Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
Treponema socranskii strain D56BRIII6 16S ribosomal RNA gene, partial sequence	468	468	100%	7e-132	100%	NR_028690.1
Treponema socranskii subsp. paredis strain ATCC 35535 16S ribosomal RNA gene, partial sequence	462	462	100%	3e-130	99%	NR_024869.1
Treponema socranskii subsp. buccale strain ATCC 35534 16S ribosomal RNA gene, partial sequence	462	462	100%	3e-130	99%	NR_024868.1
Treponema parvum ATCC 700770 strain OMZ 833 16S ribosomal RNA gene, partial sequence	279	279	100%	3e-75	87%	NR_025131.1
Treponema porcinum strain 14V28 16S ribosomal RNA gene, partial sequence	274	274	100%	2e-73	86%	NR_042942.1
Treponema amylovorum strain HA2P 16S ribosomal RNA gene, partial sequence	268	268	100%	7e-72	86%	NR_026377.1
Treponema bryantii strain RUS-1 16S ribosomal RNA gene, partial sequence	252	252	100%	7e-67	85%	NR_104781.1
Treponema maltophilum strain BR 16S ribosomal RNA gene, partial sequence	252	252	100%	7e-67	85%	NR_029296.1
Treponema brennaborense strain DD5/3 16S ribosomal RNA, partial sequence	246	246	100%	3e-65	84%	NR_074742.1
Treponema brennaborense strain DD5/3 16S ribosomal RNA gene, partial sequence	243	243	100%	5e-64	84%	NR_029348.1
Treponema bryantii strain RUS-1 16S ribosomal RNA, partial sequence	243	243	100%	5e-64	84%	NR_118718.1

Supplementary Figure S1. BLAST search of T. socranskii sequence.

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
Treponema lecithinolyticum strain OMZ 684 16S ribosomal RNA gene, partial sequence	468	468	100%	7e-132	100%	NR_026247.1
Treponema maltophilum strain BR 16S ribosomal RNA gene, partial sequence	418	418	100%	7e-117	96%	NR_029296.1
Treponema parvum ATCC 700770 strain OMZ 833 16S ribosomal RNA gene, partial sequence	291	291	100%	2e-78	87%	NR_025131.1
Treponema brennaborense strain DD5/3 16S ribosomal RNA gene, partial sequence	287	287	100%	2e-77	87%	NR_029348.1
Treponema brennaborense strain DD5/3 16S ribosomal RNA, partial sequence	285	285	100%	7e-77	87%	NR_074742.1
Treponema porcinum strain 14V28 16S ribosomal RNA gene, partial sequence	279	279	100%	3e-75	87%	NR_042942.1
Treponema zuelzerae strain DSM 1903 16S ribosomal RNA gene, partial sequence	268	268	100%	7e-72	86%	NR_104797.1
Treponema bryantii strain RUS-1 16S ribosomal RNA gene, partial sequence	257	257	100%	2e-68	85%	NR_104781.1
Spirochaeta isovalerica strain DSM 2461 16S ribosomal RNA gene, partial sequence	252	252	100%	7e-67	85%	NR_117137.1
Spirochaeta isovalerica strain MA-2 16S ribosomal RNA gene, partial sequence	252	252	100%	7e-67	85%	NR_104798.1
Treponema medium strain G7201 16S ribosomal RNA gene, partial sequence	252	252	100%	7e-67	85%	NR_037137.1
Spirochaeta psychrophila strain MO-SPC1 16S ribosomal RNA, partial sequence	246	246	100%	3e-65	84%	NR_134185.1
Treponema amylovorum strain HA2P 16S ribosomal RNA gene, partial sequence	241	241	100%	2e-63	84%	NR_026377.1
Spirochaeta alkalica strain Z-7491 16S ribosomal RNA gene, partial sequence	241	241	100%	2e-63	84%	NR_026301.1

Supplementary Figure S2. BLAST search of T. lecithinolyticum sequence.

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                                481          .         5         .         .         .         .         :         . 560
1 E.COLI              100.0%     CCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGNAATTACNGGGCGTAAAGCGCACGCAGGCGGTTTG
2 SOCRANSKII           68.0%     ---------------------CACGTAAGGTGCGAGCGTTGTTCGGAATTATTGGGCGTAAAGGGCATGCAGGCGGGTCG
3 PALLIDUM             36.3%     ACGTGCCAGCAGCCGCGGTAACACGTAAGGGCGAGCGTTGTTCGGAATTATTGGGCGTAAAGGGCATGCAGGCGGACTG
4 LECITHINOLYTICUM     66.8%     ---------------------CACGTAAGGTGCGAGCGTTGTTCGGAATTATTGGGCGTAAAGGGCATGTAGGCGGATGA

                                561          .         .         .         6         .         .         .         . 640
1 E.COLI              100.0%     TTAANTCANATGTGAAATCCCCGGGCTCAACCTGGNAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTANAGGGGGGT
2 SOCRANSKII           68.0%     CCAAGCTTGGTAAGAAATACCGGGGCTCAACTCCGGAGCTATATTGAGAACTGGCGAGCTAGAGTTGCCGAAGGGTATCC
3 PALLIDUM             36.3%     GTAAGCCTGGTGTGAAATCCCCGAGCTCAACTTGGGAACTGCACTGGGTACTGCTGGTCTAGAATCACGGAGGGGAAACC
4 LECITHINOLYTICUM     66.8%     GCAAGCTTGGTGTGAAATGCTACAGCTTAAGTGTGGCACAGCATTGAGAACTGCACATCTTGAATTACTGAAGGGTAACT

                                641          :         .         .         .         .         7         .         . 720
1 E.COLI              100.0%     ANAATTCCAGGTGTAGCGGTGAAATGCGTANAGATCTGGAGGAATACCGGTGGCNAAGGCGGCCCCCTGGACNAANACTG
2 SOCRANSKII           68.0%     GGAATTCCGCGTGAACGGGTGAAATCTGTAGATATGCGGAAGAACACCCATGGCGAAGGCAGGATACCGGCGGACGACTG
3 PALLIDUM             36.3%     GGAATTCCAAGTGTAGGGGTGGAATCTGTAGATATTTGGAAGAACACCGGTGGCGAAGGCGGGTTTCTGGCCGATCATTG
4 LECITHINOLYTICUM     66.8%     AGAATTCCACGTGTAGGGGTGAAATCTGTAGATATGTGGAAGAATACCAATGGCGAAGGCAAGTTACCGGCAGATAATTG

                                721          .         .         :         .         .         .         .         8 800
1 E.COLI              100.0%     ACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGNTAGTCCACGCCGTAAACGATGTCNACTTGNAG
2 SOCRANSKII           68.0%     ACGCTGAGGTGCGAACGTGCGGGGAGCAAACAGG-------------------------------------------
3 PALLIDUM             36.3%     ACGCTGAGGTGCGAACGTGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACACAGTAAACGATGTACACTAGGTG
4 LECITHINOLYTICUM     66.8%     ACGCTGAGGTGCGAAAGTGCGGGGAGCGAACAGG-------------------------------------------
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Supplementary Figure S3. CLUSTAL sequences alignement.