

BLAST ®

Basic Local Alignment Search Tool

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TAGC

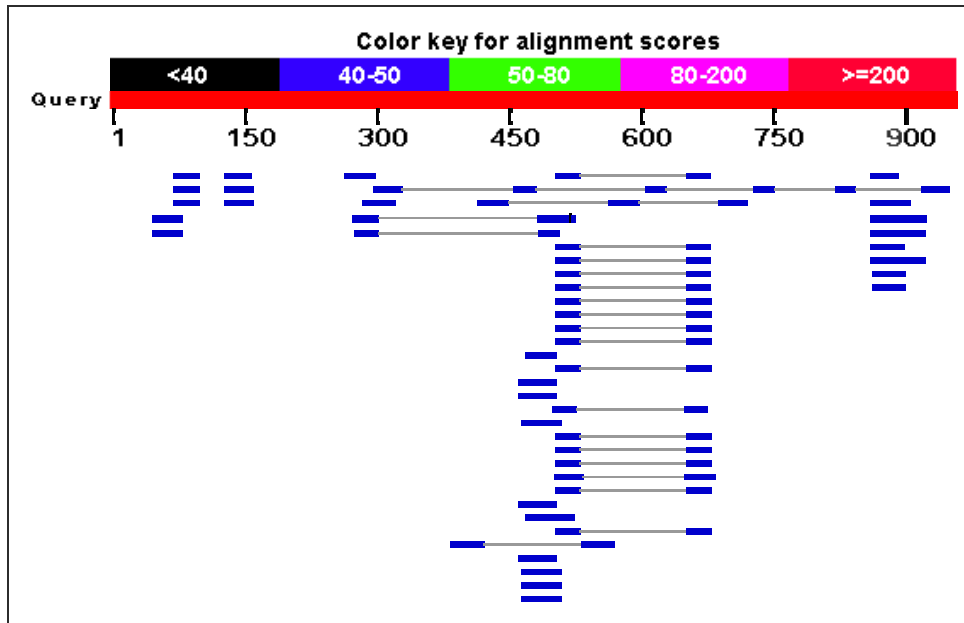
RID [Y0UXA0MU015](#) (Expires on 08-06 13:29 pm)

Query ID lc|44643
Description None
Molecule type nucleic acid
Query Length 952

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 78 Blast Hits on the Query Sequence



☰ Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Rhodospiridium toruloides strain CECT1137, genomic scaffold, scaffold RHTO0S09	46.4	46.4	3%	0.62	93%	LK052944.1
Micromonas pusilla CCMP1545 predicted protein, mRNA	46.4	260	16%	0.62	94%	XM_003057172.1
Allochroamatium vinosum DSM 180, complete genome	46.4	46.4	3%	0.62	93%	CP001896.1
Mizuhopecten yessoensis clone PYES020 microsatellite sequence	46.4	46.4	3%	0.62	89%	DQ221710.1
Allochroamatium vinosum sulfate adenylyltransferase (sat), putative adenylylsulfate reductase membrane anchor (aprM), adenylylsulfate reductase beta subunit (aprB), and adenylylsulfate reductase alpha subunit (aprA) genes, complete cds	46.4	46.4	3%	0.62	93%	U84759.2
Chromatium vinosum adenylylsulfate reductase membrane anchor (aprM) gene, complete cds	46.4	46.4	3%	0.62	93%	U84761.1
PREDICTED: Cynoglossus semilaevis KH domain containing, RNA binding, signal transduction associated 2 (khdrbs2), mRNA	44.6	44.6	4%	2.2	85%	XM_008321812.1
Lethenteron camtschaticum clone BAC 424C19, BAC 204J11 homeobox protein Hox-epsilon14 (Hox-epsilon14) gene, partial cds; and homeobox protein Hox-epsilon13 (Hox-epsilon13) and homeobox protein Hox-epsilon11 (Hox-epsilon11) genes, complete cds, complete sequence	44.6	133	7%	2.2	86%	KF318004.1
Zebrafish DNA sequence from clone CH1073-109O7 in linkage group 22, complete sequence	44.6	44.6	4%	2.2	82%	CU855918.10
Zebrafish DNA sequence from clone CH73-64M11 in linkage group 6, complete sequence	44.6	44.6	3%	2.2	91%	CU468923.8
Drosophila melanogaster 211000022280518 sequence	42.8	85.5	5%	7.6	96%	DS483774.1
Burkholderia pseudomallei genome assembly BP_3921g ,chromosome : 1	42.8	85.5	5%	7.6	93%	LK936442.1
Babesia bigemina genome assembly Bbig001 ,chromosome : III	42.8	128	10%	7.6	89%	LK391709.1
Burkholderia pseudomallei MSHR520 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP004368.1
Burkholderia pseudomallei MSHR146 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP004042.1
Burkholderia pseudomallei MSHR511 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP004023.1
Burkholderia pseudomallei NCTC 13178 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP004001.1
Burkholderia pseudomallei NAU20B-16 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP004003.1
Burkholderia pseudomallei NCTC 13179 chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP003976.1
Burkholderia pseudomallei MSHR305 chromosome 2, complete sequence	42.8	85.5	5%	7.6	93%	CP006470.1
Burkholderia pseudomallei BPC006 chromosome I, complete sequence	42.8	85.5	5%	7.6	93%	CP003781.1

PREDICTED: Pan paniscus myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA	42.8	42.8	3%	7.6	88%	XM_003830660.1
Burkholderia pseudomallei 1026b chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	CP002833.1
Tetrapapispora phaffii CBS 4417 hypothetical protein (TPHA0B04740) mRNA, complete cds	42.8	42.8	3%	7.6	89%	XM_003684529.1
Tetrapapispora phaffii CBS 4417 chromosome 2, complete genome	42.8	42.8	3%	7.6	89%	HE612857.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Dlc1:tm 1e(EUCOMM)Wtsi; transgenic	42.8	42.8	4%	7.6	83%	JN964474.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Dlc1:tm 1a(EUCOMM)Wtsi; transgenic	42.8	42.8	4%	7.6	83%	JN948505.1
Polymorphum gilvum SL003B-26A1, complete genome	42.8	85.5	5%	7.6	96%	CP002568.1
Leishmania infantum JPCM5 genome chromosome 14	42.8	42.8	6%	7.6	77%	FR796446.1
Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), RefSeqGene on chromosome 6	42.8	42.8	4%	7.6	84%	NG_009224.2
Rattus norvegicus CH230-425P24 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	42.8	42.8	6%	7.6	78%	AC132503.4
Burkholderia pseudomallei MSHR346 chromosome I, complete sequence	42.8	85.5	5%	7.6	93%	CP001408.1
Hipposideros pratti clone P02 microsatellite sequence	42.8	42.8	3%	7.6	84%	EU224387.1
Rattus norvegicus BAC CH230-34B22 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	42.8	42.8	6%	7.6	78%	AC128786.3
Burkholderia pseudomallei 1106a chromosome I, complete sequence	42.8	85.5	5%	7.6	93%	CP000572.1
Burkholderia pseudomallei 668 chromosome I, complete sequence	42.8	85.5	5%	7.6	93%	CP000570.1
Zebrafish DNA sequence from clone DKEY-69C5 in linkage group 16, complete sequence	42.8	42.8	3%	7.6	88%	CR854835.8
Burkholderia ambifaria AMMD chromosome 1, complete sequence	42.8	85.5	6%	7.6	88%	CP000440.1
Burkholderia pseudomallei 1710b chromosome I, complete sequence	42.8	85.5	5%	7.6	93%	CP000124.1
Mus musculus chromosome 8, clone RP24-280K15, complete sequence	42.8	42.8	4%	7.6	83%	AC138593.14
Molluscum contagiosum virus subtype 1 clone H-M hypothetical protein (H-M.2) and hypothetical protein (H-M.1) genes, partial cds	42.8	42.8	3%	7.6	86%	U86886.1
Molluscum contagiosum virus subtype 1, complete genome	42.8	42.8	3%	7.6	86%	U60315.1
Mus musculus 6 BAC RP24-549J13 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	42.8	42.8	5%	7.6	78%	AC157101.9
Burkholderia pseudomallei strain K96243, chromosome 1, complete sequence	42.8	85.5	5%	7.6	93%	BX571965.1
Homo sapiens BAC clone RP11-186C15 from 2, complete sequence	42.8	85.5	7%	7.6	86%	AC096558.1
Mus musculus chromosome 8, clone RP24-231N10, complete sequence	42.8	42.8	4%	7.6	83%	AC103378.21
Homo sapiens genomic DNA,						

chromosome 6, clone:RP11-688E1, complete sequence	42.8	42.8	4%	7.6	84%	AP006200.1
Zebrafish DNA sequence from clone CH211-172J16, complete sequence	42.8	42.8	3%	7.6	88%	AL935041.4
Homo sapiens genomic DNA, chromosome 6q21, clone:57112, complete sequence	42.8	42.8	4%	7.6	84%	AB041511.1
Homo sapiens genomic DNA, chromosome 6q21, anti-oncogene region, section 1/4	42.8	42.8	4%	7.6	84%	AP002528.1

Alignments

Rhodospiridium toruloides strain CECT1137, genomic scaffold, scaffold RHTO0S09

Sequence ID: **emb|LK052944.1|** Length: 938378 Number of Matches: 1

Range 1: 359899 to 359928

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:

```

Query 856      CACACACGCGCAGCTGCTCACACACGCGCA 885
                |||
Sbjct 359928  CACACACGCTCAGCTGCTCACACACGCTCA 359899

```

Micromonas pusilla CCMP1545 predicted protein, mRNA

Sequence ID: **ref|XM_003057172.1|** Length: 1692 Number of Matches: 6

Range 1: 643 to 673

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	30/32(94%)	1/32(3%)	Plus/Minus	

Features:

```

Query 297  GCAGCTGCGAGAGCTCTCTCGTGACGTGAG 328
                |||
Sbjct 673  GCAGCTGCGAGAGCTCTCTCG-GACGCGAG 643

```

Range 2: 643 to 673

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Minus	

Features:

```

Query 913  GCAGCTGCGAGAGCTCTCTCGTCTGCGAG 943
                |||
Sbjct 673  GCAGCTGCGAGAGCTCTCTCGGACGCGAG 643

```

Range 3: 651 to 673

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:

```

Query 815  GCAGCTGCGAGAGCTCTCTCTCG 837
                |||
Sbjct 673  GCAGCTGCGAGAGCTCTCTCTCG 651

```

Range 4: 651 to 673

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:

```

Query 725  GCAGCTGCGAGAGCTCTCTCTCG 747
                |||
Sbjct 673  GCAGCTGCGAGAGCTCTCTCTCG 651

```

Range 5: 651 to 673

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:

```
Query 602 GCAGCTGCGAGAGCTCTCTCTCG 624
      |||
Sbjct 673 GCAGCTGCGAGAGCTCTCTCTCG 651
```

Range 6: 651 to 673

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:

```
Query 455 GCAGCTGCGAGAGCTCTCTCTCG 477
      |||
Sbjct 673 GCAGCTGCGAGAGCTCTCTCTCG 651
```

Allochromatium vinosum DSM 180, complete genome

Sequence ID: **gb|CP001896.1|** Length: 3526903 Number of Matches: 1
Range 1: 1296649 to 1296678

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Plus	

Features:
conserved hypothetical protein

```
Query 71 GACGTGCATCTGACAGATCTGTTTCATCGTC 100
      |||
Sbjct 1296649 GACGTGCATCTGTTCGGATCTGTTTCATCGTC 1296678
```

Mizuhopecten yessoensis clone PYES020 microsatellite sequence

Sequence ID: **gb|DQ221710.1|** Length: 189 Number of Matches: 1
Range 1: 120 to 152

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	32/36(89%)	3/36(8%)	Plus/Minus	

Features:

```
Query 264 TCAGTCCCTCACACACGCGCAGGTCACACACGCGCA 299
      |||
Sbjct 152 TCAGTCGCTCACACACGCGC---TCACACACGCGCA 120
```

Allochromatium vinosum sulfate adenylyltransferase (sat), putative adenylylsulfate reductase membrane anchor (aprM), adenylylsulfate reductase beta subunit (aprB), and adenylylsulfate reductase alpha subunit (aprA) genes, complete cds

Sequence ID: **gb|U84759.2|CVU84759** Length: 5090 Number of Matches: 1
Range 1: 2213 to 2242

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Plus	

Features:

```
Query 71 GACGTGCATCTGACAGATCTGTTTCATCGTC 100
      |||
Sbjct 2213 GACGTGCATCTGTTCGGATCTGTTTCATCGTC 2242
```