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BLASTN 2.8.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Sch&auml;ffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped
BLAST and PSI-BLAST: a new generation of protein database search programs",
Nucleic Acids Res. 25:3389-3402.

RID: XDBVH8TH014


Database: nr
Query= CE-1_Alg-SR1_A04_01
Length=1121

                                                                  Score     E
Sequences producing significant alignments:                       (Bits)  Value

gi|749444531|gb|KJ635658.1|  Oophila sp. LA2008 18S ribosomal ...   1852    0E00
gi|563323151|gb|KF791553.1|  Chlorococcum sp. JB19 small subun...   1838    0E00
gi|1857164|gb|U70586.1|CEU70586  Chlorococcum ellipsoideum 18S...   1812    0E00
gi|1027363285|gb|KU521558.1|  Chlorococcum sp. 51.3 18S riboso...   1811    0E00
gi|928192344|dbj|AB983622.1|  Chlorococcum aquaticum gene for ...   1803    0E00
gi|669688692|gb|KM020099.1|  Chlorococcum minutum strain SAG 2...   1803    0E00
gi|429535705|dbj|AB713407.1|  Chlorococcum sp. J7 gene for 18S...   1803    0E00
gi|29469378|gb|AY220600.1|  Chlamydomonad sp. Tow8/18T-6w 18S ...   1802    0E00
gi|29469377|gb|AY220599.1|  Chlamydomonad sp. Pic6/3P-1w 18S r...   1802    0E00
gi|29423437|gb|AY220092.1|  Chlamydomonad sp. Pic 9/21 P-2w 18...   1798    0E00
gi|944383245|gb|KR607490.1|  Chlorococcum minutum strain SAG 2...   1797    0E00
gi|226235461|dbj|AB490288.1|  Chlorococcum sp. YF382 gene for ...   1793    0E00
gi|226235460|dbj|AB490287.1|  Chlorococcum sp. YF282 gene for ...   1792    0E00
gi|29423439|gb|AY220094.1|  Chlamydomonad sp. WTwin 8/18 P-1d ...   1792    0E00
gi|1003701883|gb|KT781103.1|  Chlorococcum sp. KQ-2016 18S rib...   1784    0E00
gi|844175872|gb|KP726222.1|  Chlorococcum sp. KLL-G015 clone c...   1783    0E00
gi|1297465723|gb|KY091671.1|  Oophila amblystomatis isolate Ki...   1779    0E00
gi|480359416|gb|KC492081.1|  Chlamydomonadaceae sp. A10 18S ri...   1775    0E00
gi|1101280142|gb|KU361142.1|  Chlamydomonas sp. SA-2016 18S ri...   1772    0E00
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gi|844175901|gb|KP726223.1|  Chlorococcum sp. KLL-G015 clone b...   1769    0E00
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gi|1371548643|gb|MG784550.1|  Chlorococcum sp. K2/5 18S riboso...   1767    0E00
gi|557844142|gb|KF144186.1|  Chlorococcum sp. GRK7-WB4 18S rib...   1767    0E00
gi|557844141|gb|KF144185.1|  Chlorococcum sp. GRK6-DB6 18S rib...   1767    0E00
gi|226235459|dbj|AB490286.1|  Chlorococcum sp. RK261 gene for ...   1767    0E00
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gi|557844143|gb|KF144187.1|  Chlorococcum sp. GRK7-WB5 18S rib...   1758    0E00
gi|480359414|gb|KC492079.1|  Chlorococcum sp. A5 18S ribosomal...   1747    0E00
gi|557844140|gb|KF144184.1|  Chlorococcum sp. GRK6-DB5 18S rib...   1743    0E00
gi|83316205|gb|DQ303098.1|  Chlorococcum sp. KNU-F-2002-C1 18S...   1735    0E00
gi|1440109552|gb|MH703751.1|  Chlorococcum oleofaciens strain ...   1732    0E00
gi|1392939113|dbj|AB936290.1|  Chlorococcum tatrense gene for ...   1732    0E00
gi|1276739976|gb|MG491516.1|  Chlorococcum oleofaciens strain ...   1732    0E00
gi|1276739974|gb|MG491514.1|  Chlorococcum citriforme strain A...   1732    0E00
gi|1276739971|gb|MG491511.1|  Neospongiococcum gelatinosum str...   1732    0E00
gi|1190062224|dbj|AB936286.1|  Chlorococcum elkhartiense gene ...   1732    0E00
gi|928192330|dbj|AB983608.1|  Chlorococcum oleofaciens gene fo...   1732    0E00
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gi|669688693|gb|KM020100.1|  Chlorococcum citriforme strain SA...   1732    0E00
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gi|509379|emb|Z28972.1|  P.insigne mRNA for nuclear encoded sm...   1732    0E00
gi|960515937|gb|KT279470.1|  Tetracystis sp. YACCYB50 18S ribo...   1731    0E00
gi|749444532|gb|KJ635659.1|  Oophila sp. KY2008 18S ribosomal ...   1727    0E00
gi|928192346|dbj|AB983624.1|  Macrochloris rubrioleum gene for...   1727    0E00
gi|928192338|dbj|AB983616.1|  Chlorococcum microstigmatum gene...   1727    0E00
gi|669688694|gb|KM020101.1|  Chlorococcum oleofaciens strain S...   1727    0E00
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gi|669688616|gb|KM020023.1|  Chlorococcum sp. SAG 2467 18S rib...   1727    0E00
gi|557844139|gb|KF144183.1|  Chlorococcum cf. sphacosum SAG 23...   1727    0E00
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gi|359385180|emb|FR865591.1|  Chlorococcum sp. CCAP 11/52 geno...   1727    0E00
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gi|1276739973|gb|MG491513.1|  Chlorococcum sphacosum strain AC...   1724    0E00
gi|32344960|gb|AY122332.1|  Chlorococcum robustum clone Kr_86_...   1724    0E00
gi|1145763|gb|U41176.1|COU41176  Chlorococcum oleofaciens 18S ...   1724    0E00
gi|1276718679|gb|MG491216.1|  Chlorococcum oleofaciens strain ...   1723    0E00
gi|1280145636|gb|MG582207.1|  Chlorococcum sphacosum strain AC...   1723    0E00
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gi|669688617|gb|KM020024.1|  Tetracystis tetraspora strain SAG...   1721    0E00
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gi|749444530|gb|KJ635657.1|  Oophila sp. CT2007 18S ribosomal ...   1719    0E00
gi|928192345|dbj|AB983623.1|  Chlorococcum nivale gene for 18S...   1719    0E00
gi|510020203|emb|HE860252.1|  Chlorochytrium lemnae partial 18...   1719    0E00
gi|510020202|emb|HE860251.1|  Chlorochytrium lemnae partial 18...   1719    0E00
gi|33325057|gb|AF514408.1|  Macrochloris sp. 105-99 strain CCC...   1718    0E00
gi|944383239|gb|KR607484.1|  Chloromonas perforata strain SAG ...   1717    0E00
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gi|442572058|gb|JQ315635.1|  Chlamydomonadaceae sp. KMMCC 249 ...   1716    0E00
gi|242347799|gb|GQ122379.1|  Chlamydomonadaceae sp. KMMCC FC-9...   1712    0E00
gi|389621737|gb|JN880460.1|  Protosiphon botryoides isolate UT...   1710    0E00
gi|389621736|gb|JN880459.1|  Protosiphon botryoides isolate FR...   1710    0E00
gi|389621735|gb|JN880458.1|  Protosiphon botryoides isolate UT...   1710    0E00
gi|389621734|gb|JN880457.1|  Protosiphon botryoides f. parieti...   1710    0E00
gi|166084192|gb|EF024715.1|  Uncultured Haematococcaceae clone...   1710    0E00
gi|1276739970|gb|MG491510.1|  Chlorococcum isabeliense strain ...   1705    0E00
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gi|1857184|gb|U70794.1|CPU70794  Chloromonas perforata strain ...   1701    0E00
gi|1276739972|gb|MG491512.1|  Chlorococcum diplobionticum stra...   1700    0E00
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gi|13469692|dbj|AB049415.1|  Chlorosarcinopsis minor gene for ...   1697    0E00
gi|669688772|gb|KM020179.1|  Rhopalosolen saccatus strain SAG ...   1696    0E00
gi|563323137|gb|KF791539.1|  Chlorococcum sp. JB1 small subuni...   1696    0E00
gi|166083647|gb|EF024170.1|  Uncultured eukaryote clone Elev_1...   1696    0E00
gi|1341122453|gb|MG022715.1|  Chlamydopodium starrii isolate C...   1696    0E00
gi|1341122452|gb|MG022714.1|  Chlamydopodium starrii isolate C...   1696    0E00
gi|960515919|gb|KT279452.1|  Tetracystis sp. YACCYB32 18S ribo...   1696    0E00
gi|928192347|dbj|AB983625.1|  Chlamydopodium starrii gene for ...   1696    0E00
gi|1276718680|gb|MG491217.1|  Chlorococcum oleofaciens strain ...   1693    0E00
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ALIGNMENTS
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          Length=1741

 Score = 1851.5 bits (2052),  Expect = 0E00
 Identities = 1085/1110 (97%), Gaps = 14/1110 (1%)
 Strand = Plus/Plus

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Sbjct  13    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  72
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Sbjct  73    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  132

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
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Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
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Sbjct  553   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  612

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
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Sbjct  613   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  672

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
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Sbjct  793   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  851

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Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
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Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
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Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
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 Score = 1838.0 bits (2037),  Expect = 0E00
 Identities = 1082/1110 (97%), Gaps = 14/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
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Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
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Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  142

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
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Sbjct  143   GCTAATACATGCGTAAATCCCGACTTCTGGGAGGGACGTATTTATTAGATAAAAGGCCAG  202

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Sbjct  203   CCGAGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  262

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Sbjct  323   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  382

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
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Sbjct  383   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  442

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Sbjct  503   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  562

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Sbjct  683   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  742
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Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
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Sbjct  743   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  802

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
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Sbjct  803   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  861

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
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Sbjct  862   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  921

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Sbjct  922   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  981

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
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Sbjct  982   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1039

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1040  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1098

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1100  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1128


>gb|U70586.1|CEU70586 Chlorococcum ellipsoideum 18S nuclear ribosomal RNA gene, partial sequence
          Length=1702

 Score = 1811.9 bits (2008),  Expect = 0E00
 Identities = 1077/1110 (97%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  123

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  183

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  184   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  243

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  303

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  363

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  423
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Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  424   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  483

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  484   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  543

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  544   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  603

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  604   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  663

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  664   GCTCCTGGGCTTCACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  723

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  724   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  783

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  784   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  842

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  843   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  902

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  903   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  962

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  963   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1020

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1021  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1079

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1081  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1109


>gb|KU521558.1| Chlorococcum sp. 51.3 18S ribosomal RNA gene, partial sequence
          Length=1697

 Score = 1811.0 bits (2007),  Expect = 0E00
 Identities = 1082/1115 (97%), Gaps = 19/1115 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  60

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  120
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Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  180

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  181    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  240

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  300

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  360

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  420

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  480

Query  485    AATATCTTAACGAGTATCCATT-GGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
              |||||||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Sbjct  481    AATATCTTAACGAGTATCCATTGGGAGGGCAAGTCTGGTTCCAGCAGCCGCGGTAATTCC  540

Query  544    AGCTCCAATAGCGTATATTTAAGTTGTTG-CAGTTAAAAAGC-TCGTAGTTGGATTTCGG  601
              ||||||||||| ||||||||||||||||| |||||||||||| |||||||||||||||||
Sbjct  541    AGCTCCAATAGGGTATATTTAAGTTGTTGCCAGTTAAAAAGCTTCGTAGTTGGATTTCGG  600

Query  602    GTGTGTCGACGCGGTCTGCC-TCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGG  660
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  601    GTGTGTCGACGCGGTCTGCCTTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGG  660

Query  661    ACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACA  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661    ACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACA  720

Query  721    AGAGTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACT  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721    AGAGTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACT  780

Query  781    CTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781    CTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA  840

Query  841    TTTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-A  899
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  841    -TTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAA  899

Query  900    AGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATT  958
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  900    AGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATT  959

Query  959    AGATACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCAT  1016
              |||||||||||||| | |||| |||||||||||||||||||||||||||| |||||||||
Sbjct  960    AGATACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCAT  1018

Query  1017   TGATTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC---GGGGGA-TAW  1070
              ||| |||||||||||||| ||||||||||  |||||||||| |||||   |||||| || 
Sbjct  1019   TGA-TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGGAGTAT  1077
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Query  1071  TGCCGCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
              | |||||||||   |||||| ||| || ||||||
Sbjct  1078  GGTCGCAAGGCTGAAACTTAAAGGAATT-GACGGA  1111


>dbj|AB983622.1| Chlorococcum aquaticum gene for 18S rRNA, partial sequence, strain: UTEX2222
          Length=1745

 Score = 1802.8 bits (1998),  Expect = 0E00
 Identities = 1075/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||| |||||||||||||||||||||||||||||||| ||||| |||||
Sbjct  201   CCGGGCTTGCCCGACTTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  621   AGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGG  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800
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Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126


>gb|KM020099.1| Chlorococcum minutum strain SAG 213-7 18S ribosomal RNA gene, partial sequence
          Length=1771

 Score = 1802.8 bits (1998),  Expect = 0E00
 Identities = 1075/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  142

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  143   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  202

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||||
Sbjct  203   CCGGGCTTGCCCGACTTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  262

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  322

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  382

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  383   GCTTCCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  442

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  443   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGCACAATGTA  502
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Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  503   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  562

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  563   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  622

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  623   AGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGG  682

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  683   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  742

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  743   TGTTCAAAGCAAGCCAACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  802

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  803   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  861

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  862   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  921

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  922   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  981

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  982   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1039

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1040  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1098

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1100  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1128


>dbj|AB713407.1| Chlorococcum sp. J7 gene for 18S rRNA, partial sequence
          Length=1732

 Score = 1802.8 bits (1998),  Expect = 0E00
 Identities = 1075/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  85

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  86    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  144

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  145   GCTAATACATGCGCAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  204
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Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  205   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  264

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  324

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  384

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  444

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  445   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGCACAATGTA  504

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  564

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  624

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  625   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  684

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  685   GCTCCTGGGCTTGACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  744

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  804

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  805   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  863

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  864   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  923

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  924   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  983

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||| ||||
Sbjct  984   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCTTTGA-  1041

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1042  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1100

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1102  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1130
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>gb|AY220600.1| Chlamydomonad sp. Tow8/18T-6w 18S ribosomal RNA gene, partial sequence
 gi|29469379|gb|AY220601.1| Chlamydomonad sp. Tow2/24P-4w 18S ribosomal RNA gene, partial
sequence
          Length=1689

 Score = 1802.0 bits (1997),  Expect = 0E00
 Identities = 1071/1103 (97%), Gaps = 15/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATA  120

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  180

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             ||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Sbjct  181   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGCGCCGGCGATG  240

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  300

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  360

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  420

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  421   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  480

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  540

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  541   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGCGTCGAC  600

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  660

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  720

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  780

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
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             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  781   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  839

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  840   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  899

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  900   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  959

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  960   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1017

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1018  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1077

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1078  GAAACTTAAAGGAATT-GACGGA  1099


>gb|AY220599.1| Chlamydomonad sp. Pic6/3P-1w 18S ribosomal RNA gene, partial sequence
          Length=1689

 Score = 1802.0 bits (1997),  Expect = 0E00
 Identities = 1071/1103 (97%), Gaps = 15/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATA  120

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  180

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             ||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Sbjct  181   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGCGCCGGCGATG  240

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  300

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  360

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  420

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  421   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  480

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  540

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  541   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGCGTCGAC  600

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  660

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  720

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  780

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  781   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  839

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  840   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  899

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  900   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  959

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  960   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1017

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1018  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1077

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1078  GAAACTTAAAGGAATT-GACGGA  1099


>gb|AY220092.1| Chlamydomonad sp. Pic 9/21 P-2w 18S ribosomal RNA gene, partial sequence
          Length=1790

 Score = 1798.3 bits (1993),  Expect = 0E00
 Identities = 1074/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  43    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  102

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Sbjct  103   AAATCAGTTATAGTTTATTTGATGGTACTTCCTACTTGG-ATAACCGTAGGAAATCTAGA  161

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  162   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  221

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
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             ||||||||||||||||||||||||||||||||||||  |||||||||| |||||||||||
Sbjct  222   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAACGAATCGCATGGCCTTGTGCC  281

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  341

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  401

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  402   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  461

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  462   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  521

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  522   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  581

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  582   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  641

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  642   GGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTCCACCTTTCTGCTGGGGACGG  701

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  702   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  761

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  762   TGTTCAAAGCAAGCCAACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  821

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  822   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  880

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  881   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  940

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  941   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  1000

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  1001  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1058

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1059  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1117

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1119  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1147
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>gb|KR607490.1| Chlorococcum minutum strain SAG 213-7 small subunit ribosomal RNA gene, partial
sequence
          Length=1717

 Score = 1797.4 bits (1992),  Expect = 0E00
 Identities = 1070/1103 (97%), Gaps = 15/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATA  120

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  180

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             |||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  181   TGCCCGACTTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCCGGCGATG  240

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  300

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  360

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  420

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  421   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGCACAATGTAAATATCT  480

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  540

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  541   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGAGTCGAC  600

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  601   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGGGCTCCTG  660

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  720

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AGCAAGCCAACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  780

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  781   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  839
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Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  840   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  899

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  900   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  959

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  960   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1017

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1018  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1077

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1078  GAAACTTAAAGGAATT-GACGGA  1099


>dbj|AB490288.1| Chlorococcum sp. YF382 gene for 18S rRNA, partial sequence
          Length=1738

 Score = 1792.9 bits (1987),  Expect = 0E00
 Identities = 1074/1111 (96%), Gaps = 16/1111 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  123

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  183

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGC  243
             ||||||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||
Sbjct  184   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGC  243

Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  424   TAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  483

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
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Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             | |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  604   GGGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACG  663

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  724   GTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  842

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  843   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  902

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  962

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||| ||||||||
Sbjct  963   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA  1021

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1022  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1080

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1081  GCAAGGCTGANACTTAAAGGAATT-GACGGA  1110


>dbj|AB490287.1| Chlorococcum sp. YF282 gene for 18S rRNA, partial sequence
          Length=1779

 Score = 1792.0 bits (1986),  Expect = 0E00
 Identities = 1074/1111 (96%), Gaps = 16/1111 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  33    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  92

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  93    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  151

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  152   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  211

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGC  243
             ||||||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||
Sbjct  212   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGC  271
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Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  272   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  331

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  332   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  391

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  392   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  451

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  452   TAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  511

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  512   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  571

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  572   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  631

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             | |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  632   GGGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACG  691

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  692   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  751

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  752   GTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  811

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  812   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  870

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  871   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  930

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  931   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  990

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||| ||||||||
Sbjct  991   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA  1049

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1050  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1108

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1109  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1138


>gb|AY220094.1| Chlamydomonad sp. WTwin 8/18 P-1d 18S ribosomal RNA gene, partial sequence
          Length=1791
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 Score = 1792.0 bits (1986),  Expect = 0E00
 Identities = 1074/1111 (96%), Gaps = 16/1111 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  43    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  102

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  103   AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  161

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  162   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  221

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGC  243
             ||||||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||
Sbjct  222   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGC  281

Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  341

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  401

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  402   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  461

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  462   TAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  521

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  522   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  581

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  582   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  641

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             | |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  642   GGGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACG  701

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  702   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  761

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  762   GTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  821

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  822   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  880

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  881   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  940
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Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  941   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  1000

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||| ||||||||
Sbjct  1001  TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA  1059

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1060  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1118

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1119  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1148


>gb|KT781103.1| Chlorococcum sp. KQ-2016 18S ribosomal RNA gene, partial sequence
          Length=1689

 Score = 1783.9 bits (1977),  Expect = 0E00
 Identities = 1067/1103 (96%), Gaps = 15/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATA  120

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  180

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             |||||||| |||||||||||||||||||||||||||||||| ||||| ||||||||||||
Sbjct  181   TGCCCGACTTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCCGGCGATG  240

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  241   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGGTAGAGGCCTACCATGGTGG  300

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  360

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  420

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  421   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  480

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  481   TAACGAGTATCCATTGGAGGGCAAGCCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  540

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  541   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGAGTCGAC  600
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Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  601   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGGGCTCCTG  660

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  720

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  780

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  781   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  839

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  840   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  899

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  900   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  959

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  960   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1017

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1018  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1077

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1078  GAAACTTAAAGGAATT-GACGGA  1099


>gb|KP726222.1| Chlorococcum sp. KLL-G015 clone c 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
          Length=2466

 Score = 1783.0 bits (1976),  Expect = 0E00
 Identities = 1072/1111 (96%), Gaps = 16/1111 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4     ATTAAGCCGTGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  63

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  64    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  122

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  182

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGC  243
             ||||||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||
Sbjct  183   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGC  242

Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  243   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  302

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  362

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  422

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  423   TAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  482

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  542

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  543   AGCTCCAATAGCGTATATTTAAGTTGTTGCGGTTAAAAAGCTCGTAGTTGGATTTCGGGT  602

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             | |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  603   GGGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACG  662

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  663   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  722

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  723   GTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  782

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  783   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  841

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  842   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  901

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  902   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  961

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||| ||||||||
Sbjct  962   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA  1020

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1021  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1079

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1080  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1109


>gb|KY091671.1| Oophila amblystomatis isolate Kingston 18S ribosomal RNA gene, partial sequence
          Length=1689

 Score = 1778.5 bits (1971),  Expect = 0E00
 Identities = 1066/1102 (96%), Gaps = 16/1102 (1%)
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 Strand = Plus/Plus

Query  14    TGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTT  73
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTT  60

Query  74    ATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATACA  133
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  61    ATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATACA  119

Query  134   TGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTG  193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   TGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTG  179

Query  194   CCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGCCGGCGATGT  252
             |||||||||||||||||||||||||||  | ||||||||| |||||||||||||||||||
Sbjct  180   CCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGCCGGCGATGT  239

Query  253   TTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGT  312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGT  299

Query  313   AACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCAC  372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   AACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCAC  359

Query  373   ATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAA  432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   ATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAA  419

Query  433   TAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCTT  492
             |||||||||||||||||| |||| ||||||||||||||||||| ||||||||||||||||
Sbjct  420   TAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCTT  479

Query  493   AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAAT  552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAAT  539

Query  553   AGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGACG  612
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  540   AGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGGGTCGACG  599

Query  613   CGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGG  672
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  600   CGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGGGCTCCTGG  659

Query  673   GCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAA  732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  660   GCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAA  719

Query  733   GCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTT  792
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   GCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTT  779

Query  793   GTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTCA  852
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  780   GTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTCA  838

Query  853   TTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCAA  911
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  839   TTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCAA  898

Query  912   GGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCGT  970
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Sbjct  899   GGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCGT  958

Query  971   AGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCTG  1028
             || | |||| |||||||||||||||||||||||||||| ||| |||||||| ||||||||
Sbjct  959   AGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA-TGACCCTG  1016

Query  1029  CCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT-  1082
             |||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1017  CCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTG  1076

Query  1083  TGACTTAAGGGAGTTGGACGGA  1103
               |||||| ||| || ||||||
Sbjct  1077  AAACTTAAAGGAATT-GACGGA  1097


>gb|KC492081.1| Chlamydomonadaceae sp. A10 18S ribosomal RNA gene, partial sequence
          Length=1784

 Score = 1774.9 bits (1967),  Expect = 0E00
 Identities = 1070/1110 (96%), Gaps = 19/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  43    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  102

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Sbjct  103   AAATCAGTTATAGTTTATTTGATGGTACTTCCTACTTGG-ATAACCGTAGGAAATCTAGA  161

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  162   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  221

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||||||||||||||||||||||  |||||||||| |||||||||||
Sbjct  222   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAACGAATCGCATGGCCTTGTGCC  281

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  341

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  401

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Sbjct  402   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGAC--GGGGAGGT  459

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  460   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  519

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  579

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  580   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  639

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Sbjct  640   GGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTCCACCTTTCTGCTGGGGACGG  699

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  700   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  759

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760   TGTTCAAAGCAAGCCAACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  819

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  820   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  878

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  879   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  938

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||  ||||||||||||||| ||||||||||||
Sbjct  939   TTTGCCAAGGATGTTTTCATTGATCAAGAA--AAAGTTGGGGGCTCGAAGACGATTAGAT  996

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  997   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1054

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1055  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1113

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1115  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1143


>gb|KU361142.1| Chlamydomonas sp. SA-2016 18S ribosomal RNA gene, partial sequence
          Length=1655

 Score = 1772.2 bits (1964),  Expect = 0E00
 Identities = 1056/1089 (96%), Gaps = 15/1089 (1%)
 Strand = Plus/Plus

Query  26    TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  60

Query  86    ATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCC  145
             ||||||| |||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATGGTACTTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCC  119

Query  146   GACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   GACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  179

Query  206   CGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATGTTTCATTCAAATTT  265
             ||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Sbjct  180   CGAATCATGATAACTTCACGAATCGCACGGCCTCGCGCCGGCGATGTTTCATTCAAATTT  239

Query  266   CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  299

Query  326   GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  300   GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  359

Query  386   AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  419

Query  446   TGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCTTAACGAGTATCCAT  505
             ||||| |||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  420   TGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCTTAACGAGTATCCAT  479

Query  506   TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAA  565
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAA  539

Query  566   GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGACGCGGTCTGCCTCTG  625
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  540   GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGCGTCGACGCGGTCTGCCTCTG  599

Query  626   GTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTG  685
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  600   GTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTG  659

Query  686   GGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCCACGCT  745
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  660   GGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCGACGCT  719

Query  746   CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  805
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  779

Query  806   ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTCATTGTCAGAGGTGA  865
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  780   ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTCATTGTCAGAGGTGA  838

Query  866   AATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCAAGGATGTTTTCATT  924
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  839   AATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCAAGGATGTTTTCATT  898

Query  925   GATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCGTAGKCYTCAA-CAT  982
             |||||||||||||||||||||||||| |||||||||||||||||||||| | |||| |||
Sbjct  899   GATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCGTAGTC-TCAACCAT  957

Query  983   AAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCTGCCAGCA-CTTATG  1040
             ||||||||||||||||||||||||| |||||||||||| |||||||||||||| ||||||
Sbjct  958   AAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCTGCCAGCACCTTATG  1016

Query  1041  AGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT-TGACTTAAGGGAG  1095
             ||||  |||||||||| |||||  |||||| ||  | |||||||||   |||||| |||
Sbjct  1017  AGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAA  1076

Query  1096  TTGGACGGA  1104
             || ||||||
Sbjct  1077  TT-GACGGA  1084


>gb|KU361141.1| Chlamydomonas irregularis 18S ribosomal RNA gene, partial sequence
          Length=1652

 Score = 1772.2 bits (1964),  Expect = 0E00
 Identities = 1056/1089 (96%), Gaps = 15/1089 (1%)
 Strand = Plus/Plus

Query  26    TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1      TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  60

Query  86     ATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCC  145
              ||||||| |||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  61     ATGGTACTTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCC  119

Query  146    GACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120    GACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  179

Query  206    CGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATGTTTCATTCAAATTT  265
              ||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Sbjct  180    CGAATCATGATAACTTCACGAATCGCACGGCCTCGCGCCGGCGATGTTTCATTCAAATTT  239

Query  266    CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240    CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  299

Query  326    GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300    GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  359

Query  386    AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360    AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  419

Query  446    TGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCTTAACGAGTATCCAT  505
              ||||| |||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  420    TGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCTTAACGAGTATCCAT  479

Query  506    TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAA  565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480    TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAA  539

Query  566    GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGACGCGGTCTGCCTCTG  625
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  540    GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGCGTCGACGCGGTCTGCCTCTG  599

Query  626    GTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTG  685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  600    GTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTG  659

Query  686    GGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCCACGCT  745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  660    GGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCGACGCT  719

Query  746    CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720    CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  779

Query  806    ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTCATTGTCAGAGGTGA  865
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  780    ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTCATTGTCAGAGGTGA  838

Query  866    AATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCAAGGATGTTTTCATT  924
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  839    AATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCAAGGATGTTTTCATT  898

Query  925    GATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCGTAGKCYTCAA-CAT  982
              |||||||||||||||||||||||||| |||||||||||||||||||||| | |||| |||
Sbjct  899    GATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCGTAGTC-TCAACCAT  957

Query  983    AAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCTGCCAGCA-CTTATG  1040
              ||||||||||||||||||||||||| |||||||||||| |||||||||||||| ||||||
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Sbjct  958   AAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCTGCCAGCACCTTATG  1016

Query  1041  AGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT-TGACTTAAGGGAG  1095
             ||||  |||||||||| |||||  |||||| ||  | |||||||||   |||||| |||
Sbjct  1017  AGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAA  1076

Query  1096  TTGGACGGA  1104
             || ||||||
Sbjct  1077  TT-GACGGA  1084


>gb|KP726223.1| Chlorococcum sp. KLL-G015 clone b 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
          Length=2466

 Score = 1769.5 bits (1961),  Expect = 0E00
 Identities = 1069/1111 (96%), Gaps = 16/1111 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4     ATTAAGCCGTGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  63

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  64    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  122

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   GCTAATACATGCGTAGATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  182

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGC  243
             ||||||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||
Sbjct  183   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGC  242

Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  302

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  362

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  422

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||| ||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  423   TAGTGACAATAGATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  482

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  542

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  602

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             | |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  603   GGGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACG  662
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Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  663   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  722

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||
Sbjct  723   GTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCACGGAATCACACGATAGGACTCTG  782

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  783   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  841

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  842   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  901

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  902   ATTTGCCAAGGATGCTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  961

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||| ||||||||
Sbjct  962   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA  1020

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1021  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1079

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1080  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1109


>gb|KY091670.1| Oophila amblystomatis isolate Suddent Tract 18S ribosomal RNA gene, complete
sequence
          Length=1699

 Score = 1767.7 bits (1959),  Expect = 0E00
 Identities = 1067/1108 (96%), Gaps = 17/1108 (2%)
 Strand = Plus/Plus

Query  9     AGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAAT  68
             || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AGCCNTGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAAT  60

Query  69    CAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTA  128
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  61    CAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAGCTA  119

Query  129   ATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGG  188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   ATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGG  179

Query  189   GCTTGCCCGACCTTAGGCGAATCATGATAACTTCA-CGAATCGCACGGCCTTGTGCCGGC  247
             ||||||||||||||||||||||||||||||||  | ||||||||| ||||||||||||||
Sbjct  180   GCTTGCCCGACCTTAGGCGAATCATGATAACTCAAACGAATCGCATGGCCTTGTGCCGGC  239

Query  248   GATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATG  307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   GATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATG  299

Query  308   GTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   GTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  359
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Query  368   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  419

Query  428   GACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAAT  487
             ||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||
Sbjct  420   GACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAAT  479

Query  488   ATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCT  547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   ATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCT  539

Query  548   CCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGT  607
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  540   CCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGGGT  599

Query  608   CGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCT  667
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  600   CGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGGGCT  659

Query  668   CCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGT  727
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  660   CCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGT  719

Query  728   TCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCT  787
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   TCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCT  779

Query  788   ATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTA  847
             |||||||||||||||| |||||||||||||||||||||||||||||||||||| ||||||
Sbjct  780   ATCTTGTTGGTCTGTANGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTA  838

Query  848   TTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTT  906
             ||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  839   TTTCATTGTCAGANGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTT  898

Query  907   GCCAA-GGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATAC  964
             ||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  899   GCCAAGGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATAC  958

Query  965   CGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTG  1022
             |||||||| | |||| |||||||||||||||||||||||||||| ||| |||||||| ||
Sbjct  959   CGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGCTCCATTGA-TG  1016

Query  1023  ACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCA  1077
             |||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||||
Sbjct  1017  ACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCA  1076

Query  1078  AGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||   |||||| ||| || ||||||
Sbjct  1077  AGGCTGAAACTTAAAGGAATT-GACGGA  1103


>gb|MG784552.1| Chlorococcum sp. K2/11 18S ribosomal RNA gene, partial sequence
          Length=1752

 Score = 1766.8 bits (1958),  Expect = 0E00
 Identities = 1067/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  84
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Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  85     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  143

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  203

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  204    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  263

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  323

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  383

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  443

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  444    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  503

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  563

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  564    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  623

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
               ||||||||||||||||||||||||||||||||||||||||||||||| ||||   |||
Sbjct  624    CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  683

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
               |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  684    TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  743

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  744    TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  803

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  804    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  862

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  863    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  922

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  923    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  982

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  983    ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1040
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Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1041  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1099

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1101  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1129


>gb|MG784550.1| Chlorococcum sp. K2/5 18S ribosomal RNA gene, partial sequence
          Length=1750

 Score = 1766.8 bits (1958),  Expect = 0E00
 Identities = 1067/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   ||| 
Sbjct  622   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  682   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  741
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Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|KF144186.1| Chlorococcum sp. GRK7-WB4 18S ribosomal RNA gene, partial sequence
          Length=1753

 Score = 1766.8 bits (1958),  Expect = 0E00
 Identities = 1067/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  84

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  85    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  143

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  203

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  204   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  263

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  323

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  383

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  443
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Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  444   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  503

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  563

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  564   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  623

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   |||
Sbjct  624   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  683

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  684   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  743

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  744   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  803

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  804   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  862

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  863   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  922

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  923   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  982

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  983   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1040

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1041  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1099

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1101  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1129


>gb|KF144185.1| Chlorococcum sp. GRK6-DB6 18S ribosomal RNA gene, partial sequence
          Length=1754

 Score = 1766.8 bits (1958),  Expect = 0E00
 Identities = 1067/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  28    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  87

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  88    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  146
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Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  206

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  207    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  266

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  326

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  386

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  446

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  447    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  506

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  626

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
               ||||||||||||||||||||||||||||||||||||||||||||||| ||||   |||
Sbjct  627    CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  686

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
               |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  687    TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  746

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747    TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  806

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  807    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  865

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  866    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  925

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  926    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  985

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  986    ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1043

Query  1021   TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1044   TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1102
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Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1104  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1132


>dbj|AB490286.1| Chlorococcum sp. RK261 gene for 18S rRNA, partial sequence
          Length=1794

 Score = 1766.8 bits (1958),  Expect = 0E00
 Identities = 1067/1110 (96%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  46    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  105

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  106   AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  164

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  224

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  225   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  284

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  285   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  344

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  345   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  404

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  405   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  464

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  465   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  524

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  584

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  585   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  644

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   ||| 
Sbjct  645   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  704

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  705   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  764

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  765   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  824
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Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  825   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  883

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  884   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  943

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  944   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  1003

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  1004  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1061

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1062  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1120

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1122  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1150


>emb|FR865523.1| Chlamydomonas debaryana genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA
gene, ITS2, 28S rRNA gene, culture collection CCAP 11/1
          Length=2519

 Score = 1758.7 bits (1949),  Expect = 0E00
 Identities = 1065/1110 (95%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACCTCCTNCTTGG-ATAACCGTAGGAAATCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
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Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   ||| 
Sbjct  622   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  682   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|KF144187.1| Chlorococcum sp. GRK7-WB5 18S ribosomal RNA gene, partial sequence
          Length=1768

 Score = 1757.8 bits (1948),  Expect = 0E00
 Identities = 1065/1110 (95%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  41    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  100

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  101   AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  159

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  160   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  219

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  220   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  279

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  280   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  339

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  340   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  399

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  400   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  459

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  460   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  519

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  579

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  580   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  639

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   ||| 
Sbjct  640   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  699

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  700   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  759

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  819

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  820   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  878

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  879   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  938

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  939   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  998

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              ||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  999   CCCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1056

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||| ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1057  TGACCCCGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1115

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
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Sbjct  1117  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1145


>gb|KC492079.1| Chlorococcum sp. A5 18S ribosomal RNA gene, partial sequence
          Length=1789

 Score = 1747.0 bits (1936),  Expect = 0E00
 Identities = 1064/1110 (95%), Gaps = 18/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  46    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  105

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  106   AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  164

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  224

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  225   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGCC  284

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  285   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  344

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  345   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  404

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  405   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGG-GGT  463

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  464   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  523

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct  524   AATATCTTAACGAGTATCCATTGGA--GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  581

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  582   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  641

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||   ||| 
Sbjct  642   CGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCAGCTGAATACGC  701

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||||||||  |||| |||||  ||||||||||||||||||||||
Sbjct  702   TCTCCTGGGCTTAACTGCTTGGGAAGTGGAGTCAGCAGAGTGACCTTGAGCAAACAAGAG  761

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  762   TGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  821

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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Sbjct  822    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  880

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  881    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  940

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  941    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  1000

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  1001  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1058

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1059  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1117

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
              |||||||   |||||| ||| || ||||||
Sbjct  1119  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1147


>gb|KF144184.1| Chlorococcum sp. GRK6-DB5 18S ribosomal RNA gene, partial sequence
          Length=1754

 Score = 1743.3 bits (1932),  Expect = 0E00
 Identities = 1064/1111 (95%), Gaps = 17/1111 (2%)
 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  28     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  87

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  88     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGA  146

Query  125    GCTAATACATGCGTAAAT-CCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCA  183
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  147    GCTAATACATGCGTAAATTCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCA  206

Query  184    GCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGC  243
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  207    GCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTTGTGC  266

Query  244    CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267    CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  326

Query  304    CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  327    CATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  385

Query  364    GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  386    GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  445

Query  424    TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
              ||||||||||||||||||||| ||||| |||| ||||| ||||||||||||| |||||||
Sbjct  446    TAGTGACAATAAATAACAATATTGGGCATTTATGTCTGATAATTGGAATGAGTACAATGT  505

Query  484    AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  506   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  565

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  566   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGAT  625

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             |||| | ||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  626   GTGTTGTCGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACG  685

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
              |||||||||||| ||||  ||||||  ||||||||||||||||||||||||||||||||
Sbjct  686   AGCTCCTGGGCTTTACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  745

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   GTGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  805

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  806   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  864

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  865   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  924

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  925   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  984

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  985   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA  1043

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1044  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1102

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1103  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1132


>gb|DQ303098.1| Chlorococcum sp. KNU-F-2002-C1 18S ribosomal RNA gene, partial sequence
          Length=1547

 Score = 1735.2 bits (1923),  Expect = 0E00
 Identities = 1037/1071 (96%), Gaps = 15/1071 (1%)
 Strand = Plus/Plus

Query  44    TGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG  103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG  60

Query  104   TATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGT  163
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    -ATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGT  119

Query  164   ATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCA  223
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  120   ATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACTTTAGGCGAATCATGATAACTTCA  179

Query  224   CGAATCGCACGGCCTTGTGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCG  283
             ||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  180   CGAATCGCATGGCCTCGTGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCG  239

Query  284   ATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCC  343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   ATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCC  299

Query  344   GGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTAC  403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   GGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTAC  359

Query  404   CCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGT  463
             ||||||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Sbjct  360   CCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGT  419

Query  464   AATTGGAATGAGAACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTG  523
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  420   AATTGGAATGAGTACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTG  479

Query  524   CCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAG  583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   CCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAG  539

Query  584   CTCGTAGTTGGATTTCGGGTGTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGT  643
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  540   CTCGTAGTTGGATTTCGGGTGAGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGT  599

Query  644   GCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAA  703
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  600   TCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAA  659

Query  704   GTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGG  763
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  660   GTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGG  719

Query  764   AATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAG  823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   AATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAG  779

Query  824   AGGGACAGTCGGGGGCATTTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAA  883
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  780   AGGGACAGTCGGGGGCA-TTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAA  838

Query  884   AGACGAACTTCTGCG-AAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTG  942
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  839   AGACGAACTTCTGCGAAAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTG  898

Query  943   GGGGCTCG-AGACGATTAGATACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGG  1000
             |||||||| |||||||||||||||||||||| | |||| |||||||||||||||||||||
Sbjct  899   GGGGCTCGAAGACGATTAGATACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGG  957

Query  1001  ATTGGCA-GTGTTCCATTGATTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-G  1057
             ||||||| |||||||||||| |||||||||||||| ||||||||||  |||||||||| |
Sbjct  958   ATTGGCAGGTGTTCCATTGA-TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGG  1016

Query  1058  GTTC--GGGGGA-TAWTGCCGCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||  |||||| ||  | |||||||||   |||||| ||| || ||||||
Sbjct  1017  GTTCCGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATT-GACGGA  1066


>gb|MH703751.1| Chlorococcum oleofaciens strain Ru-1-1 small subunit ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer
2, complete sequence; and large subunit ribosomal RNA gene, partial sequence
          Length=2678
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 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84     AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  622    TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920
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Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>dbj|AB936290.1| Chlorococcum tatrense gene for 18S ribosomal RNA, partial sequence
          Length=1745

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  201   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  620
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Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  621   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126


>gb|MG491516.1| Chlorococcum oleofaciens strain ACSSI 208 small subunit ribosomal RNA gene,
partial sequence
          Length=1724

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  200   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319
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Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  620   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|MG491514.1| Chlorococcum citriforme strain ACSSI 200 small subunit ribosomal RNA gene, partial
sequence
          Length=1726

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
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 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84     AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  622    TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
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Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|MG491511.1| Neospongiococcum gelatinosum strain ACSSI 217 small subunit ribosomal RNA gene,
partial sequence
          Length=1720

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
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Sbjct  622   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>dbj|AB936286.1| Chlorococcum elkhartiense gene for 18S ribosomal RNA, partial sequence
          Length=1745

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  201   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
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Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  621   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126
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>dbj|AB983608.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence, strain: SAG 213-11

gi|928192331|dbj|AB983609.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence, strain: UTEX 1770
gi|928192332|dbj|AB983610.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence, strain: UTEX 2224
gi|928192333|dbj|AB983611.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence, strain: SAG 66.80

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 gi|928192334|dbj|AB983612.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence,
strain: UTEX 2227
 gi|928192335|dbj|AB983613.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence,
strain: SAG 64.80
 gi|928192336|dbj|AB983614.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence,
strain: SAG 30.93
 gi|928192337|dbj|AB983615.1| Chlorococcum oleofaciens gene for 18S rRNA, partial sequence,
strain: TKAC1016
          Length=1744

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  200   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  620   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|KM020103.1| Neospongiococcum gelatinosum strain SAG 64.80 18S ribosomal RNA gene, partial
sequence
          Length=1765

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
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Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  622   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|KM020100.1| Chlorococcum citriforme strain SAG 62.80 18S ribosomal RNA gene, partial sequence
          Length=1770

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
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Sbjct  142    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  622    TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  981    ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021   TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039   TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076   CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
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Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|JN968580.1| Chlorococcum sphacosum strain SAG 66.80 18S ribosomal RNA gene, partial sequence
 gi|379318163|gb|JN968584.1| Neospongiococcum gelatinosum strain SAG 64.80 18S ribosomal RNA gene,
partial sequence
          Length=1743

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  200   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             ||||||||||||||||||||||||| ||||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  620   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799
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Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>emb|Z28972.1| P.insigne mRNA for nuclear encoded small subunit ribosomal RNA
          Length=1788

 Score = 1731.6 bits (1919),  Expect = 0E00
 Identities = 1060/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  42    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  101

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  102   AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  159

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  160   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  219

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  220   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  279

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  280   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  339

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  340   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  399

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  400   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  459

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  460   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  519
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Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  579

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  580   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  639

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  640   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  699

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  700   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  759

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  819

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  820   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  878

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  879   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  938

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  939   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  998

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  999   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1056

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1057  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1115

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1117  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1145


>gb|KT279470.1| Tetracystis sp. YACCYB50 18S ribosomal RNA gene, partial sequence
          Length=1597

 Score = 1730.7 bits (1918),  Expect = 0E00
 Identities = 1022/1049 (97%), Gaps = 14/1049 (1%)
 Strand = Plus/Plus

Query  66    AATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAG  125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAG  60

Query  126   CTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGC  185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGC  120

Query  186   CGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCG  245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  121   CGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCCG  180
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Query  246   GCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCA  305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCA  240

Query  306   TGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  300

Query  366   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  360

Query  426   GTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAA  485
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAA  420

Query  486   ATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  480

Query  546   CTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGT  605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  481   CTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGC  540

Query  606   GTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGG  665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGG  600

Query  666   CTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGT  725
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CTCCTGGGCTTCACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGT  660

Query  726   GTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGC  785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGC  720

Query  786   CTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCG  845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  721   CTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCG  779

Query  846   TATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCAT  904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  780   TATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCAT  839

Query  905   TTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATA  963
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  840   TTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATA  899

Query  964   CCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATT  1021
             ||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| |
Sbjct  900   CCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-T  957

Query  1022  GACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGC  1076
             ||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||
Sbjct  958   GACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGC  1017

Query  1077  AAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||   |||||| ||| || ||||||
Sbjct  1018  AAGGCTGAAACTTAAAGGAATT-GACGGA  1045


>gb|KJ635659.1| Oophila sp. KY2008 18S ribosomal RNA gene, partial sequence
          Length=1671
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 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  20     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  79

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  80     AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  137

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  138    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  197

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  198    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  257

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  258    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  317

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  377

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  437

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  438    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  497

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  498    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  557

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  558    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  617

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  618    TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  677

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  678    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  737

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  738    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  797

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  798    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  856

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  857    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  916
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Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||| ||||||||| ||||||||||||
Sbjct  917   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTGGGGGGCTCGAAGACGATTAGAT  976

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  977   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1034

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1035  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1093

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1095  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1123


>dbj|AB983624.1| Macrochloris rubrioleum gene for 18S rRNA, partial sequence, strain: CCCryo
340b-08
          Length=1744

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  200   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  620   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>dbj|AB983616.1| Chlorococcum microstigmatum gene for 18S rRNA, partial sequence, strain: UTEX
1777
 gi|928192339|dbj|AB983617.1| Chlorococcum microstigmatum gene for 18S rRNA, partial sequence,
strain: SAG 11-52
 gi|928192340|dbj|AB983618.1| Chlorococcum microstigmatum gene for 18S rRNA, partial sequence,
strain: SAG 11-43
 gi|928192341|dbj|AB983619.1| Chlorococcum microstigmatum gene for 18S rRNA, partial sequence,
strain: TKAC1035
 gi|928192342|dbj|AB983620.1| Chlorococcum microstigmatum gene for 18S rRNA, partial sequence,
strain: TKAC1036
          Length=1744

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
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             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |
Sbjct  200   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  620   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
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             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|KM020101.1| Chlorococcum oleofaciens strain SAG 213-11 18S ribosomal RNA gene, partial
sequence
          Length=1770

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||| || |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGGACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  622   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801
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Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|KM020023.1| Chlorococcum sp. SAG 2467 18S ribosomal RNA gene, partial sequence; internal
transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 26S ribosomal RNA gene, partial sequence
          Length=2429

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |
Sbjct  202   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
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Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  622   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|KF144183.1| Chlorococcum cf. sphacosum SAG 2398 isolate GRK6-DB1 18S ribosomal RNA gene,
partial sequence
          Length=1741

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  73

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  74    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  131

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
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             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  132   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  191

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  192   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  251

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  252   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTGCC  311

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  371

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  431

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  432   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  491

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  492   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  551

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  552   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  611

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  612   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  671

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  672   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  731

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  732   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  791

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  792   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  850

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  851   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  910

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  911   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  970

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  971   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1028

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1029  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1087

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
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Sbjct  1089  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1117


>gb|JN968582.1| Tetracystis tetraspora strain SAG 98.80 18S ribosomal RNA gene, partial sequence
          Length=1743

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||| |||||
Sbjct  200   CCGGGCTTGCCCGACCTTTGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  620   TGCCGGCGCGGTCTGCCTCTGGTATGTACTGCGCTCGGCGCACCTTTCTGCTGGGGACGG  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             | |||||||||| ||||  ||||||  ||| |||||||||||||||||||||||||||||
Sbjct  680   GTTCCTGGGCTTCACTGTCTGGGACTCGGAGTCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACATCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||| |
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATT-AA  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>emb|FR865591.1| Chlorococcum sp. CCAP 11/52 genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA
gene, ITS2, 28S rRNA gene, culture collection CCAP 11/52
          Length=2518

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |
Sbjct  201   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500
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Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  621   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126


>gb|GU117582.1| Pleurastrum sp. CCCryo 006-99 18S small subunit ribosomal RNA gene, partial
sequence
          Length=1712

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  60

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  61    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  118

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  119   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  178
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Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  179   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  238

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  298

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  358

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  418

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  419   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  478

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  538

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  539   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  598

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  599   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  658

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  659   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  718

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  778

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  779   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  837

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  838   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  897

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  898   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  957

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  958   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1015

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1016  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1074

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1076  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1104
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>gb|GU117573.1| Pleurastrum sp. CCCryo 340b-08 18S small subunit ribosomal RNA gene and internal
transcribed spacer 1, partial sequence
          Length=2031

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  202   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  622   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|FJ946902.1| Chlorococcales sp. II4 18S ribosomal RNA gene, partial sequence
          Length=1786

 Score = 1727.1 bits (1914),  Expect = 0E00
 Identities = 1059/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  40    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  99

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  100   AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  157

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  158   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  217

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  218   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  277

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  278   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  337

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  338   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  397

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  398   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  457

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  458   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  517

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  518   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  577

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  578   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  637

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  638   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  697

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  698   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  757

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  758   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  817

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  818   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  876

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  877   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  936

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  937   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  996

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  997   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1054

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1055  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1113

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1115  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1143


>gb|KM020102.1| Chlorococcum sphacosum strain SAG 66.80 18S ribosomal RNA gene, partial sequence
          Length=1771

 Score = 1725.3 bits (1912),  Expect = 0E00
 Identities = 1060/1111 (95%), Gaps = 17/1111 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGG-CTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGC  243
             ||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||
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Sbjct  202   CCGGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGG  261

Query  244   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   CGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTAC  321

Query  304   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   CATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAAC  381

Query  364   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGG  441

Query  424   TAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGT  483
             ||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||
Sbjct  442   TAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGT  501

Query  484   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  561

Query  544   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGT  603
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  562   AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGAT  621

Query  604   GTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACG  663
             |||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  622   GTGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACG  681

Query  664   GGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  723
              |||||||||||||||||  ||||||  ||||||||||||||||||||||||||||||||
Sbjct  682   AGCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGA  741

Query  724   GTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   GTGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  801

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  802   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  860

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  861   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGC  920

Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  921   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  980

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA  1039

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1040  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1098

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1099  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1128
```

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>gb|MG491513.1| Chlorococcum sphacosum strain ACSSI 209 small subunit ribosomal RNA gene, partial
sequence
          Length=1672

 Score = 1724.4 bits (1911),  Expect = 0E00
 Identities = 1056/1106 (95%), Gaps = 16/1106 (1%)
 Strand = Plus/Plus

Query  9     AGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAAT  68
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAAT  60

Query  69    CAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTA  128
             |||||||||||||||||||||||| |  |||| || |||||||||| || ||||||||||
Sbjct  61    CAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTA  118

Query  129   ATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGG  188
             |||| ||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  119   ATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGG  178

Query  189   GCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCG  248
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||||
Sbjct  179   GCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCG  238

Query  249   ATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGG  308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   ATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGG  298

Query  309   TGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTA  368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   TGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTA  358

Query  369   CCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTG  428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   CCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTG  418

Query  429   ACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATA  488
             |||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||||||
Sbjct  419   ACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATA  478

Query  489   TCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTC  548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   TCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTC  538

Query  549   CAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTC  608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| 
Sbjct  539   CAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTT  598

Query  609   GACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTC  668
             ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| ||||
Sbjct  599   GACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTC  658

Query  669   CTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTT  728
             |||||||||||||  ||||||  |||||||||||||||||||||||||||||||||||||
Sbjct  659   CTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTT  718

Query  729   CAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTA  788
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   CAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTA  778

Query  789   TCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTAT  848
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  779   TCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTAT  837
```

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Query  849   TTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTG  907
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  838   TTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTG  897

Query  908   CCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCG  966
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  898   CCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCG  957

Query  967   TCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGAC  1024
             |||||| | |||| |||||||||||||||||||||||||||| |||||||||||| ||||
Sbjct  958   TCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGAC  1015

Query  1025  CCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAG  1079
             |||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||||||
Sbjct  1016  CCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAG  1075

Query  1080  GCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||   |||||| ||| || ||||||
Sbjct  1076  GCTGAAACTTAAAGGAATT-GACGGA  1100


>gb|AY122332.1| Chlorococcum robustum clone Kr_86_30 18S ribosomal RNA gene, partial sequence
          Length=1764

 Score = 1723.5 bits (1910),  Expect = 0E00
 Identities = 1058/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  86

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  87    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  144

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||| |||| |||||||||||||||||||||||||||||||||
Sbjct  145   GCTAATACGTGCGTAAATCCCNACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  204

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |
Sbjct  205   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGC  264

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  324

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  384

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  444

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  445   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  504

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  564
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Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  565   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  624

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  625   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  684

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  685   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  744

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  804

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  805   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  863

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  864   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  923

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  924   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  983

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  984   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1041

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1042  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1100

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1102  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1130


>gb|U41176.1|COU41176 Chlorococcum oleofaciens 18S ribosomal RNA gene
          Length=1745

 Score = 1723.5 bits (1910),  Expect = 0E00
 Identities = 1058/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  201   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  260
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Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| || ||||||||||||| 
Sbjct  621   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTNTCTGCTGGGGACGA  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCCTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126
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>gb|MG491216.1| Chlorococcum oleofaciens strain CAMU MZ-Ch4 small subunit ribosomal RNA gene, partial sequence
          Length=1689

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 Score = 1722.6 bits (1909),  Expect = 0E00
 Identities = 1055/1105 (95%), Gaps = 16/1105 (1%)
 Strand = Plus/Plus

Query  10    GSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATC  69
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATC  60

Query  70    AGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAA  129
             ||||||||||||||||||||||| |  |||| || |||||||||| || |||||||||||
Sbjct  61    AGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAA  118

Query  130   TACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGG  189
             ||| ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  119   TACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGG  178

Query  190   CTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGA  249
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||
Sbjct  179   CTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCGA  238

Query  250   TGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGT  309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   TGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGT  298

Query  310   GGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTAC  369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   GGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTAC  358

Query  370   CACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGA  429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   CACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGA  418

Query  430   CAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATAT  489
             ||||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||
Sbjct  419   CAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATAT  478

Query  490   CTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCC  549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   CTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCC  538

Query  550   AATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCG  609
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |
Sbjct  539   AATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTG  598

Query  610   ACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCC  669
             |||||||||||||||||||||||||||| ||| |||| |||||||||||||||| |||||
Sbjct  599   ACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTCC  658

Query  670   TGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTC  729
             ||||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  659   TGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTC  718

Query  730   AAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTAT  789
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   AAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTAT  778

Query  790   CTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATT  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  779   CTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATT  837

Query  850   TCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGC  908
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  838   TCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGC  897
```

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Query  909   CAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGT  967
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  898   CAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGT  957

Query  968   CGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACC  1025
             ||||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||
Sbjct  958   CGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACC  1015

Query  1026  CTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGG  1080
             ||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||
Sbjct  1016  CTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGG  1075

Query  1081  CT-TGACTTAAGGGAGTTGGACGGA  1104
             ||   |||||| ||| || ||||||
Sbjct  1076  CTGAAACTTAAAGGAATT-GACGGA  1099


>gb|MG582207.1| Chlorococcum sphacosum strain ACSSI 188 small subunit ribosomal RNA gene, partial
sequence
          Length=1704

 Score = 1722.6 bits (1909),  Expect = 0E00
 Identities = 1055/1105 (95%), Gaps = 16/1105 (1%)
 Strand = Plus/Plus

Query  10    GSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATC  69
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATC  60

Query  70    AGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAA  129
             ||||||||||||||||||||||| |  |||| || |||||||||| || |||||||||||
Sbjct  61    AGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAA  118

Query  130   TACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGG  189
             ||| ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  119   TACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGG  178

Query  190   CTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGA  249
             |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||
Sbjct  179   CTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCGA  238

Query  250   TGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGT  309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   TGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGT  298

Query  310   GGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTAC  369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   GGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTAC  358

Query  370   CACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGA  429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   CACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGA  418

Query  430   CAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATAT  489
             ||||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||
Sbjct  419   CAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATAT  478

Query  490   CTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCC  549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   CTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCC  538

Query  550   AATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCG  609
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |
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Sbjct  539   AATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTG  598

Query  610   ACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCC  669
             |||||||||||||||||||||||||||| ||| |||| |||||||||||||||| |||||
Sbjct  599   ACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTCC  658

Query  670   TGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTC  729
             ||||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  659   TGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTC  718

Query  730   AAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTAT  789
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   AAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTAT  778

Query  790   CTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATT  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  779   CTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATT  837

Query  850   TCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGC  908
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  838   TCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGC  897

Query  909   CAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGT  967
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  898   CAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGT  957

Query  968   CGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACC  1025
             ||||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||
Sbjct  958   CGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACC  1015

Query  1026  CTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGG  1080
             ||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||
Sbjct  1016  CTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGG  1075

Query  1081  CT-TGACTTAAGGGAGTTGGACGGA  1104
             ||   |||||| ||| || ||||||
Sbjct  1076  CTGAAACTTAAAGGAATT-GACGGA  1099


>gb|KR607491.1| Chlorococcum oleofaciens strain SAG 213-11 small subunit ribosomal RNA gene,
partial sequence
          Length=1716

 Score = 1721.7 bits (1908),  Expect = 0E00
 Identities = 1054/1103 (95%), Gaps = 16/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             ||||||||||||||||||||| |  |||| || |||||||||| || |||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAATA  119

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  120   CGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  179

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             ||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Sbjct  180   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCGATG  239

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  299

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  359

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  419

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  420   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  479

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  539

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Sbjct  540   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTGAC  599

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             |||||||||||||||||||||||||| ||| |||| |||||||||||||||| |||||||
Sbjct  600   GCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTCCTG  659

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  660   GGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  719

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   AGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  779

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  780   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  838

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  839   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  898

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  899   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  958

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  959   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1016

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1017  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1076

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1077  GAAACTTAAAGGAATT-GACGGA  1098


>gb|KM020024.1| Tetracystis tetraspora strain SAG 98.80 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 26S ribosomal RNA gene, partial sequence
          Length=2442
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 Score = 1720.8 bits (1907),  Expect = 0E00
 Identities = 1059/1111 (95%), Gaps = 17/1111 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||| |||||
Sbjct  202   CCGGGCTTGCCCGACCTTTGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  622   TGCCGGCGCGGTCTGCCTCTGGTATGTACTGCGCTCGGCGCACCTTTCTGCTGGGGACGG  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             | |||||||||| ||||  ||||||  ||| |||||||||||||||||||||||||||||
Sbjct  682   GTTCCTGGGCTTCACTGTCTGGGACTCGGAGTCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAG-CAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  783
             ||||||||| |||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTG  801

Query  784   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTT  843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  802   GCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TT  860

Query  844   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGC  902
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||
Sbjct  861   CGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACATCTGCGAAAGC  920
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Query  903   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  921   ATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  980

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| |||||||||| |
Sbjct  981   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATT-A  1038

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1039  ATGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1098

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1099  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1128


>gb|FJ946903.1| Chlorococcales sp. VI8 18S ribosomal RNA gene, partial sequence
          Length=1786

 Score = 1719.9 bits (1906),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| ||||||||||||||||| | |||||||||||||||||||||||||||||||||
Sbjct  40    ATTAAGCCATGCATGTCTAAGTATNANCTGCTTATACGGTGAAACTGCGAATGGCTCATT  99

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  100   AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  157

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  158   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  217

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  218   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  277

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  278   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  337

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  338   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  397

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  398   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  457

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  458   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  517

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  518   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  577

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  578   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  637
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Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  638   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  697

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  698   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  757

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  758   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  817

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  818   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  876

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  877   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  936

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  937   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  996

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  997   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1054

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1055  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1113

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1115  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1143


>gb|KJ635657.1| Oophila sp. CT2007 18S ribosomal RNA gene, partial sequence
          Length=1744

 Score = 1719.0 bits (1905),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| ||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  20    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  79

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  80    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  136

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  196

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  197   CCGGGCTTGCCCGACCTGAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  256

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  316
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Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  376

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  436

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  437   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  496

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  556

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  616

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||  |||  ||||||||||| ||||  ||||||||||||||||||||
Sbjct  617   TGGCGGCGCGGTCTGGTTCTACTATGTACTGCGTTCGGCACACCTTTCTGCTGGGGACGG  676

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  677   GCTCCTGGGCTTCACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  736

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  737   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  796

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  797   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  855

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  856   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  915

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  916   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  975

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  976   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1033

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1034  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1092

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1094  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1122


>dbj|AB983623.1| Chlorococcum nivale gene for 18S rRNA, partial sequence, strain: UTEX2225
          Length=1743

 Score = 1719.0 bits (1905),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus
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Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  138

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  198

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  199   CCGGGCTTGCCCGACCTGAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  258

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  318

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  378

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  438

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  439   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  498

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  558

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  559   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  618

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||  |||  ||||||||||| ||||  ||||||||||||||||||||
Sbjct  619   TGGCGGCGCGGTCTGGTTCTACTATGTACTGCGTTCGGCACACCTTTCTGCTGGGGACGG  678

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  679   GCTCCTGGGCTTCACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  738

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  798

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  799   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  857

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  858   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  917

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  918   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  977
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Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  978   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1035

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1036  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1094

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1096  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1124


>emb|HE860252.1| Chlorochytrium lemnae partial 18S rRNA gene, culture collection CAUP:H6905
          Length=1647

 Score = 1719.0 bits (1905),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  25    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  84

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  85    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  202   CCGGGCTTGCCCGACCTGAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||  |||  ||||||||||| ||||  ||||||||||||||||||||
Sbjct  622   TGGCGGCGCGGTCTGGTTCTACTATGTACTGCGTTCGGCACACCTTTCTGCTGGGGACGG  681
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Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTCACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
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>emb|HE860251.1| Chlorochytrium lemnae partial 18S rRNA gene, culture collection CAUP:H6904
          Length=1633

 Score = 1719.0 bits (1905),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  25    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  84

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  85    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  141

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  201

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  202   CCGGGCTTGCCCGACCTGAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  261

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  321

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  381
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Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  441

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  442   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  501

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  561

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  621

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || |||||||||  |||  ||||||||||| ||||  ||||||||||||||||||||
Sbjct  622   TGGCGGCGCGGTCTGGTTCTACTATGTACTGCGTTCGGCACACCTTTCTGCTGGGGACGG  681

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||||||||||||||||||||||||||||||||||
Sbjct  682   GCTCCTGGGCTTCACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  741

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  801

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  802   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  860

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  861   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  920

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  921   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  980

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  981   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1038

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1039  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1097

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1099  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1127


>gb|AF514408.1| Macrochloris sp. 105-99 strain CCCryo 105-99 18S ribosomal RNA gene, partial
sequence
          Length=1764

 Score = 1718.1 bits (1904),  Expect = 0E00
 Identities = 1057/1110 (95%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Sbjct  36     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  95

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  96     AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  153

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  154    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  213

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  214    CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  273

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  274    GGCGATGTSTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  333

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  334    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  393

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  394    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  453

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  454    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  513

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  514    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  573

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  574    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  633

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  634    TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  693

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  694    GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  753

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  754    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  813

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  814    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  872

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  873    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  932

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  933    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  992

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
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Sbjct  993   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1050

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1051  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1109

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1111  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1139


>gb|KR607484.1| Chloromonas perforata strain SAG 11.43 small subunit ribosomal RNA gene, partial
sequence
          Length=1716

 Score = 1717.2 bits (1903),  Expect = 0E00
 Identities = 1053/1103 (95%), Gaps = 16/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             ||||||||||||||||||||| |  |||| || |||||||||| || |||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAATA  119

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  120   CGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  179

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             ||||||||||||||||||||||||||||||||||||||||||| ||| ||| ||||||||
Sbjct  180   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGCGGCGATG  239

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  299

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  359

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  419

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  420   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  479

Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  539

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Sbjct  540   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTGAC  599

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             |||||||||||||||||||||||||| ||| |||| |||||||||||||||| |||||||
Sbjct  600   GCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTCCTG  659

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
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                ||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  660   GGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  719

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   AGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  779

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  780   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  838

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  839   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  898

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  899   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  958

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  959   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1016

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1017  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1076

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1077  GAAACTTAAAGGAATT-GACGGA  1098


>gb|KM870774.1| Uncultured eukaryote clone TE212F 18S ribosomal RNA gene, complete sequence
          Length=1730

 Score = 1717.2 bits (1903),  Expect = 0E00
 Identities = 1056/1110 (95%), Gaps = 15/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  85

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  86    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  143

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  144   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  203

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  204   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  263

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  323

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  383

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  443

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  444   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  503

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  563

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  564   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  623

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  624   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  683

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  684   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  743

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  744   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  803

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Sbjct  804   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGGCATTC  863

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  864   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  923

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  924   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  983

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  984   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1041

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1042  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1100

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| |||| ||||
Sbjct  1102  CAAGGCTGAAACTTAAAGGAATTGG-CGGA  1130


>gb|JQ315635.1| Chlamydomonadaceae sp. KMMCC 249 18S ribosomal RNA gene, partial sequence
          Length=1666

 Score = 1716.3 bits (1902),  Expect = 0E00
 Identities = 1025/1058 (96%), Gaps = 15/1058 (1%)
 Strand = Plus/Plus

Query  57    GGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGA  116
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1     GGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGA  59

Query  117   AATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAA  176
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  60    AATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAA  119

Query  177   AAGGCCAGCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGC  236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   AAGGCCAGCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGC  179

Query  237   CTTGTGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGA  296
             || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  180   CTCGCGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGA  239

Query  297   GGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCT  356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   GGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCT  299

Query  357   GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACAC  416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACAC  359

Query  417   GGGGAGGTAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGA  476
             |||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Sbjct  360   GGGGAGGTAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGT  419

Query  477   ACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGG  536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  420   ACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGG  479

Query  537   TAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGAT  596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGAT  539

Query  597   TTCGGGTGTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCT  656
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  540   TTCGGGTGCGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCT  599

Query  657   GGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCA  716
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  600   GGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGGCCTTGAGCA  659

Query  717   AACAAGAGTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAG  776
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  660   AACAAGAGTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAG  719

Query  777   GACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGG  836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   GACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGG  779

Query  837   GGCATTTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTG  896
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  780   GGCA-TTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTG  838

Query  897   CG-AAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGAC  954
             || |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  839   CGAAAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGAC  898

Query  955   GATTAGATACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTT  1012
             |||||||||||||||||| | |||| |||||||||||||||||||||||||||| |||||
Sbjct  899   GATTAGATACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTT  957

Query  1013  CCATTGATTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-  1067
             ||||||| |||||||||||||| ||||||||||  |||||||||| |||||  ||||||
Sbjct  958   CCATTGA-TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAG  1016

Query  1068  TAWTGCCGCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1103
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             ||  | |||||||||   |||||| ||| || ||||||
Sbjct  1017  TATGGTCGCAAGGCTGAAACTTAAAGGAATT-GACGGA  1053


>gb|GQ122379.1| Chlamydomonadaceae sp. KMMCC FC-97 18S ribosomal RNA gene, partial sequence
          Length=1667

 Score = 1711.8 bits (1897),  Expect = 0E00
 Identities = 1024/1058 (96%), Gaps = 15/1058 (1%)
 Strand = Plus/Plus

Query  57    GGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGA  116
             |||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Sbjct  1     GGCTCATTAAATCAGTTATAGTTTATTTGATGGTACTTCCTACTTGG-ATAACCGTAGGA  59

Query  117   AATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAA  176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  60    AATCTAGAGCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAA  119

Query  177   AAGGCCAGCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGC  236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   AAGGCCAGCCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGC  179

Query  237   CTTGTGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGA  296
             || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  180   CTCGCGCCGGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGA  239

Query  297   GGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCT  356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   GGCCTACCATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCT  299

Query  357   GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACAC  416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   GAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACAC  359

Query  417   GGGGAGGTAGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGA  476
             |||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||| 
Sbjct  360   GGGGAGGTAGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGT  419

Query  477   ACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGG  536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  420   ACAATGTAAATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGG  479

Query  537   TAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGAT  596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TAATTCCAGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGAT  539

Query  597   TTCGGGTGTGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCT  656
             |||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  540   TTCGGGTGCGTCGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGGTGCACCTTTCTGCT  599

Query  657   GGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCA  716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  600   GGGGACGGGCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCA  659

Query  717   AACAAGAGTGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAG  776
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  660   AACAAGAGTGTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAG  719

Query  777   GACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGG  836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   GACTCTGGCCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGG  779

Query  837   GGCATTTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTG  896
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                |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  780   GGCA-TTCGTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTG  838

Query  897   CG-AAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGAC  954
             || |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  839   CGAAAGCATTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGAC  898

Query  955   GATTAGATACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTT  1012
             |||||||||||||||||| | |||| |||||||||||||||||||||||||||| |||||
Sbjct  899   GATTAGATACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTT  957

Query  1013  CCATTGATTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-  1067
             ||||||| |||||||||||||| ||||||||||  |||||||||| |||||  ||||||
Sbjct  958   CCATTGA-TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAG  1016

Query  1068  TAWTGCCGCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1103
             ||  | |||||||||   |||||| ||| || ||||||
Sbjct  1017  TATGGTCGCAAGGCTGAAACTTAAAGGAATT-GACGGA  1053


>gb|JN880460.1| Protosiphon botryoides isolate UTEX B 99 18S ribosomal RNA gene, partial sequence
          Length=1695

 Score = 1710.0 bits (1895),  Expect = 0E00
 Identities = 1056/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  10    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  68

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  69    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  126

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  127   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  186

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  187   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  246

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  247   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  306

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  307   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  366

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  367   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  426

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  427   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  486

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  487   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  546

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  547   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  606

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  607   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  666

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  667   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  726

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  727   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  786

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  787   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  845

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  846   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  905

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  906   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  965

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  966   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1023

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1024  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1082

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1084  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1112


>gb|JN880459.1| Protosiphon botryoides isolate FRT2000 18S ribosomal RNA gene, partial sequence
          Length=1745

 Score = 1710.0 bits (1895),  Expect = 0E00
 Identities = 1056/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  20    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  78

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  79    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  136

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  196

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  197   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  256

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  316

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  376

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  436

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  437   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  496

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  556

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  616

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  617   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  676

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  677   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  736

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  737   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  796

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  797   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  855

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  856   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  915

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  916   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  975

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  976   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1033

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1034  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1092

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1094  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1122


>gb|JN880458.1| Protosiphon botryoides isolate UTEX 47 18S ribosomal RNA gene, partial sequence
          Length=1720

 Score = 1710.0 bits (1895),  Expect = 0E00
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 Identities = 1056/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  20     ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  78

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  79     AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  136

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137    GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  196

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  197    CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  256

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  316

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  376

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  436

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  437    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  496

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  556

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  616

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  617    TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  676

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  677    GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  736

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  737    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  796

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  797    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  855

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  856    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  915

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
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             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  916   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  975

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  976   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1033

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1034  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1092

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1094  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1122


>gb|JN880457.1| Protosiphon botryoides f. parieticola isolate UTEX 46 18S ribosomal RNA gene,
partial sequence
          Length=1718

 Score = 1710.0 bits (1895),  Expect = 0E00
 Identities = 1056/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  20    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  78

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  79    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  136

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  196

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  197   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  256

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  316

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  376

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  436

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  437   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  496

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  556

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  616
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Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  617   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  676

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  677   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  736

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  737   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  796

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  797   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  855

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  856   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  915

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  916   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  975

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  976   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1033

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1034  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1092

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1094  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1122


>gb|EF024715.1| Uncultured Haematococcaceae clone Elev_18S_1205 18S ribosomal RNA gene, partial
sequence
          Length=1775

 Score = 1710.0 bits (1895),  Expect = 0E00
 Identities = 1056/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  40    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  98

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  99    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  156

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  157   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  216

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  217   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  276

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  277   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  336
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Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  337   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  396

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  397   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  456

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  457   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  516

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  517   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  576

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  577   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  636

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  637   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  696

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  697   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  756

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  757   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  816

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  817   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  875

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  876   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  935

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  936   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  995

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  996   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1053

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1054  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1112

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1114  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1142


>gb|MG491510.1| Chlorococcum isabeliense strain ACSSI 207 small subunit ribosomal RNA gene,
partial sequence
          Length=1715

 Score = 1705.5 bits (1890),  Expect = 0E00
 Identities = 1054/1110 (94%), Gaps = 17/1110 (2%)
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 Strand = Plus/Plus

Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||| |||||| |||||||||||||||||||||||
Sbjct  24     ATTAAGCCATGCATGTCTAAGTATAAACTACTTATATGGTGAAACTGCGAATGGCTCATT  83

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84     AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141    GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  201    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  260

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| | |  ||||||||||||||||||| ||||||||
Sbjct  441    AGTGACAATAAATAACAATACTGGGCATCTTTGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  620

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||   ||||||||||||||||||| ||||||||||  |||||||||||||||||||||| 
Sbjct  621    TGCTTACGCGGTCTGCCTCTGGTAAGTACTGCGCTAAGTGCACCTTTCTGCTGGGGACGA  680

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681    GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
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Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||| ||||||||| ||||||||||||
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAAGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCAC-TTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             ||||||||||||||| ||| |||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACTTTAAGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126


>dbj|AB983621.1| Chlorococcum rugosum gene for 18S rRNA, partial sequence, strain: UTEX 1785
          Length=1742

 Score = 1705.5 bits (1890),  Expect = 0E00
 Identities = 1054/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||| |||||| |||||||||||||||||||||||
Sbjct  22    ATTAAGCCATGCATGTCTAAGTATAAACTACTTATATGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  138

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  198

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  199   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  258

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  318

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  378

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  438

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| | |  ||||||||||||||||||| ||||||||
Sbjct  439   AGTGACAATAAATAACAATACTGGGCATCTTTGTCTGGTAATTGGAATGAGTACAATGTA  498

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  558

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  559   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  618

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||   ||||||||||||||||||| ||||||||||  ||||||||||||||||||||||
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Sbjct  619   TGCTTACGCGGTCTGCCTCTGGTAAGTACTGCGCTAAGTGCACCTTTCTGCTGGGGACGA  678

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  679   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  738

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  798

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  799   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  857

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  858   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  917

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  918   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  977

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||| ||||||||| ||||||||||||
Sbjct  978   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAAGGATTGGCAGGTGTTCCATTGA-  1035

Query  1021  TGACCCTGCCAGCAC-TTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             ||||||||||||||| ||| |||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1036  TGACCCTGCCAGCACTTTAAGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1094

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1096  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1124


>gb|KM020106.1| Chlorococcum isabeliense strain SAG 65.80 18S ribosomal RNA gene, partial
sequence
          Length=1761

 Score = 1705.5 bits (1890),  Expect = 0E00
 Identities = 1054/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||| |||||| |||||||||||||||||||||||
Sbjct  24    ATTAAGCCATGCATGTCTAAGTATAAACTACTTATATGGTGAAACTGCGAATGGCTCATT  83

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  84    AAATCAGTTATAGTTTATTTGATGGTACTT--TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  201   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| | |  ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATCTTTGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||   ||||||||||||||||||| ||||||||||  |||||||||||||||||||||| 
Sbjct  621   TGCTTACGCGGTCTGCCTCTGGTAAGTACTGCGCTAAGTGCACCTTTCTGCTGGGGACGA  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  859

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  860   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  919

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  920   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  979

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||| ||||||||| |||||||||||| 
Sbjct  980   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAAGGATTGGCAGGTGTTCCATTGA-  1037

Query  1021  TGACCCTGCCAGCAC-TTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             ||||||||||||||| ||| |||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1038  TGACCCTGCCAGCACTTTAAGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1096

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1126


>gb|KC149964.1| Protosiphon botryoides isolate GTD4b-3 18S ribosomal RNA gene, partial sequence
          Length=1759

 Score = 1705.5 bits (1890),  Expect = 0E00
 Identities = 1055/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
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            |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  42   ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  100

Query  65   AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
            |||||||||||||||||||||||||| |||  |||| || |||||||||| || ||||||
Sbjct  101  AAATCAGTTATAGTTTATTTGATGGTTCCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  158

Query  125  GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  159  GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  218

Query  185  CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  219  CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  278

Query  245  GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  279  GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  338

Query  305  ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  339  ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  398

Query  365  GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  399  GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  458

Query  425  AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
            |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  459  AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  518

Query  485  AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519  AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  578

Query  545  GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  579  GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  638

Query  605  TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
            ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  639  TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  698

Query  665  GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
            |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  699  GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  758

Query  725  TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  759  TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  818

Query  785  CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  819  CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  877

Query  845  GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  878  GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  937

Query  904  TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  938  TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  997

Query  963  ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
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                |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  998   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1055

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1056  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1114

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1116  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1144


>gb|FJ946907.1| Chlorococcales sp. VPL9-6 18S ribosomal RNA gene, partial sequence
          Length=1718

 Score = 1705.5 bits (1890),  Expect = 0E00
 Identities = 1055/1110 (95%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  68

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  69    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  126

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  127   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  186

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||| | ||||||| |
Sbjct  187   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCATGCCCTTGTGGC  246

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  247   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  306

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  307   ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  365

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  366   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  425

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  426   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  485

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  486   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  545

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  546   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  605

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| | ||||||||||||||||||||||||||| ||| |||| ||||||||||||||||
Sbjct  606   TGTTGTCGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  665

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
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             |||||||||||| | ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  666   GCTCCTGGGCTTCATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  725

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  726   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  785

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  786   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  844

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  904

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  905   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  964

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||| ||||| 
Sbjct  965   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCTATTGA-  1022

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1023  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1081

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1083  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1111


>gb|M63001.1|CAUUGEAC Characium vacuolatum 18S ribosomal RNA gene
          Length=1793

 Score = 1704.6 bits (1889),  Expect = 0E00
 Identities = 1054/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  43    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  102

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  103   AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  161

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  162   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  221

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| ||||||||||||||||||||||||||||||| | ||| ||| |
Sbjct  222   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCATGCCCTCGTGGC  281

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  341

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342   ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  400

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
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Sbjct  401   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  460

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  461   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  520

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  521   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  580

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  581   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  640

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| | |||||||||||||||||| |||||||| ||| |||| ||||||||||||||||
Sbjct  641   TGTTGTCGCGGTCTGCCTCTGGTACGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  700

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  701   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  760

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  761   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  820

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  821   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  879

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  880   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  939

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  940   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  999

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||| |||||
Sbjct  1000  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCAATTGA-  1057

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1058  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1116

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1118  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1146


>gb|KM870658.1| Uncultured eukaryote clone TE108A 18S ribosomal RNA gene, complete sequence
          Length=1730

 Score = 1702.8 bits (1887),  Expect = 0E00
 Identities = 1055/1111 (94%), Gaps = 17/1111 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  85

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
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             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  86    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  143

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  144   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  203

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||| |
Sbjct  204   CCGGGCTTGCCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGC  263

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  323

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  383

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  443

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  444   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  503

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCG  563

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  564   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  623

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| |||||||||||||||||||||||||||||  || |||| ||||| ||||||||||
Sbjct  624   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTCCGATGCATCTTTCCGCTGGGGACGA  683

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||| ||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  684   GCTCCTGGGCTTAATTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  743

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  744   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  803

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  804   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  862

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  863   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  922

Query  904   -TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGA  961
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  923   TTTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGA  982

Query  962   TACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGA  1019
             ||||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  983   TACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA  1041

Query  1020  TTGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCC  1074
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              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |
Sbjct  1042  -TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTC  1100

Query  1075  GCAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||||   |||||| ||| || ||||||
Sbjct  1101  GCAAGGCTGAAACTTAAAGGAATT-GACGGA  1130


>gb|U41177.1|PBU41177 Protosiphon botryoides 18S ribosomal RNA gene
          Length=1744

 Score = 1702.8 bits (1887),  Expect = 0E00
 Identities = 1054/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  200   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| ||||||| 
Sbjct  620   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  680   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
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Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              ||||||||| | |||| ||||| |||||||||||||||||||||| ||||||||||||
Sbjct  979   NCCGTCGTAGTC-TCAACCATAANCGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|U70794.1|CPU70794 Chloromonas perforata strain SAG 11-43 18S ribosomal RNA gene, partial
sequence
          Length=1700

 Score = 1701.0 bits (1885),  Expect = 0E00
 Identities = 1052/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  61

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  62    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  119

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  120   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  179

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |
Sbjct  180   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTCGTGGC  239

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   GGCGATGTNTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  299

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  300   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTAAGAAACG  359

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||| |
Sbjct  360   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACNNNGAGNT  419
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Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  420   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  479

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  539

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  540   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  599

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| ||||||||||||||||||||||||||||| ||| |||| |||||||||||||||| 
Sbjct  600   TGTTGACGCGGTCTGCCTCTGGTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGA  659

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  660   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  719

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  779

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  780   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  838

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  839   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  898

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Sbjct  899   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAANACGATTAGAT  958

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  959   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1016

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1017  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1075

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1077  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1105


>gb|MG491512.1| Chlorococcum diplobionticum strain ACSSI 202 small subunit ribosomal RNA gene,
partial sequence
          Length=1702

 Score = 1700.1 bits (1884),  Expect = 0E00
 Identities = 1053/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  5     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  64

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  65    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  122
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Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  182

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||| ||||||||||||||||||||||||||||| ||||| |||||
Sbjct  183   CCGGGCTTGCCCGACCTTTGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCC  242

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  302

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  362

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  422

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| || |||||||||||||||| ||||||||
Sbjct  423   AGTGACAATAAATAACAATACTGGGCATTTATGTTTGGTAATTGGAATGAGTACAATGTA  482

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  542

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  543   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTA  602

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || || ||||||||||||||||||||||||||||| | |||||||||||||  ||||
Sbjct  603   TGCCGGCGTGGTCTGCCTCTGGTATGTACTGCGCTCGGCGTACCTTTCTGCTGGAAACGG  662

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             | |||||||||| ||||  ||||||  ||| |||||||||||||||||||||||||||||
Sbjct  663   GTTCCTGGGCTTCACTGTCTGGGACTCGGAGTCAGCGAAGTGACCTTGAGCAAACAAGAG  722

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  723   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  782

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  783   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  841

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Sbjct  842   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACATCTGCGAAAGCA  901

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  902   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  961

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  962   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1019

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1020  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1078
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Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1080  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1108


>gb|U70587.1|CDU70587 Chlorococcum diplobionticum 18S ribosomal RNA gene, partial sequence
          Length=1708

 Score = 1700.1 bits (1884),  Expect = 0E00
 Identities = 1053/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  5     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  64

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  65    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  122

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  182

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||| ||||||||||||||||||||||||||||| ||||| |||||
Sbjct  183   CCGGGCTTGCCCGACCTTTGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCC  242

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  302

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  362

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  422

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| || |||||||||||||||| ||||||||
Sbjct  423   AGTGACAATAAATAACAATACTGGGCATTTATGTTTGGTAATTGGAATGAGTACAATGTA  482

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  542

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTA  602

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             || || || ||||||||||||||||||||||||||||| | |||||||||||||  ||||
Sbjct  603   TGCCGGCGTGGTCTGCCTCTGGTATGTACTGCGCTCGGCGTACCTTTCTGCTGGAAACGG  662

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             | |||||||||| ||||  ||||||  ||| |||||||||||||||||||||||||||||
Sbjct  663   GTTCCTGGGCTTCACTGTCTGGGACTCGGAGTCAGCGAAGTGACCTTGAGCAAACAAGAG  722

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  723   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  782
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Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  783   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  841

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Sbjct  842   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACATCTGCGAAAGCA  901

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  902   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  961

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  962   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1019

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1020  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1078

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1080  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1108


>gb|KC196723.1| Macrochloris radiosa isolate UTEX 1964 18S ribosomal RNA gene, partial sequence
          Length=1688

 Score = 1699.2 bits (1883),  Expect = 0E00
 Identities = 1049/1103 (95%), Gaps = 16/1103 (1%)
 Strand = Plus/Plus

Query  12    CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAG  61

Query  72    TTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATA  131
             |||||||||||||||||||||||  |||| || |||||||||| || |||||||||||||
Sbjct  62    TTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAATA  119

Query  132   CATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCT  191
             | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||| ||
Sbjct  120   CGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGACT  179

Query  192   TGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATG  251
             || |||| ||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Sbjct  180   TGTCCGAACTTAGGCGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCGATG  239

Query  252   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGG  299

Query  312   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   TAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCA  359

Query  372   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360   CATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACA  419

Query  432   ATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCT  491
             ||||||||||||||||||| |||| ||||||||||||||||||| |||||||||||||||
Sbjct  420   ATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCT  479
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Query  492   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480   TAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAA  539

Query  552   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGAC  611
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Sbjct  540   TAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTGAC  599

Query  612   GCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTG  671
             ||||||||||||||||||| |||||| ||| |||| |||||||||||||||| | |||||
Sbjct  600   GCGGTCTGCCTCTGGTATGCACTGCGTTCGATGCATCTTTCTGCTGGGGACGTGTTCCTG  659

Query  672   GGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  731
             ||||||| ||  ||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  660   GGCTTAATTGTCTGGGACACGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAA  719

Query  732   AGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  791
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   AGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCT  779

Query  792   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTC  851
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  780   TGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTC  838

Query  852   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCA  910
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  839   ATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCA  898

Query  911   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCG  969
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  899   AGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCG  958

Query  970   TAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCT  1027
             ||| | |||| |||||||||||||||||||||||||||| |||||||||||| |||||||
Sbjct  959   TAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCT  1016

Query  1028  GCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT  1082
             ||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||||||||
Sbjct  1017  GCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCT  1076

Query  1083  -TGACTTAAGGGAGTTGGACGGA  1104
                |||||| ||| || ||||||
Sbjct  1077  GAAACTTAAAGGAATT-GACGGA  1098


>dbj|AB049415.1| Chlorosarcinopsis minor gene for 18S rRNA
          Length=1740

 Score = 1697.3 bits (1881),  Expect = 0E00
 Identities = 1053/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACTGTGAAACTGCGAATGGCTCATT  82

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  83    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200
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Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||||  ||||||||||||||||||||||||||||| ||||| |||||
Sbjct  201   CCGGGCTTGCCCGACCTATGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCC  260

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Sbjct  261   GGCGATGTTTCATTCAAATTTCTGCCCTATCAATTGTCGATGGTAGGATAGAGGCCTACC  320

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ATGATGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  380

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  440

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  441   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  500

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AACATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  560

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  620

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              | || ||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  621   CGCCGTCGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGG  680

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  |||||||||||| ||||||||||||||||||||
Sbjct  681   GCTCCTGGGCTTCACTGTCTGGGACTCGGAATCAGCGAANTGACCTTGAGCAAACAAGAG  740

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  800

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |||
Sbjct  801   CCTATCTTGTTGGTCTGTAGGA-CGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACATCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| 
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125
```

```
>gb|KM020179.1| Rhopalosolen saccatus strain SAG 26.95 18S ribosomal RNA gene, partial sequence
          Length=1752

 Score = 1696.5 bits (1880),  Expect = 0E00
 Identities = 1052/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  66

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  67    AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  125

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  126   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  185

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||| |||||| | ||||||| |
Sbjct  186   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGGATCGCATGCCCTTGTGGC  245

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  246   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  305

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  306   ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGCGCCTGAGAAACG  364

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365   GCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  425   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  484

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  604

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| |||||||||||||  |||||||||||||||||| |||| |||||||||||||||| 
Sbjct  605   TGTTGACGCGGTCTGCCATTGGTATGTACTGCGCTCGATGCATCTTTCTGCTGGGGACGA  664

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  665   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Sbjct  725   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACATGATAGGACTCTGG  784

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  843
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Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  844   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  903

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  963

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| ||||||||||||||||||||| |||||| |||||| ||||| 
Sbjct  964   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGNTTGGCAGGTGTTCTATTGA-  1021

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1022  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1080

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1082  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1110


>gb|KF791539.1| Chlorococcum sp. JB1 small subunit ribosomal RNA gene, partial sequence
          Length=1743

 Score = 1696.5 bits (1880),  Expect = 0E00
 Identities = 1053/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  23    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             |||||||||||||||||||||||||||| |  |||| || |||||||||| || ||||||
Sbjct  82    AAATCAGTTATAGTTTATTTGATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGA  139

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  199

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||||
Sbjct  200   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTCGTGCC  259

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  319

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   AGGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  379

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559
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Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  619

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||||
Sbjct  620   CGTCGACGCGGTCTGCCTCTGGTACGTACTGCGCTCGGTGCACCTTTCTGCCGGGGACGG  679

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             | |||||||||| ||||  ||||||  ||| || |||| ||||||||||||||| |||||
Sbjct  680   GTTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAATAAGAG  739

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  799

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGT-TTTTGGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||| ||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTCTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|EF024170.1| Uncultured eukaryote clone Elev_18S_510 18S ribosomal RNA gene, partial sequence
 gi|166083832|gb|EF024355.1| Uncultured Haematococcaceae clone Elev_18S_1005 18S ribosomal RNA
gene, partial sequence
          Length=1776

 Score = 1696.5 bits (1880),  Expect = 0E00
 Identities = 1053/1110 (94%), Gaps = 17/1110 (2%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct  40    ATTAAGCCATGCATGTCTAAGTATAAACCT-TTATACGGTGAAACTGCGAATGGCTCATT  98

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||  |||| || |||||||||| || ||||||
Sbjct  99    AAATCAGTTATAGTTTATTTGATGGTACCTT-TACTCGG-ATAACCGTAGTAATTCTAGA  156

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  157   GCTAATACGTGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  216

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
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             |||||||||||||||| ||||||| |||||| ||||||||||||||||||||||||||||
Sbjct  217   CCGGGCTTGCCCGACCCTAGGCGAGTCATGACAACTTCACGAATCGCACGGCCTTGTGCC  276

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  277   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  336

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  337   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  396

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  397   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATCACCCAATCCCGACACGGGGAGGT  456

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  457   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  516

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  517   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  576

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  577   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  636

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||  |||||||||||||||||||||||||||||  |||||||||||||||| |||||||
Sbjct  637   TGCTGACGCGGTCTGCCTCTGGTATGTACTGCGGCCGGTGCACCTTTCTGCCGGGGACGA  696

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||| ||||  ||||||  ||| || |||| |||||||||||||||||||||
Sbjct  697   GCTCCTGGGCTTCACTGTCTGGGACTCGGAGTCGGCGAGGTGACCTTGAGCAAACAAGAG  756

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  757   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  816

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  817   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  875

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  876   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  935

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  936   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  995

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  996   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-  1053

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1054  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1112

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1114  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1142
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>gb|MG022715.1| Chlamydopodium starrii isolate CCAP 209/1B small subunit ribosomal RNA gene,
partial sequence
          Length=1233

 Score = 1695.5 bits (1879),  Expect = 0E00
 Identities = 1052/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  46    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  105

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  106   AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  164

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  165   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  224

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||| |||||| | ||| ||| |
Sbjct  225   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGGATCGCATGCCCTCGTGGC  284

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  285   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  344

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  345   ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGCGCCTGAGAAACG  403

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  404   GCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  463

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  464   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  523

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  524   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  583

Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  584   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  643

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| |||||||||||||  |||||||||||||||||| |||| ||||||||||||||||
Sbjct  644   TGTTGACGCGGTCTGCCATTGGTATGTACTGCGCTCGATGCATCTTTCTGCTGGGGACGA  703

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  704   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  763

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| |||||||||||||||||||||||||||| |||||||||||||||
Sbjct  764   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACATGATAGGACTCTGG  823

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  824   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  882
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Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  883   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  942

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  943   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  1002

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||| ||||| 
Sbjct  1003  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCTATTGA-  1060

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1061  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1119

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1121  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1149


>gb|MG022714.1| Chlamydopodium starrii isolate CCAP 209/1A small subunit ribosomal RNA gene,
partial sequence
          Length=1266

 Score = 1695.5 bits (1879),  Expect = 0E00
 Identities = 1052/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  47    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  106

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  107   AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  165

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  166   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  225

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||| |||||| | ||| ||| |
Sbjct  226   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGGATCGCATGCCCTCGTGGC  285

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  286   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  345

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  346   ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGCGCCTGAGAAACG  404

Query  365   GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  405   GCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  464

Query  425   AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
             |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  465   AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  524

Query  485   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525   AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  584
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Query  545   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  585   GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  644

Query  605   TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
             ||| |||||||||||||  |||||||||||||||||| |||| |||||||||||||||| 
Sbjct  645   TGTTGACGCGGTCTGCCATTGGTATGTACTGCGCTCGATGCATCTTTCTGCTGGGGACGA  704

Query  665   GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
             |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  705   GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  764

Query  725   TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
             ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Sbjct  765   TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACATGATAGGACTCTGG  824

Query  785   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  825   CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  883

Query  845   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  884   GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  943

Query  904   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  944   TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  1003

Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||| ||||| 
Sbjct  1004  ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCTATTGA-  1061

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1062  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1120

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1122  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1150


>gb|KT279452.1| Tetracystis sp. YACCYB32 18S ribosomal RNA gene, partial sequence
          Length=1598

 Score = 1695.5 bits (1879),  Expect = 0E00
 Identities = 1015/1049 (96%), Gaps = 15/1049 (1%)
 Strand = Plus/Plus

Query  66    AATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAG  125
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  1     AATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGG-ATAACCGTAGGAAATCTAGAG  59

Query  126   CTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGC  185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  60    CTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGC  119

Query  186   CGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCG  245
             |||||||||||||| |||||||||||||||||||||||||||||||| ||||| ||||||
Sbjct  120   CGGGCTTGCCCGACTTTAGGCGAATCATGATAACTTCACGAATCGCATGGCCTCGTGCCG  179

Query  246   GCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCA  305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  180   GCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCA  239
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Query  306   TGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  299

Query  366   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  359

Query  426   GTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAA  485
             ||||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||||
Sbjct  360   GTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGCACAATGTAA  419

Query  486   ATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  420   ATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  479

Query  546   CTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGT  605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  480   CTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGA  539

Query  606   GTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGG  665
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  540   GTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTTCACCTTTCTGCTGGGGACGGG  599

Query  666   CTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGT  725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  600   CTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGT  659

Query  726   GTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGC  785
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  660   GTTCAAAGCAAGCCGACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGC  719

Query  786   CTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCG  845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  720   CTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCG  778

Query  846   TATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCAT  904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  779   TATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCAT  838

Query  905   TTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATA  963
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  839   TTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATA  898

Query  964   CCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATT  1021
             ||||||||| | |||| |||||||||||||||||||||||||||| |||||||||||| |
Sbjct  899   CCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-T  956

Query  1022  GACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGC  1076
             ||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | |||
Sbjct  957   GACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGC  1016

Query  1077  AAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             ||||||   |||||| ||| || ||||||
Sbjct  1017  AAGGCTGAAACTTAAAGGAATT-GACGGA  1044


>dbj|AB983625.1| Chlamydopodium starrii gene for 18S rRNA, partial sequence, strain: SAG 16.87
          Length=1744

 Score = 1695.5 bits (1879),  Expect = 0E00
 Identities = 1052/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus
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Query  5      ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22     ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  81

Query  65     AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
              ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  82     AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  140

Query  125    GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
              |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  141    GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  200

Query  185    CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
              |||||||||||||||| |||||||||||||||||||||||| |||||| | ||| ||| |
Sbjct  201    CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGGATCGCATGCCCTCGTGGC  260

Query  245    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261    GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  320

Query  305    ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
              ||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  321    ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGCGCCTGAGAAACG  379

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380    GCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  439

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  440    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  499

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  560    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  619

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| |||||||||||||  |||||||||||||||||| |||| |||||||||||||||| 
Sbjct  620    TGTTGACGCGGTCTGCCATTGGTATGTACTGCGCTCGATGCATCTTTCTGCTGGGGACGA  679

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  680    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  739

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Sbjct  740    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACATGATAGGACTCTGG  799

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  800    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  858

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  859    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  918

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  919    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  978
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Query  963   ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
             |||||||||| | |||| |||||||||||||||||||||||||||| |||||| |||||
Sbjct  979   ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCTATTGA-  1036

Query  1021  TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
             |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1037  TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1095

Query  1076  CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
             |||||||   |||||| ||| || ||||||
Sbjct  1097  CAAGGCTGAAACTTAAAGGAATT-GACGGA  1125


>gb|MG491217.1| Chlorococcum oleofaciens strain CAMU MZ-Ch27 small subunit ribosomal RNA gene,
partial sequence
          Length=1665

 Score = 1692.8 bits (1876),  Expect = 0E00
 Identities = 1039/1089 (95%), Gaps = 16/1089 (1%)
 Strand = Plus/Plus

Query  26    TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTG  60

Query  86    ATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGAGCTAATACATGCGTAAATCCC  145
             ||||||| |  |||| || |||||||||| || |||||||||||||| ||||||||||||
Sbjct  61    ATGGTACTTT-TACTCGG-ATAACCGTAGTAATTCTAGAGCTAATACGTGCGTAAATCCC  118

Query  146   GACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  205
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119   GACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAGCCGGGCTTGCCCGACCTTAGG  178

Query  206   CGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCCGGCGATGTTTCATTCAAATTT  265
             ||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Sbjct  179   CGAATCATGATAACTTCACGAATCGCACGCCCTTGTGGCGGCGATGTTTCATTCAAATTT  238

Query  266   CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   CTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTGGTAACGGGTGACGGA  298

Query  326   GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   GGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGC  358

Query  386   AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   AGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATAC  418

Query  446   TGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTAAATATCTTAACGAGTATCCAT  505
             ||||| |||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  419   TGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTAAATATCTTAACGAGTATCCAT  478

Query  506   TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTTAA  565
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  479   TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAANAGCGTATATTTAA  538

Query  566   GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTGTGTCGACGCGGTCTGCCTCTG  625
             |||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Sbjct  539   GTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATGTGTTGACGCGGTCTGCCTCTG  598

Query  626   GTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGGGCTCCTGGGCTTAACTGCTTG  685
             |||||||||||| ||| |||| |||||||||||||||| |||||||||||||||||  ||
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Sbjct  599   GTATGTACTGCGTTCGATGCATCTTTCTGCTGGGGACGAGCTCCTGGGCTTAACTGTCTG  658

Query  686   GGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCCACGCT  745
             ||||  |||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  659   GGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAGTGTTCAAAGCAAGCCTACGCT  718

Query  746   CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  805
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   CTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGGCCTATCTTGTTGGTCTGTAGG  778

Query  806   ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTCGTATTTCATTGTCAGAGGTGA  865
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  779   ACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTCGTATTTCATTGTCAGAGGTGA  837

Query  866   AATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCATTTGCCAAGGATGTTTTCATT  924
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  838   AATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCATTTGCCAAGGATGTTTTCATT  897

Query  925   GATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGATACCGTCGTAGKCYTCAA-CAT  982
             |||||||||||||||||||||||||| |||||||||||||||||||||| | |||| |||
Sbjct  898   GATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGATACCGTCGTAGTC-TCAACCAT  956

Query  983   AAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGATTGACCCTGCCAGCA-CTTATG  1040
             ||||||||||||||||||||||||| |||||||||||| |||||||||||||| ||||||
Sbjct  957   AAACGATGCCGACTAGGGATTGGCAGGTGTTCCATTGA-TGACCCTGCCAGCACCTTATG  1015

Query  1041  AGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCGCAAGGCT-TGACTTAAGGGAG  1095
             ||||  |||||||||| |||||  |||||| ||  | |||||||||   |||||| |||
Sbjct  1016  AGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAA  1075

Query  1096  TTGGACGGA  1104
             || ||||||
Sbjct  1076  TT-GACGGA  1083


>gb|M84319.1|CAURD18S Characium saccatum 18S ribosomal RNA (18S rDNA) gene
          Length=2233

 Score = 1692.8 bits (1876),  Expect = 0E00
 Identities = 1051/1110 (94%), Gaps = 16/1110 (1%)
 Strand = Plus/Plus

Query  5     ATTAAGSCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  64
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  40    ATTAAGCCATGCATGTCTAAGTATAAACTGCTTATACGGTGAAACTGCGAATGGCTCATT  99

Query  65    AAATCAGTTATAGTTTATTTGATGGTACCTCCTACTTGGTATAACCGTAGGAAATCTAGA  124
             ||||||||||||||||||||||||||||||| |||| || |||||||||| || ||||||
Sbjct  100   AAATCAGTTATAGTTTATTTGATGGTACCTCTTACTCGG-ATAACCGTAGTAATTCTAGA  158

Query  125   GCTAATACATGCGTAAATCCCGACTTCTGGAAGGGACGTATTTATTAGATAAAAGGCCAG  184
             |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  159   GCTAATACGTGCGTAAATCCCGACTTATGGAAGGGACGTATTTATTAGATAAAAGGCCAG  218

Query  185   CCGGGCTTGCCCGACCTTAGGCGAATCATGATAACTTCACGAATCGCACGGCCTTGTGCC  244
             |||||||||||||||| |||||||||||||||||||||||| |||||| | ||| ||| |
Sbjct  219   CCGGGCTTGCCCGACCCTAGGCGAATCATGATAACTTCACGGATCGCATGCCCTCGTGGC  278

Query  245   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  279   GGCGATGTTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGAGGCCTACC  338

Query  305   ATGGTGGTAACGGGTGACGGAGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACG  364
             ||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||
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Sbjct  339    ATGGTGGTAACGGGT-ACGGAGGATTAGGGTTCGATTCCGGAGAGGGNGCCTGAGAAACG  397

Query  365    GCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGT  424
              || |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  398    GCGACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGNAGGT  457

Query  425    AGTGACAATAAATAACAATACTGGGCGTTTACGTCTGGTAATTGGAATGAGAACAATGTA  484
              |||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Sbjct  458    AGTGACAATAAATAACAATACTGGGCATTTATGTCTGGTAATTGGAATGAGTACAATGTA  517

Query  485    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  518    AATATCTTAACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  577

Query  545    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGGTG  604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  578    GCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGATG  637

Query  605    TGTCGACGCGGTCTGCCTCTGGTATGTACTGCGCTCGGTGCACCTTTCTGCTGGGGACGG  664
              ||| |||||||||||||  |||||||||||||||||| |||| ||||||||||||||||
Sbjct  638    TGTTGACGCGGTCTGCCATTGGTATGTACTGCGCTCGATGCATCTTTCTGCTGGGGACGA  697

Query  665    GCTCCTGGGCTTAACTGCTTGGGACCTGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  724
              |||||||||||||||||  ||||||  |||||||||||||||||||||||||||||||||
Sbjct  698    GCTCCTGGGCTTAACTGTCTGGGACTCGGAATCAGCGAAGTGACCTTGAGCAAACAAGAG  757

Query  725    TGTTCAAAGCAAGCCCACGCTCTGAATTTTTTAGCATGGAATCACACGATAGGACTCTGG  784
              ||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  758    TGTTCAAAGCAAGCCTACGCTCTGAATTTTTTAGCATGGAATCACATGATAGGACTCTGG  817

Query  785    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCATTTC  844
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  818    CCTATCTTGTTGGTCTGTAGGACCGGAGTAATGATTAAGAGGGACAGTCGGGGGCA-TTC  876

Query  845    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCG-AAGCA  903
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  877    GTATTTCATTGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACTTCTGCGAAAGCA  936

Query  904    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCG-AGACGATTAGAT  962
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  937    TTTGCCAAGGATGTTTTCATTGATCAAGAACGAAAGTTGGGGGCTCGAAGACGATTAGAT  996

Query  963    ACCGTCGTAGKCYTCAA-CATAAACGATGCCGACTAGGGATTGGCA-GTGTTCCATTGAT  1020
              |||||||||| | |||| |||||||||||||||||||||||||||| |||||| |||||
Sbjct  997    ACCGTCGTAGTC-TCAACCATAAACGATGCCGACTAGGGATTGGCAGGTGTTCTATTGA-  1054

Query  1021   TGACCCTGCCAGCA-CTTATGAGAATYCAAAGTTTTT-GGTTC--GGGGGA-TAWTGCCG  1075
              |||||||||||||| ||||||||||  |||||||||| |||||  |||||| ||  | ||
Sbjct  1055   TGACCCTGCCAGCACCTTATGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCG  1113

Query  1076   CAAGGCT-TGACTTAAGGGAGTTGGACGGA  1104
              |||||||   |||||| ||| || ||||||
Sbjct  1115   CAAGGCTGAAACTTAAAGGAATT-GACGGA  1143
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