

Figure S1_BLAST hints for three green algae 18-5.8-28S rRNA

BLAST hint for *Haematococcus pluvialis* 18-5.8-28S rRNA sequence



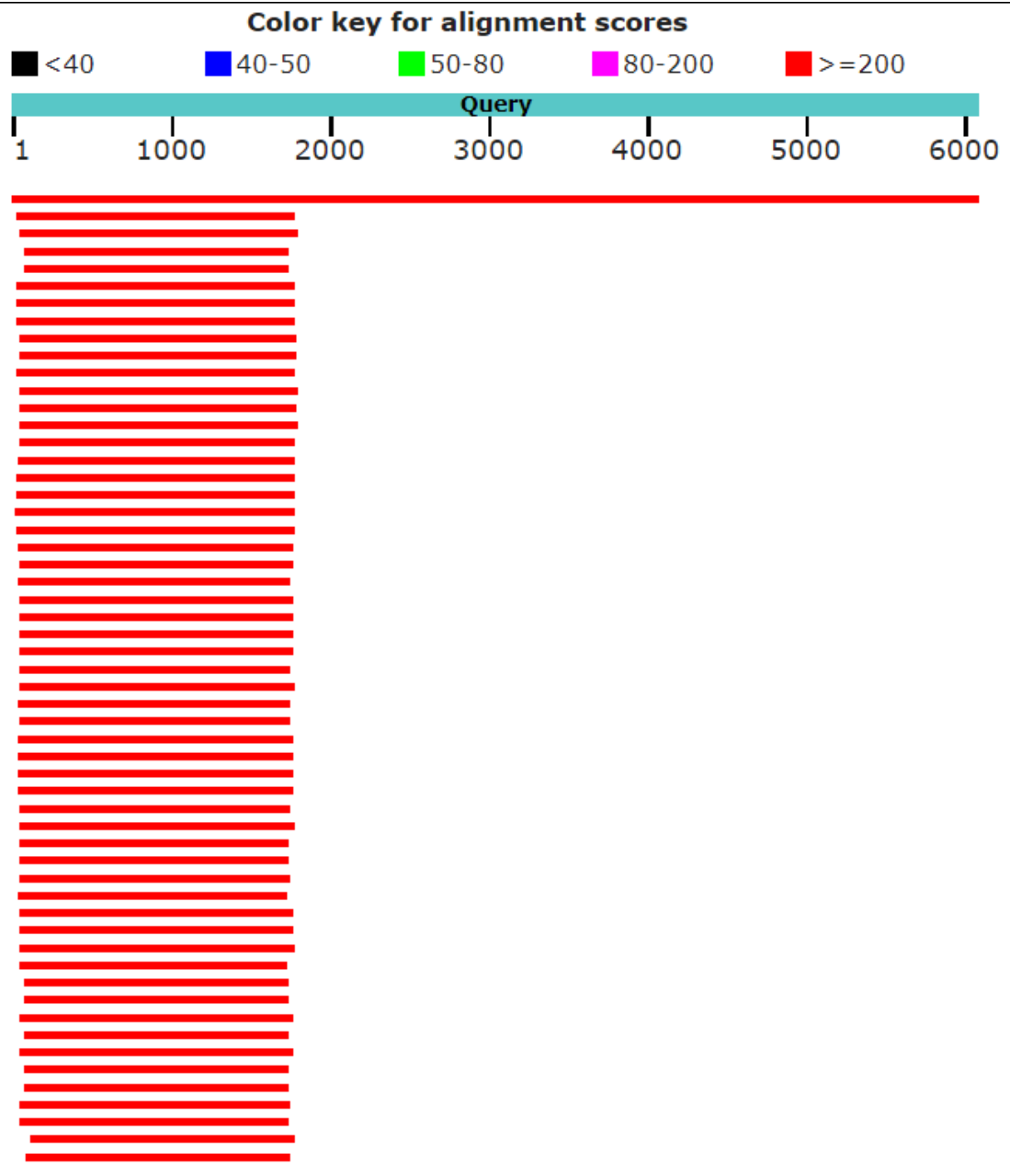
Sequence alignment result for *Haematococcus pluvialis* 18-5.8-28S rRNA sequence

Haematococcus pluvialis strain KMMCC 1354 18S ribosomal RNA gene, partial sequence
 Sequence ID: [JQ315539.1](#) Length: 2040 Number of Matches: 1

Range 1: 1 to 2040 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
3738 bits(2024)	0.0	2036/2041(99%)	3/2041(0%)	Plus/Plus
Query 142	ACCG-TAGTAATTCTAGAGCTAATACGTGCG-TATATCCC	ACTTCTGGAAGGGACGTAT	199	
Sbjct 1	ACCGCTAGT-ATTCTAGAGCTAATACGTGCGCTATATCCC	ACTTCTGGAAGGGACGTAT	59	
Query 200	TTATTAGATAAAAAGGCCAGCCGGGCTTGCCCGACCTATGGCGAATCATGATAACTTCACG	259		
Sbjct 60	TTATTAGATAAAAAGGCCAGCCGGGCTTGCCCGACCTATGGCGAATCATGATAACTTCACG	119		
Query 260	AATCGCACGGCCTTGCGCCGGCGATGTTTCATTCAAATTTCTGCCTATCAACTTTCGAT	319		
Sbjct 120	AATCGCACGGCCTTGCGCCGGCGATGTTTCATTCAAATTTCTGCCTATCAACTTTCGAT	179		
Query 320	GGTAGGATAGAGGCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGG	379		
Sbjct 180	GGTAGGATAGAGGCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGG	239		
Query 380	AGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCC	439		
Sbjct 240	AGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCC	299		
Query 440	AATCCCGACACGGGGAGGTAGTGACAATAAATAACAATACCGGGCATCAATGTCTGGTAA	499		
Sbjct 300	AATCCCGACACGGGGAGGTAGTGACAATAAATAACAATACCGGGCATCAATGTCTGGTAA	359		
Query 500	TTGGAATGAGAACAATTTAAATCCCTTAAACGAGTATCCATTGGAGGGCAAGTCTGGTGCC	559		
Sbjct 360	TTGGAATGAGAACAATTTAAATCCCTTAAACGAGTATCCATTGGAGGGCAAGTCTGGTGCC	419		
Query 560	AGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCT	619		
Sbjct 420	AGCAGCCGCGGTAATTCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCT	479		
Query 620	CGTAGTTGGATTTTCGGGTGGGTTCCAGCGGTCTGCCTCTGGTATGTA	679		
Sbjct 480	CGTAGTTGGATTTTCGGGTGGGTTCCAGCGGTCTGCCTCTGGTATGTA	539		
Query 680	CCTTTCTGCCGGGACGTGTTCTGGGCTTCATTGTCCGGGACTCGAATTCGGCGAGGAT	739		
Sbjct 540	CCTTTCTGCCGGGACGTGTTCTGGGCTTCATTGTCCGGGACTCGAATTCGGCGAGGAT	599		
Query 740	ACTTTGAGTAAAACAGCGTGTTCAAAGCAAGCCTACGCTCTGAATGCATTAGCATGGAAT	799		
Sbjct 600	ACTTTGAGTAAAACAGCGTGTTCAAAGCAAGCCTACGCTCTGAATGCATTAGCATGGAAT	659		
Query 800	ATCACGATAGGACTCTGGCCTATCTTGTGGTCTGTAGGACCGGAGTAATGATTAAGAGG	859		
Sbjct 660	ATCACGATAGGACTCTGGCCTATCTTGTGGTCTGTAGGACCGGAGTAATGATTAAGAGG	719		
Query 860	GACAGTCGGGGGCATTTCGATATTTTCATTGTCAGAGGTGAAATTC	919		
Sbjct 720	GACAGTCGGGGGCATTTCGATATTTTCATTGTCAGAGGTGAAATTC	779		

BLAST hint for *Aegagropila linnaei* 18-5.8-28S rRNA sequence



Sequence alignment result for *Aegagropila linnaei* 18-5.8-28S rRNA sequence

Aegagropila linnaei gene for 18S ribosomal RNA, partial sequence, Lake Akan

Sequence ID: [AB062698.1](#) Length: 1738 Number of Matches: 1

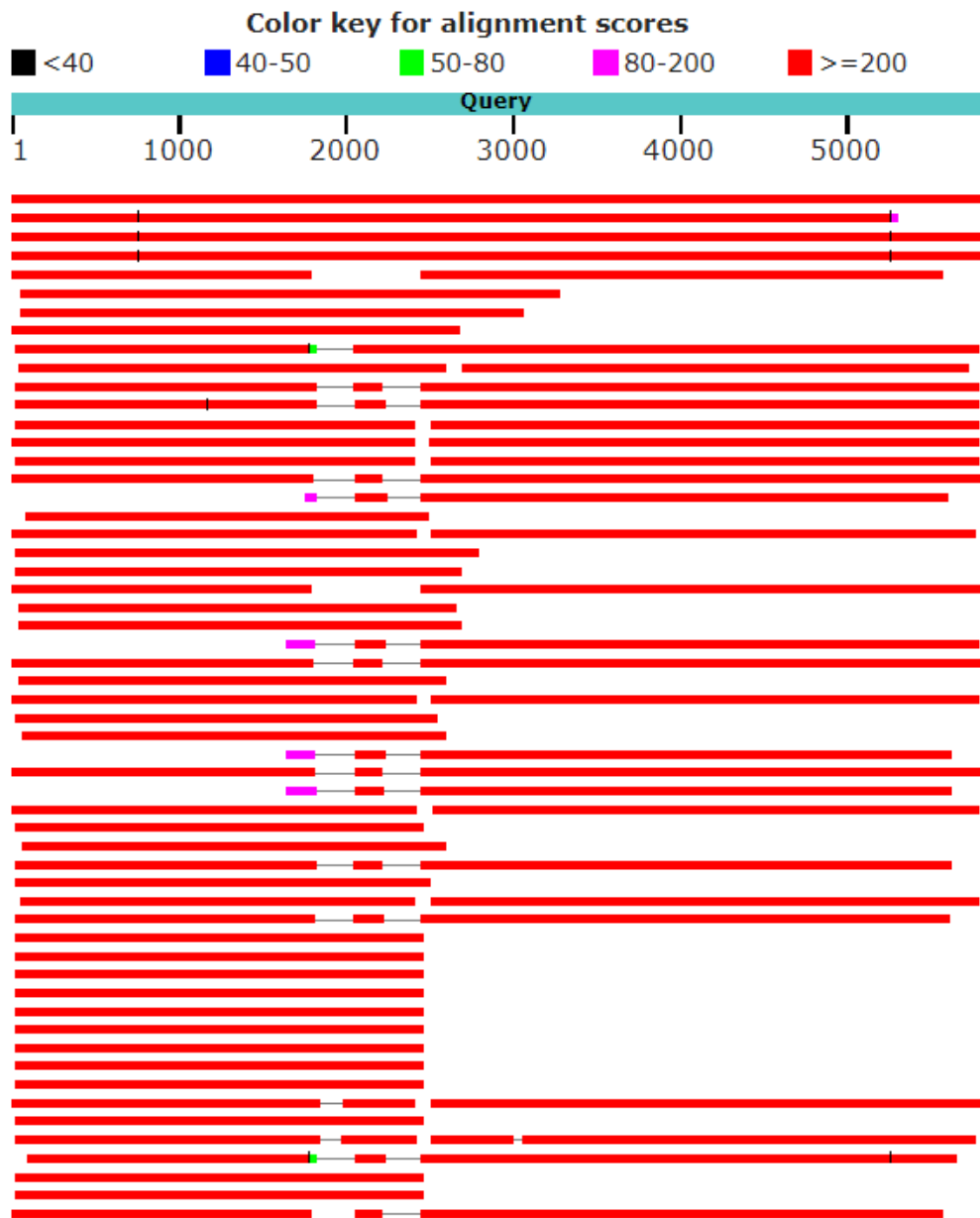
▶ [See 3 more title\(s\)](#)

Range 1: 1 to 1738 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
3205 bits(1735)	0.0	1738/1739(99%)	1/1739(0%)	Plus/Plus
Query 20	TCGTGATGCTTGTCTCAAAGATTAAGCCATGCATGTGTAGGTATAACCGATTATACCG			79
Sbjct 1	TCGTGATGCTTGTCTCAAAGATTAAGCCATGCATGTGTAGGTATAACCGATTATACCG			60
Query 80	GAAAAC TGCGAATGGCTCGGTAATCAGTTATAGTTTATTTGATAGTGCTCACTACTCGG			139
Sbjct 61	GAAAAC TGCGAATGGCTCGGTAATCAGTTATAGTTTATTTGATAGTGCTCACTACTCGG			120
Query 140	ATAACCGTAGTAACGCTAGAGCTAATACGTGCGTAAATCCCGACTCTAGGAAGGGACGTA			199
Sbjct 121	ATAACCGTAGTAACGCTAGAGCTAATACGTGCGTAAATCCCGACTCTAGGAAGGGACGTA			180
Query 200	TTTATTAGATAAAAAGGCCGACCGGTTTCCCGATCTGCGCTGAATCATGGTAACTTCACG			259
Sbjct 181	TTTATTAGATAAAAAGGCCGACCGGTTTCCCGATCTGCGCTGAATCATGGTAACTTCACG			240
Query 260	GATTGCATGGCCTTCGTGCCAGCGACGTGTCATTCAAGTTTCTGCCCCATCATGGTTTCG			319
Sbjct 241	GATTGCATGGCCTTCGTGCCAGCGACGTGTCATTCAAGTTTCTGCCCCATCATGGTTTCG			300
Query 320	ACTGTAATGTATTGGATTACAGTGCCGATAACGGGTAGCGGAGGATTAGGGTTCGATTCC			379
Sbjct 301	ACTGTAATGTATTGGATTACAGTGCCGATAACGGGTAGCGGAGGATTAGGGTTCGATTCC			360
Query 380	GGAGAGGGCGCCTGAGAAATGGCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAAATTAC			439
Sbjct 361	GGAGAGGGCGCCTGAGAAATGGCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAAATTAC			420
Query 440	CCAATCCCAACTCAGGGAGGTAGTGACAAGAAATAACAATGCGGAGCCATAGGTTCTGCA			499
Sbjct 421	CCAATCCCAACTCAGGGAGGTAGTGACAAGAAATAACAATGCGGAGCCATAGGTTCTGCA			480
Query 500	ATTGGAATGAGTACAATTTAAACCACTTAACGAGTACCTATTGGAGGGCAAGTCTGGTGC			559
Sbjct 481	ATTGGAATGAGTACAATTTAAACCACTTAACGAGTACCTATTGGAGGGCAAGTCTGGTGC			540
Query 560	CAGCAGCCGCGGTAATCCAGTCCAATAGCGTATATGTAAGTTGTTGCGATTAAAAAGC			619
Sbjct 541	CAGCAGCCGCGGTAATCCAGTCCAATAGCGTATATGTAAGTTGTTGCGATTAAAAAGC			600
Query 620	CCGTAGCTGAACCTCGGGCAGCCCGACGGTCCCGCCTTACGGTGAGTACTGTCCTGGGCT			679
Sbjct 601	CCGTAGCTGAACCTCGGGCAGCCCGACGGTCCCGCCTTACGGTGAGTACTGTCCTGGGCT			660

BLAST hint for *Chlorella ellipsoidea* 18-5.8-28S rRNA sequence



Sequence alignment result for *Chlorella ellipsoidea* 18-5.8-28S rRNA sequence

Chlorella sorokiniana 18S rRNA gene, strain Prag A14

Sequence ID: [X74001.1](#) Length: 1797 Number of Matches: 1

Range 1: 2 to 1796 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
3299 bits(1786)	0.0	1792/1795(99%)	0/1795(0%)	Plus/Plus
Query 1	ACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTA			60
Sbjct 2	ACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTA			61
Query 61	AGTATAAACTGCTTTATACTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTAT			120
Sbjct 62	AGTATAAACTGCTTTATACTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTAT			121
Query 121	TTGATGGTACCTACTACTCGGATACCCGTAAGTAAATCTAGAGCTAATACGTGCGTAAATC			180
Sbjct 122	TTGATGGTACCTACTACTCGGATACCCGTAAGTAAATCTAGAGCTAATACGTGCGTAAATC			181
Query 181	CCGACTTCTGGAAGGGACGTATTTATTAGATAAAAAGGCCGACCGGGCTCTGCCCGACTCG			240
Sbjct 182	CCGACTTCTGGAAGGGACGTATTTATTAGATAAAAAGGCCGACCGGGCTCTGCCCGACTCG			241
Query 241	CGGTGAATCATGATAAATTACGAATCGCATGGCCTCGTGCCGGCGATGTTTCATTCAAAA			300
Sbjct 242	CGGTGAATCATGATAAATTACGAATCGCATGGCCTCGTGCCGGCGATGTTTCATTCAAAA			301
Query 301	TTTCTGCCCTATCAACTTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGAC			360
Sbjct 302	TTTCTGCCCTATCAACTTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGAC			361
Query 361	GGAGGATTAGGGTTCGATTCGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA			420
Sbjct 362	GGAGGATTAGGGTTCGATTCGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA			421
Query 421	GGCAGCAGGCGCGCAAATTACCCAATCCTGACACAGGGAGGTAGTGACAATAAATAACAA			480
Sbjct 422	GGCAGCAGGCGCGCAAATTACCCAATCCTGACACAGGGAGGTAGTGACAATAAATAACAA			481
Query 481	TACTGGGCCTTTTTCAGGTCTGGTAATTGGAATGAGTACAATCTAAACCCCTTAACGAGGA			540
Sbjct 482	TACTGGGCCTTTTTCAGGTCTGGTAATTGGAATGAGTACAATCTAAACCCCTTAACGAGGA			541
Query 541	TCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATCCAGCTCCAATAGCGTATA			600
Sbjct 542	TCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATCCAGCTCCAATAGCGTATA			601
Query 601	TTTAAGTTGCTGCAGTTAAAAAGCTCGTAGTTGGATTTTCGGGTGGGGCCTGCCGGTCCGC			660
Sbjct 602	TTTAAGTTGCTGCAGTTAAAAAGCTCGTAGTTGGATTTTCGGGTGGGGCCTGCCGGTCCGC			661
Query 661	CGTTTCGGTGTGCACTGGCAGGGCCACCTTGTTCGGGGGACGGGCTCCTGGGCTTCAC			720
Sbjct 662	CGTTTCGGTGTGCACTGGCAGGGCCACCTTGTTCGGGGGACGGGCTCCTGGGCTTCAC			721