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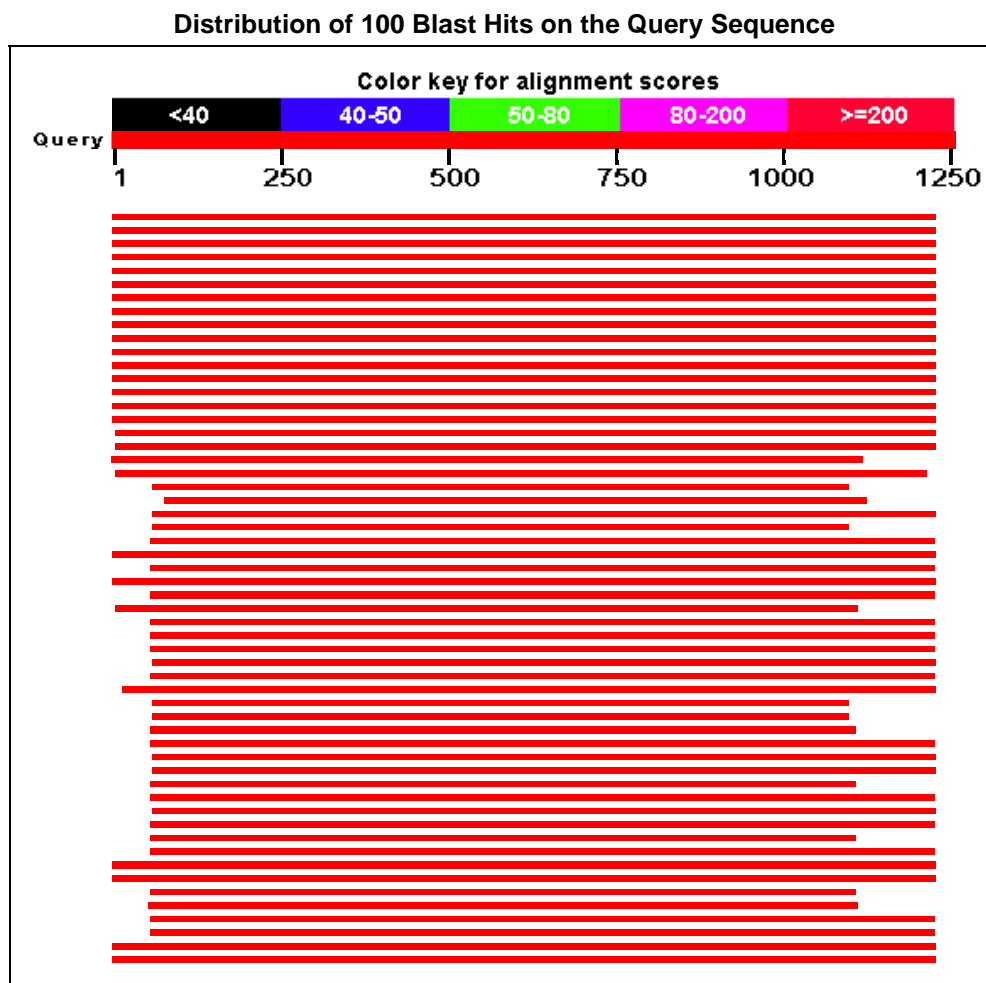
Nucleotide Sequence (1253 letters)

RID [ZE156ZPY015](#) (Expires on 09-16 01:32 am)

Query ID lcl|Query_79857
Description None
Molecule type nucleic acid
Query Length 1253

Database Name rRNA_typestrains/prokaryotic_16S_riboso
Description 16S ribosomal RNA (Bacteria and Archaea)
Program BLASTN 2.2.32+

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Dyadobacter koreensis strain NBRC 101116 16S ribosomal RNA gene, partial sequence	1873	1873	97%	0.0	95%	NR_113977.1
Dyadobacter koreensis strain KCTC 12537 16S ribosomal RNA gene, partial sequence	1873	1873	97%	0.0	95%	NR_044041.1
Dyadobacter psychrophilus strain BZ26 16S ribosomal RNA gene, partial sequence	1868	1868	97%	0.0	95%	NR_117212.1
Dyadobacter ginsengisoli strain Gsoil 043 16S ribosomal RNA gene, partial sequence	1838	1838	97%	0.0	94%	NR_041372.1
Dyadobacter hamtensis strain HHS 11 16S ribosomal RNA gene, partial sequence	1838	1838	97%	0.0	94%	NR_042226.1
Dyadobacter jejuensis strain AM1R11 16S ribosomal RNA gene, partial sequence	1825	1825	97%	0.0	94%	NR_109488.1
Dyadobacter fermentans strain NS114 16S ribosomal RNA gene, partial sequence	1794	1794	97%	0.0	94%	NR_027533.1
Dyadobacter alkalitolerans strain 12116 16S ribosomal RNA gene, partial sequence	1790	1790	97%	0.0	93%	NR_044476.1
Dyadobacter soli strain MJ20 16S ribosomal RNA gene, partial sequence	1788	1788	97%	0.0	93%	NR_117263.1
Dyadobacter tibetensis strain Y620-1 16S ribosomal RNA gene, partial sequence	1777	1777	97%	0.0	93%	NR_109648.1
Dyadobacter fermentans strain NS114 16S ribosomal RNA gene, complete sequence	1777	1777	97%	0.0	93%	NR_074368.1
Dyadobacter arcticus strain R-S7-29 16S ribosomal RNA gene, partial sequence	1757	1757	97%	0.0	93%	NR_109479.1
Dyadobacter crusticola strain CP183-8 16S ribosomal RNA gene, partial sequence	1744	1744	97%	0.0	93%	NR_042335.1
Dyadobacter beijingensis strain A54 16S ribosomal RNA gene, partial sequence	1705	1705	97%	0.0	92%	NR_043725.1
Persicitalea jodogahamensis strain NBRC 103568 16S ribosomal RNA gene, partial sequence	1225	1225	97%	0.0	85%	NR_114246.1
Persicitalea jodogahamensis strain Shu-9-SY12-35C 16S ribosomal RNA gene, partial sequence	1225	1225	97%	0.0	85%	NR_041525.1
Runella slithyformis strain DSM 19594 16S ribosomal RNA gene, complete sequence	1155	1155	97%	0.0	84%	NR_074339.1
Runella slithyformis strain ATCC 29530 16S ribosomal RNA gene,	1129	1129	97%	0.0	84%	NR_044735.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
complete sequence						
Imperialibacter roseus strain P4 16S ribosomal RNA, partial sequence	1125	1125	89%	0.0	85%	NR_132295.1
Runella defluvii strain EMB13 16S ribosomal RNA gene, partial sequence	1123	1123	96%	0.0	84%	NR_043766.1
Larkinella insperata strain LMG 22510 16S ribosomal RNA gene, complete sequence	1110	1110	82%	0.0	86%	NR_042402.1
Siphonobacter aquaeclarae strain P2 16S ribosomal RNA gene, partial sequence	1109	1109	83%	0.0	86%	NR_116562.1
Mongoliitalea lutea strain MIM18 16S ribosomal RNA gene, partial sequence	1105	1105	92%	0.0	84%	NR_122086.1
Larkinella arboricola strain Z0532 16S ribosomal RNA gene, partial sequence	1094	1094	82%	0.0	86%	NR_116968.1
Arcicella aurantiaca strain TNR-18 16S ribosomal RNA gene, partial sequence	1088	1088	92%	0.0	84%	NR_116735.1
Algoriphagus faecimaris strain LYX05 16S ribosomal RNA gene, partial sequence	1088	1088	97%	0.0	83%	NR_108679.1
Arcicella aquatica strain NO-502 16S ribosomal RNA gene, partial sequence	1088	1088	92%	0.0	84%	NR_029000.1
Algoriphagus hitonicola strain 7-UAH 16S ribosomal RNA gene, partial sequence	1085	1085	97%	0.0	83%	NR_044249.1
Runella limosa strain EMB111 16S ribosomal RNA gene, partial sequence	1085	1085	92%	0.0	84%	NR_043771.1
Runella zeae strain NS12 16S ribosomal RNA gene, partial sequence	1085	1085	87%	0.0	85%	NR_025004.1
Algoriphagus boritolerans strain T-22 16S ribosomal RNA gene, partial sequence	1083	1083	92%	0.0	84%	NR_041271.1
Algoriphagus boritolerans strain NBRC 101277 16S ribosomal RNA gene, partial sequence	1079	1079	92%	0.0	84%	NR_113997.1
Flectobacillus roseus strain GFA-11 16S ribosomal RNA gene, partial sequence	1079	1079	92%	0.0	84%	NR_116312.1
Arcicella rigui strain NSW-5 16S ribosomal RNA gene, partial sequence	1072	1072	92%	0.0	84%	NR_108997.1
Arcicella rosea strain TW5 16S ribosomal RNA gene, partial sequence	1072	1072	92%	0.0	84%	NR_042707.1
Flectobacillus lacus strain CL-GP79 16S ribosomal RNA gene, partial sequence	1064	1064	96%	0.0	83%	NR_043554.1
Larkinella bovis strain NBRC 106324 16S ribosomal RNA gene, partial sequence	1061	1061	82%	0.0	85%	NR_114299.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Larkinella bovis strain M2T2B15 16S ribosomal RNA gene, partial sequence	1061	1061	82%	0.0	85%	NR_117267.1
Algoriphagus lutimaris strain S1-3 16S ribosomal RNA gene, partial sequence	1061	1061	83%	0.0	85%	NR_104489.1
Algoriphagus alkaliphilus strain AC-74 16S ribosomal RNA gene, complete sequence	1059	1059	92%	0.0	84%	NR_042278.1
Marinoscillum furvescens strain NBRC 15994 16S ribosomal RNA gene, partial sequence	1051	1051	92%	0.0	83%	NR_113833.1
Marinoscillum furvescens strain NBRC 15994 16S ribosomal RNA gene, partial sequence	1051	1051	92%	0.0	83%	NR_040920.1
Algoriphagus halophilus strain JC2051 16S ribosomal RNA gene, partial sequence	1050	1050	83%	0.0	85%	NR_025744.1
Algoriphagus terrigena strain DS-44 16S ribosomal RNA gene, partial sequence	1046	1046	92%	0.0	83%	NR_043616.1
Pseudarcicella hirudinis strain E92 16S ribosomal RNA gene, partial sequence	1042	1042	92%	0.0	83%	NR_108865.1
Belliella pelovolcani strain CC-SAL-25 16S ribosomal RNA gene, partial sequence	1042	1042	92%	0.0	83%	NR_116416.1
Algoriphagus zhangzhouensis strain 12C11 16S ribosomal RNA gene, partial sequence	1038	1038	83%	0.0	85%	NR_109472.1
Algoriphagus taeaanensis strain HMC4223 16S ribosomal RNA gene, partial sequence	1038	1038	92%	0.0	83%	NR_125540.1
Cytophaga hutchinsonii strain ATCC 33406 16S ribosomal RNA gene, complete sequence	1033	1033	97%	0.0	82%	NR_102866.1
Cytophaga hutchinsonii strain NBRC 15051 16S ribosomal RNA gene, partial sequence	1033	1033	97%	0.0	82%	NR_112977.1
Algoriphagus ornithinivorans strain JC2052 16S ribosomal RNA gene, partial sequence	1033	1033	83%	0.0	85%	NR_025745.1
Sporocytophaga myxococcoides strain DSM 11118 16S ribosomal RNA gene, partial sequence	1031	1031	83%	0.0	85%	NR_025463.1
Algoriphagus jejuensis strain CNU040 16S ribosomal RNA gene, partial sequence	1027	1027	92%	0.0	83%	NR_108184.1
Marinoscillum luteum strain SJP7 16S ribosomal RNA gene, partial sequence	1026	1026	92%	0.0	83%	NR_108992.1
Belliella baltica strain DSM 15883 16S ribosomal RNA gene, complete sequence	1024	1024	97%	0.0	82%	NR_102864.1
Nafulsella turpanensis strain ZLM-10 16S ribosomal RNA gene, partial sequence	1024	1024	97%	0.0	82%	NR_118330.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Algoriphagus aquaeductus strain T4 16S ribosomal RNA gene, partial sequence	1024	1024	83%	0.0	85%	NR_116214.1
Algoriphagus mannitolivorans strain JC2050 16S ribosomal RNA gene, partial sequence	1024	1024	83%	0.0	85%	NR_025743.1
Belliella baltica strain BA134 16S ribosomal RNA gene, partial sequence	1024	1024	97%	0.0	82%	NR_025599.1
Algoriphagus chungangensis strain CAU 1002 16S ribosomal RNA gene, partial sequence	1022	1022	83%	0.0	85%	NR_109527.1
Pedobacter terrae strain DS-57 16S ribosomal RNA gene, partial sequence	1020	1020	95%	0.0	83%	NR_044005.1
Algoriphagus shivajiensis strain NIO-S3 16S ribosomal RNA gene, partial sequence	1018	1018	83%	0.0	84%	NR_117207.1
Rhodocytophaga aerolata strain 5416T-29 16S ribosomal RNA gene, partial sequence	1018	1018	97%	0.0	82%	NR_116118.1
Roseivirga echinicomitans strain KMM 6058 16S ribosomal RNA gene, partial sequence	1018	1018	90%	0.0	83%	NR_043168.1
Algoriphagus machipongonensis strain PR1 16S ribosomal RNA gene, complete sequence	1016	1016	83%	0.0	85%	NR_121685.1
Algoriphagus boseongensis strain BS-R1 16S ribosomal RNA gene, partial sequence	1016	1016	83%	0.0	84%	NR_118640.1
Algoriphagus namhaensis strain DPG-3 16S ribosomal RNA gene, partial sequence	1014	1014	84%	0.0	84%	NR_109104.1
Algoriphagus marincola strain SW-2 16S ribosomal RNA gene, partial sequence	1014	1014	83%	0.0	84%	NR_025808.1
Flexibacter ruber strain NBRC 16677 16S ribosomal RNA gene, partial sequence	1013	1013	91%	0.0	83%	NR_113860.1
Algoriphagus aquatilis strain NBRC 104237 16S ribosomal RNA gene, partial sequence	1013	1013	83%	0.0	84%	NR_114262.1
Algoriphagus aquatilis strain A8-7 16S ribosomal RNA gene, partial sequence	1013	1013	83%	0.0	84%	NR_044462.1
Flexibacter ruber strain IFO 16677 16S ribosomal RNA gene, partial sequence	1013	1013	91%	0.0	83%	NR_040916.1
Spirosoma linguale strain DSM 74 16S ribosomal RNA gene, complete sequence	1011	1011	83%	0.0	84%	NR_074369.1
Cecembia lonarensis strain LW9 16S ribosomal RNA gene, partial sequence	1011	1011	92%	0.0	83%	NR_116971.1
Spirosoma spitsbergense strain SPM-9 16S ribosomal RNA gene, partial sequence	1011	1011	93%	0.0	83%	NR_044220.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pedobacter koreensis strain WPCB189 16S ribosomal RNA gene, partial sequence	1009	1009	95%	0.0	82%	NR_043538.1
Pedobacter ginsengisoli strain Gsoil 104 16S ribosomal RNA gene, partial sequence	1009	1009	88%	0.0	83%	NR_041374.1
Flectobacillus major strain ATCC 29496 16S ribosomal RNA gene, complete sequence	1007	1007	91%	0.0	83%	NR_044736.2
Algoriphagus olei strain CC-Hsuan-617 16S ribosomal RNA gene, partial sequence	1007	1007	92%	0.0	83%	NR_116592.1
Spirosoma linguale strain DSM 74 16S ribosomal RNA gene, complete sequence	1007	1007	83%	0.0	84%	NR_042403.1
Rhodonellum psychrophilum strain GCM71 16S ribosomal RNA gene, partial sequence	1005	1005	97%	0.0	82%	NR_043556.1
Pedobacter koreensis strain NBRC 101153 16S ribosomal RNA gene, partial sequence	1003	1003	95%	0.0	82%	NR_113980.1
Algoriphagus vanfongensis strain KMM 6241 16S ribosomal RNA gene, partial sequence	1003	1003	83%	0.0	84%	NR_044196.1
Pedobacter rhizosphaerae strain 01-96 16S ribosomal RNA gene, partial sequence	1003	1003	95%	0.0	82%	NR_122096.1
Pedobacter suwonensis strain 15-52 16S ribosomal RNA gene, partial sequence	1003	1003	95%	0.0	82%	NR_043543.1
Roseivirga spongicola strain UST030701-084 16S ribosomal RNA gene, partial sequence	1003	1003	87%	0.0	84%	NR_043531.1
Algoriphagus yeomjeoni strain MSS-160 16S ribosomal RNA gene, partial sequence	1003	1003	97%	0.0	82%	NR_043131.1
Flexibacter flexilis strain NBRC 15060 16S ribosomal RNA gene, partial sequence	1002	1002	83%	0.0	84%	NR_113726.1
Algoriphagus antarcticus strain LMG 21980 16S ribosomal RNA gene, partial sequence	1002	1002	92%	0.0	83%	NR_025604.1
Roseivirga ehrenbergii strain KMM 6017 16S ribosomal RNA gene, partial sequence	1002	1002	90%	0.0	83%	NR_025825.1
Flexibacter flexilis strain IFO 15060 16S ribosomal RNA gene, partial sequence	1002	1002	83%	0.0	84%	NR_112181.1
Pedobacter oryzae strain N7 16S ribosomal RNA gene, partial sequence	998	998	88%	0.0	83%	NR_116174.1
Algoriphagus winogradskyi strain LMG 21969 16S ribosomal RNA gene, partial sequence	996	996	97%	0.0	82%	NR_025601.1
Marivirga tractuosa strain DSM 4126 16S ribosomal RNA gene, complete sequence	994	994	94%	0.0	82%	NR_074493.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Spirosoma luteum strain SPM-10 16S ribosomal RNA gene, partial sequence	994	994	92%	0.0	83%	NR_044221.1
Marivirga tractuosa strain IFO 15989 16S ribosomal RNA gene, partial sequence	994	994	94%	0.0	82%	NR_040918.1
Pedobacter sandarakinus strain DS-27 16S ribosomal RNA gene, partial sequence	992	992	95%	0.0	82%	NR_043665.1
Algoriphagus aquimarinus strain LMG 21971 16S ribosomal RNA gene, partial sequence	990	990	85%	0.0	84%	NR_025602.1
Leadbetterella byssophila strain DSM 17132 16S ribosomal RNA gene, complete sequence	989	989	86%	0.0	83%	NR_074303.1
Fontibacter ferrireducens strain SgZ-2 16S ribosomal RNA gene, partial sequence	989	989	97%	0.0	82%	NR_109591.1

Alignments

Dyadobacter koreensis strain NBRC 101116 16S ribosomal RNA gene, partial sequence

Sequence ID: [ref|NR_113977.1|](#) Length: 1433 Number of Matches: 1

Range 1: 106 to 1301

Score	Expect	Identities	Gaps	Strand	Frame
1873 bits(1014)	0.0()	1158/1223(95%)	28/1223(2%)	Plus/Plus	
Features:					
Query 1		GCCCGGGGAAACCCGGATTAATACCGCATAACACAGGGGTCCCGCATGGGTACTATTTGT			60
Sbjct 106		GCCCGGGGAAACCCGGATTAATACCGCATAATACAGGGGTGCCACCT-GGTACTATTTGT			164
Query 61		TAAAGATTTTATCGGTGGTAGATGGGCATGCGTTCGATTAGCTAGTTGGTATAGGTAACGG			120
Sbjct 165		TAAAGATTTTATTGGTTGAAGATGGGCATGCGTTCGATTAGCTAGTTGG-CGGGGTAACGG			223
Query 121		CTTACCAAGGCTACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			180
Sbjct 224		CCCACCAAGGCGACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			283
Query 181		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			240
Sbjct 284		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			343
Query 241		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			300
Sbjct 344		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			403
Query 301		GGAAGAAGAGCAGGGATGCGTCCTTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC			360
Sbjct 404		GGAAGAAGAGCAGGGATGCGTCCTTGTGTGACGGTACTGAATGAATAAGCACCGGCTAAC			463
Query 361		TCCGTGCCAGCAGCCGCGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT			420
Sbjct 464		TCCGTGCCAGCAGCCGCGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT			523
Query 421		AAAGGGTGCGTAGGTGGCTTGTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			480
Sbjct 524		AAAGGGTGCGTAGGTGGCTAATTAAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			583
Query 481		TGCCATTGATACTGACAAGCTTGAACAAGTGAGGCTGCCGGAATGGATGGTGTAGCGG			540
Sbjct 584		TGCCATTGATACTGATTAGCTTGAACAAGTGAGGCTGCCGGAATGGATGGTGTAGCGG			643
Query 541		TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT			600
Sbjct 644		TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT			703
Query 601		GACACTGAGGCACGAAAGCATGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCATGCC			660

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Sbjct  704      GACACTGAGGCACGAAAGCATGGGGAGCAAACAGGATTAGATACCCCTGGTAGTCCATGCC      763
Query  661      GTAAACGATGAGGACTCGCTGTTGGCCTGTCAAGGGTCAGCGGCTTAGGGAAACCGTTAA      720
Sbjct  764      GTAAACGATGAGGACTCGCTGTTGGGCTGTCACGGCTCAGCGGCTTAGGGAAACCGTTAA      823
Query  721      GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG      780
Sbjct  824      GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG      883
Query  781      CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA      840
Sbjct  884      CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA      943
Query  841      ATCACCACAGGAATCATTAGAAATGGGTGATCCAGCAATGGCTTGTT-TGAAGGTGCTG      899
Sbjct  944      ATCACAATAGACGT-ATTAGAAATGGGTATTCCAGCAATGGCT-GTTGTGAAGGTGCTG      1001
Query  900      CATGGCTGTCGTCAGCTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC      959
Sbjct  1002     CATGGCTGTCGTCAGCTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC      1061
Query  960      CCTATGGTTAGTTGCCAGCACGTAATGGTGGGGGACTCTAATCAGACTGCCTGTGCACAC      1019
Sbjct  1062     CCTATGGTTAGTTGCCAGCACGTAATGGT-GGGGACTCTAATCAGACTGCCTGTGCAAAC      1120
Query  1020     AAGAGAGGAAGGAGGGGACGACGTCAGTCATCATGGGCCCTTTACGTCCAGGGCCAACA      1079
Sbjct  1121     -AGAGAGGAAGGAGGGGACGACGTCAGTCATCATGG-CCCTT-ACGTCCAGGGC-AACA      1176
Query  1080     CAACGTGCTTACAATGGGCGGGTACAGAAAGGGTTAGCTACCTCCACCGATGAGAATGCCA      1139
Sbjct  1177     CA-CGTGCT-ACAATGGGCGG-TACAGA-GGGTC-GCTAC-TC-AGTGATGAG-ATGCCA      1228
Query  1140     ATCCCAAAAAAGCCGTTCTCCAGTTCCGAATTGGAATCCTGCACCTCGACTCCTATGGAA      1199
Sbjct  1229     ATCCCAAAAAAGCCGTTCTC--AGTTCGGA-TTGGAGT-CTGCAACTCGACTC-TATG-AA      1282
Query  1200     GACTGGGAATCCCTTAGATAATC      1222
Sbjct  1283     G-CTGG-AATCGCT-AG-TAATC      1301

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Dyadobacter koreensis strain KCTC 12537 16S ribosomal RNA gene, partial sequence

Sequence ID: [ref|NR_044041.1|](#) Length: 1412 Number of Matches: 1

Range 1: 103 to 1298

Score	Expect	Identities	Gaps	Strand	Frame
1873 bits(1014)	0.0()	1158/1223(95%)	28/1223(2%)	Plus/Plus	
Features:					
Query 1		GCCCGGGGAAACCCGGATTAATACCGCATAACACAGGGGTCCCGCATGGGTACTATTTGT			60
Sbjct 103		GCCCGGGGAAACCCGGATTAATACCGCATAATACAGGGGTGCCACCT-GGTACTATTTGT			161
Query 61		TAAAGATTTATCGGTGGTAGATGGGCATGCGTTCGATTAGCTAGTTGGTATAGGTAACGG			120
Sbjct 162		TAAAGATTTATTGGTTGAAGATGGGCATGCGTTCGATTAGCTAGTTGG-CGGGGTAACGG			220
Query 121		CTTACCAAGGCTACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			180
Sbjct 221		CCCACCAAGGCGACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			280
Query 181		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			240
Sbjct 281		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			340
Query 241		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			300
Sbjct 341		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			400
Query 301		GGAAGAAGAGCAGGGATGCGTCTCTTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC			360
Sbjct 401		GGAAGAAGAGCAGGGATGCGTCTCTTGTGTGACGGTACTGAATGAATAAGCACCGGCTAAC			460
Query 361		TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAGCGTTGTCCGGATTATTGGGTTT			420
Sbjct 461		TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAGCGTTGTCCGGATTATTGGGTTT			520
Query 421		AAAGGGTGCCTAGGTGGCTTGTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			480
Sbjct 521		AAAGGGTGCCTAGGTGGCTAATTAAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			580
Query 481		TGCCATTGATACTGACAAGCTTGAAACAAGTGGAGGCTGCCGGAATGGATGGTGTAGCGG			540
Sbjct 581		TGCCATTGATACTGATTAGCTTGAAACAAGTGGAGGCTGCCGGAATGGATGGTGTAGCGG			640
Query 541		TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATT			600

Sbjct	641	TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT	700
Query	601	GACACTGAGGCACGAAAGCATGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCATGCC	660
Sbjct	701	GACACTGAGGCACGAAAGCATGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCATGCC	760
Query	661	GTAACGATGAGGACTCGCTGTTGGCCTGTCAAGGGTCAGCGGCTTAGGGAAACCGTTAA	720
Sbjct	761	GTAACGATGAGGACTCGCTGTTGGGCTGTCACGGCTCAGCGGCTTAGGGAAACCGTTAA	820
Query	721	GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG	780
Sbjct	821	GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG	880
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Sbjct	881	CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA	940
Query	841	ATCACCACAGGAATCATTCAGAAATGGGTGATCCAGCAATGGCTTGTT-TGAAGGTGCTG	899
Sbjct	941	ATCACAATAGACGT-ATTCAGAAATGGGTATTCCAGCAATGGCT-GTTGTGAAGGTGCTG	998
Query	900	CATGGCTGTCGTCAGCTCGTGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC	959
Sbjct	999	CATGGCTGTCGTCAGCTCGTGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC	1058
Query	960	CCTATGGTTAGTTGCCAGCACGTAATGGTGGGGACTCTAATCAGACTGCCTGTGCACAC	1019
Sbjct	1059	CCTATGGTTAGTTGCCAGCACGTAATGGT-GGGGACTCTAATCAGACTGCCTGTGCAAAAC	1117
Query	1020	AAGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGGGCCCTTTACGTCCAGGGCCAACA	1079
Sbjct	1118	-AGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGG-CCCTT-ACGTCCAGGGC-AACA	1173
Query	1080	CAACGTGCTTACAATGGGCGGTACAGAAGGGTTAGCTACCTCCACCGATGAGAATGCCA	1139
Sbjct	1174	CA-CGTGCT-ACAATGGGCGG-TACAGA-GGGTC-GCTAC-TC-AGTGATGAG-ATGCCA	1225
Query	1140	ATCCCAAAAAGCCGTTCTCCAGTTCCGAATTGGAATCCTGCACCTCGACTCCTATGGAA	1199
Sbjct	1226	ATCCCAAAAAGCCGTTCTC--AGTTCGGA-TTGAGT-CTGCAACTCGACTC-TATG-AA	1279
Query	1200	GACTGGGAATCCCTTAGATAATC	1222
Sbjct	1280	G-CTGG-AATCGCT-AG-TAATC	1298

Dyadobacter psychrophilus strain BZ26 16S ribosomal RNA gene, partial sequence

Sequence ID: [ref|NR_117212.1|](#) Length: 1501 Number of Matches: 1

Range 1: 126 to 1322

Score	Expect	Identities	Gaps	Strand	Frame
1868 bits(1011)	0.0()	1157/1223(95%)	27/1223(2%)	Plus/Plus	
Features:					
Query	1	GCCCGGGGAAACCCGGATTAATACCGCATAACACAGGGGTCCCGCATGGGTACTATTTGT			60
Sbjct	126	GCCCGGGGAAACCCGGATTAATACCGCATAACACAGGGGTACAGCAT-TGTACTATTTGT			184
Query	61	TAAAGATTTATCGGTGGTAGATGGGCATGCGTTCGATTAGCTAGTTGGTATAGGTAACGG			120
Sbjct	185	TAAAGATTTATTGGTTGAAGATGGGCATGCGTTCGATTAGCTAGTTGGTATGGGTAACGG			244
Query	121	CTTACCAAGGCTACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			180
Sbjct	245	CCTACCAAGGCGACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			304
Query	181	ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			240
Sbjct	305	ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			364
Query	241	TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			300
Sbjct	365	TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			424
Query	301	GGAAGAAGAGCAGGGATGCGTCCTTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC			360
Sbjct	425	GGAAGAAGAGCAGGGATGCGTCCTTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC			484
Query	361	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT			420
Sbjct	485	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT			544
Query	421	AAAGGGTGCGTAGGTGGCTTGTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			480
Sbjct	545	AAAGGGTGCGTAGGTGGCTATTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG			604

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Query 481  TGCCATTGATACTGACAAGCTTGAAACAAGTGGAGGCTGCCGGAATGGATGGTGTAGCGG 540
Sbjct 605  TGCCATTGATACTGAATAGCTTGAAAGAATTGGAGGCTGCCGGAATGGATGGTGTAGCGG 664
Query 541  TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT 600
Sbjct 665  TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGATTTATTT 724
Query 601  GACACTGAGGCACGAAAGCATGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCATGCC 660
Sbjct 725  GACACTGAGGCACGAAAGCATGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCATGCC 784
Query 661  GTAAACGATGAGGACTCGCTGTTGGCCTGTCAAGGGTCAGCGGCTTAGGGAAACCGTTAA 720
Sbjct 785  GTAAACGATGAGGACTCGCTGTTGGCCTGTCAAGGGTCAGCGGCTTAGGGAAACCGTTAA 844
Query 721  GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG 780
Sbjct 845  GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG 904
Query 781  CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA 840
Sbjct 905  CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA 964
Query 841  ATCACCACAGGAATCATTCAGAAATGGGTGATCCAGCAATGGCTTGTT-TGAAGGTGCTG 899
Sbjct 965  ATCACAATA-GAATTGCGCAGAAATGTGTAAAGCCAGCAATGGCT-GTTGTGAAGGTGCTG 1022
Query 900  CATGGCTGTCGTCAGCTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC 959
Sbjct 1023  CATGGCTGTCGTCAGCTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC 1082
Query 960  CCTATGGTTAGTTGCCAGCACGTAATGGTGGGGACTCTAATCAGACTGCCTGTGCACAC 1019
Sbjct 1083  CCTATGGTTAGTTGCCAGCACGTAATGGT-GGGGACTCTAGCCAGACTGCCTGTGCAAAC 1141
Query 1020  AAGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGGGCCCTTTACGTCCAGGGCCAACA 1079
Sbjct 1142  -AGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGG-CCCTT-ACGTCCAGGGC-AACA 1197
Query 1080  CAACGTGCTTACAATGGGCGGGTACAGAAGGGTTAGCTACCTCCACCGATGAGAATGCCA 1139
Sbjct 1198  CA-CGTGCT-ACAATGGGCGG-TACAGA-GGGT-AGCTACA-C-AGTGATGTG-ATGCCA 1249
Query 1140  ATCCCAAAAAGCCGTTCTCCAGTTCGGAATTGGAATCCTGCACCTCGACTCCTATGGAA 1199
Sbjct 1250  ATCCCAAAAAGCCGTTCTC--AGTTTCGGA-TTGAGT-CTGCAACTCGACTC-TATG-AA 1303
Query 1200  GACTGGGAATCCCTTAGATAATC 1222
Sbjct 1304  G-CTGG-AATCGCT-AG-TAATC 1322

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Dyadobacter ginsengisoli strain Gsoil 043 16S ribosomal RNA gene, partial sequence

Sequence ID: [ref|NR_041372.1|](#) Length: 1451 Number of Matches: 1

Range 1: 114 to 1308

Score	Expect	Identities	Gaps	Strand	Frame
1838 bits(995)	0.0()	1155/1226(94%)	35/1226(2%)	Plus/Plus	
Features:					
Query 1	GCCCCGGGAAACCCGGATTAATACCGCATAACACAGGGGTCCCGCATGGGTACTATTTGT	60			
Sbjct 114	GCCCCGGGAAACCCGGATTAATACCGCATAATACAGGGGGCCACATGGGT-CTATTTGT	172			
Query 61	TAAAGATTTATCGGTGGTAGATGGGCATGCGTTCGATTAGCTAGTTGGTATAGGTAACGG	120			
Sbjct 173	TAAAGATTTATCGGTGGTAGATGGGCATGCGTTCGATTAGCTAGTTGGCA-GGGTAACGG	231			
Query 121	CTTACCAAGGCTACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG	180			
Sbjct 232	CCTACCAAGGCGACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG	291			
Query 181	ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC	240			
Sbjct 292	ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC	351			
Query 241	TGACCCAGCCATGCCCGGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG	300			
Sbjct 352	TGACCCAGCCATGCCCGGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG	411			
Query 301	GGAAGAAGAGCAGGGATGCGTCCCTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC	360			
Sbjct 412	GGAAGAAGAGCAGGGATGCGTCCCTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC	471			
Query 361	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT	420			
Sbjct 472	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT	531			

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Query 421  AAAGGGTGCCTAGGTGGCTTGTTAAGTCAGTGGTGAATACAGCCGCTCAACGGTTGAGG 480
Sbjct 532  AAAGGGTGCCTAGGTGGCTAATTAAAGTCAGTGGTGAATACAGCCGCTCAACGGTTGAGG 591
Query 481  TGCCATTGATACTGACAAGCTTGAAACAAGTGGAGGCTGCCGAATGGATGGTGTAGCGG 540
Sbjct 592  TGCCATTGATACTGACTAGCTTGAAATAATTGGAGGCTGCCGAATGGATGGTGTAGCGG 651
Query 541  TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACG-TTTGATT 599
Sbjct 652  TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGATTG-TT 710
Query 600  TGACACTGAGGCACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGC 659
Sbjct 711  TGACACTGAGGCACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGC 770
Query 660  CGTAAACGATGAGGACTCGCTGTTGGCCTG-TCAAGGGTCAGCGGCTTAGGGAAACCGTT 718
Sbjct 771  TGTAAACGATGAGGACTCGCTGTTGG--TGTTACGCATCAGCGGCTTAGGGAAACCGTT 828
Query 719  AAGTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTC 778
Sbjct 829  AAGTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTC 888
Query 779  CGCACAAGCGGTGGAGCATGTGGTTTAATTTCGATGATACGCGAGGAACCTTACCTGGGCT 838
Sbjct 889  CGCACAAGCGGTGGAGCATGTGGTTTAATTTCGATGATACGCGAGGAACCTTACCTGGGCT 948
Query 839  AAATCACCACAGGAATCATTTCAGAAATGGGTGATCCAGCAATGG-CT-TGTTTGAAGGTG 896
Sbjct 949  AAATCA-CAGAGGAATTATGCAGAAATGTGTAAGCTAGCAATAGTCTCTG--TGAAGGTG 1005
Query 897  CTGCATGGCTGTCTGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCAGCAACGAGCGCA 956
Sbjct 1006  CTGCATGGCTGTCTGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCAGCAACGAGCGCA 1065
Query 957  ACCCCTATGGTTAGTTGCCAGCACGTAATGGTGGGGGACTCTAATCAGACTGCCTGTGCA 1016
Sbjct 1066  ACCCCTATGGTTAGTTGCCAGCACGTAATGGT-GGGGACTCTAGCCAGACTGCCTGTGCA 1124
Query 1017  CACAAGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGGGCCCTTTACGTCCAGGGCCA 1076
Sbjct 1125  AAC-AGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGG-CCCTT-ACGTCCAGGGC-A 1180
Query 1077  ACACAACGTGCTTACAATGGGCGGGTACAGAAGGGTTAGCTACCTCCACCGATGAGAATG 1136
Sbjct 1181  ACACA-CGTGCT-ACAATGGGCGG-TACAGA-GGGT-AGCTACA-C-AGCGATGTG-ATG 1232
Query 1137  CCAATCCCAAAAAGCCGTTCTCCAGTTCGAATTTGAATCCTGCACCTCGACTCCTATG 1196
Sbjct 1233  CCAATCCCAAAAAGCCGTTCTC--AGTTCGGA-TTGGAGT-CTGCAACTCGACTC-TATG 1287
Query 1197  GAAGACTGGGAATCCCTTAGATAATC 1222
Sbjct 1288  -AAG-CTGG-AATCGCT-AG-TAATC 1308

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Dyadobacter hamtensis strain HHS 11 16S ribosomal RNA gene, partial sequence

Sequence ID: [ref|NR_042226.1|](#) Length: 1446 Number of Matches: 1

Range 1: 114 to 1308

Score	Expect	Identities	Gaps	Strand	Frame
1838 bits(995)	0.0()	1152/1223(94%)	29/1223(2%)	Plus/Plus	
Features:					
Query 1		GCCCGGGGAAACCCGGATTAATACCGCATAACACAGGGGTCCCGCATGGGTACTATTTGT			60
Sbjct 114		GCCCGGGGAAACCCGGATTAATACCGCATAATACATTTGGGCCACCT-GGTTTGATTTGT			172
Query 61		TAAAGATTTTATCGGTGGTAGATGGGCATGCGTTTCGATTAGCTAGTTGGTATAGGTAACGG			120
Sbjct 173		TAAAGATTTATTGGTGATAGATGGGCATGCGTTTCGATTAGCTAGTTGGCA-GGGTAACGG			231
Query 121		CTTACCAAGGCTACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			180
Sbjct 232		CCTACCAAGGCAACGATCGATAGGGGAGCTGAGAGGTTGATCCCCACACGGGCACTGAG			291
Query 181		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			240
Sbjct 292		ATACGGGCCCCGACTCCTACGGGAGGCAGCAGTAGGGAATATTGGGCAATGGATGCAAGTC			351
Query 241		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			300
Sbjct 352		TGACCCAGCCATGCCGCGTGCCGGATGAAGGCCCTCAGGGTTGTAAACGGCTTTTATTTCG			411
Query 301		GGAAGAAGAGCAGGGATGCGTCTTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC			360

NCBI Blast:Nucleotide Sequence (1253 letters)

Sbjct	412	GGAAGAAGAGCAGGGATGCGTCCCTGTGTGACGGTACCGAATGAATAAGCACCGGCTAAC	471
Query	361	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT	420
Sbjct	472	TCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTGTCCGGATTTATTGGGTTT	531
Query	421	AAAGGGTGCGTAGGTGGCTTGTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG	480
Sbjct	532	AAAGGGGGCGTAGGTGGCTTTTTAAGTCAGTGGTGAAATACAGCCGCTCAACGGTTGAGG	591
Query	481	TGCCATTGATACTGACAAGCTTGAAACAAGTGGAGGCTGCCGGAATGGATGGTGTAGCGG	540
Sbjct	592	TGCCATTGATACTGAAGAGCTTGAAACAAGTGGAGGCTGCCGGAATGGATGGTGTAGCGG	651
Query	541	TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT	600
Sbjct	652	TGAAATGCATAGATATCATCCAGAACACCGATTGCGAAGGCAGGTGGCTACGTTTGATTT	711
Query	601	GACACTGAGGCACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGCC	660
Sbjct	712	GACACTGAGGCACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGCC	771
Query	661	GTAACGATGAGGACTCGCTGTTGGCCTGTCAAGGGTCAGCGGCTTAGGGAAACCGTTAA	720
Sbjct	772	GTAACGATGAGGACTCGCTGTTGGTCTGTCAAGGATCAGCGGCTTAGGGAAACCGTTAA	831
Query	721	GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG	780
Sbjct	832	GTCCTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGTCCG	891
Query	781	CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCTGGGCTAA	840
Sbjct	892	CACAAGCGGTGGAGCATGTGGTTTAATTCGATGATACCCGAGGAACCTTACCTGGGCTAA	951
Query	841	ATCACACAGGAATCATTCAGAAATGGGTGATCCAGCAATGGCTTGTT-TGAAGGTGCTG	899
Sbjct	952	ATCACAAATAGACGT-ATTTCAGAAATGGGTATTCCAGCAATGGCT-GTTGTGAAGGTGCTG	1009
Query	900	CATGGCTGTCGTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCACGAGCGCAACC	959
Sbjct	1010	CATGGCTGTCGTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCACGAGCGCAACC	1069
Query	960	CCTATGGTTAGTTGCCAGCACGTAATGGTGGGGACTCTAATCAGACTGCCTGTGCACAC	1019
Sbjct	1070	CCTATGGTTAGTTGCCAGCACGTAATGGT-GGGGACTCTAATCAGACTGCCTGTGCAAAC	1128
Query	1020	AAGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGGGCCCTTTACGTCCAGGGCCAACA	1079
Sbjct	1129	-AGAGAGGAAGGAGGGGACGACGTCAAGTCATCATGG-CCCTT-ACGTCCAGGGC-AACA	1184
Query	1080	CAACGTGCTTACAATGGGCGGGTACAGAAGGGTTAGCTACCTCCACCGATGAGAATGCCA	1139
Sbjct	1185	CA-CGTGCT-ACAATGGGCGG-TACAGA-GGGTC-GCTAC-TC-AGTGATGAG-ATGCCA	1236
Query	1140	ATCCCAAAAAGCCGTTCTCCAGTTCCGAATTGGAATCCTGCACCTCGACTCCTATGGAA	1199
Sbjct	1237	ATCCCAAAAAGCCGTTCTCA-A-TTCGGA-TTGAAGT-CTGCAACTCGACT--TATG-AA	1289
Query	1200	GACTGGGAATCCCTTAGATAATC	1222
Sbjct	1290	G-CTGG-AATCGCT-AG-TAATC	1308