

BLAST ®

Basic Local Alignment Search Tool

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AGTC

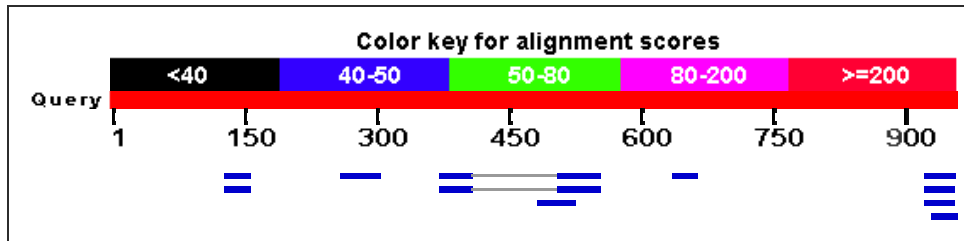
RID [Y0SCXZH801R](#) (Expires on 08-06 12:46 pm)

Query ID lc|147875
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 13 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured bacterium contig00188 genomic sequence	46.4	46.4	4%	0.62	84%	JX827820.1
Neospora caninum Liverpool putative protein kinase (incomplete catalytic triad) (NCLIV_010550) mRNA, complete cds	46.4	89.1	8%	0.62	82%	XM_003880570.1
Neospora caninum Liverpool complete genome, chromosome IV	46.4	89.1	8%	0.62	82%	FR823384.1
Saccharomycetaceae sp. 'Ashbya aceri' chromosome V, complete sequence	44.6	44.6	4%	2.2	81%	CP006024.1
Rhesus Macaque BAC CH250-136K12 () complete sequence	44.6	44.6	3%	2.2	89%	AC193550.4
Ustilago maydis 521 hypothetical protein (UM04065.1) partial mRNA	44.6	44.6	3%	2.2	93%	XM_755119.1
Mus musculus BAC clone RP24-562E3 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	88%	AC134534.3
Mus musculus BAC clone RP24-85I19 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	88%	AC154902.2
Human DNA sequence from clone RP11-187L3 on chromosome 13, complete sequence	42.8	42.8	2%	7.6	93%	AL161715.24
Homo sapiens BAC clone RP11-319N12 from 4, complete sequence	42.8	42.8	3%	7.6	93%	AC093803.3
Homo sapiens BAC clone RP11-472F4 from 4, complete sequence	42.8	42.8	3%	7.6	93%	AC025821.7

Alignments

Uncultured bacterium contig00188 genomic sequence

Sequence ID: **gb|JX827820.1|** Length: 34239 Number of Matches: 1

Range 1: 10583 to 10626

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	38/45(84%)	1/45(2%)	Plus/Plus	

Features:

```

Query 260 CTGTACGTACCCACGCGCTCTCGTTACGCGCGCTCTCGTCATC 304
          |||
Sbjct 10583 CTGTACGTGCCCAC-CGCGCTCTCGTAACGCGCGCGCGTCGTC 10626

```

Neospora caninum Liverpool putative protein kinase (incomplete catalytic triad) (NCLIV_010550) mRNA, complete cds

Sequence ID: **ref|XM_003880570.1|** Length: 8889 Number of Matches: 2

Range 1: 3798 to 3846

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	41/50(82%)	1/50(2%)	Plus/Minus	

Features:

```

Query 503 CTCGTCATCCGCGCTCTCGTCATCGCAGTACGAACGCGCTCTCGTCATCG 552
          |||
Sbjct 3846 CTCGTCCTCGTCGTCCTCGTCGTCGCCAGTA-GAACGCGCTCTCGTCGTCG 3798

```

Range 2: 3798 to 3831

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Minus	

Features:

Query 371 CTCGTCATCGCAGTACGAACGCGCTCTCGTCATCG 405
 Sbjct 3831 CTCGTCGTCCAGTA-GAACGCGCTCTCGTCGTCG 3798

Neospora caninum Liverpool complete genome, chromosome IV

Sequence ID: **emb|FR823384.1|** Length: 2317323 Number of Matches: 2
 Range 1: 789322 to 789370

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	41/50(82%)	1/50(2%)	Plus/Minus	

Features:

Query 503 CTCGTCATCCGCGCTCTCGTCATCGCAGTACGAACGCGCTCTCGTCATCG 552
 Sbjct 789370 CTCGTCCTCGTCGTCCAGTA-GAACGCGCTCTCGTCGTCG 789322

Range 2: 789322 to 789355

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Minus	

Features:

Query 371 CTCGTCATCGCAGTACGAACGCGCTCTCGTCATCG 405
 Sbjct 789355 CTCGTCGTCCAGTA-GAACGCGCTCTCGTCGTCG 789322

Saccharomycetaceae sp. 'Ashbya aceri' chromosome V, complete sequence

Sequence ID: **gb|CP006024.1|** Length: 1513917 Number of Matches: 1
 Range 1: 1484202 to 1484249

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	39/48(81%)	3/48(6%)	Plus/Minus	

Features:

Query 480 CGCGCGCTCTCGTTACGCGCGCTCTCGTCA---TCGCGCTCTCGTCA 524
 Sbjct 1484249 CGCGCGCTCTCGGCACGCGCGCTCTCCACACGCTCCGCGCTCACCTCA 1484202

Rhesus Macaque BAC CH250-136K12 () complete sequence

Sequence ID: **gb|AC193550.4|** Length: 184509 Number of Matches: 1
 Range 1: 137125 to 137156

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	31/35(89%)	3/35(8%)	Plus/Plus	

Features:

Query 916 TCATCTGTGTCACACACACTACATCTGTGTCACAC 950
 Sbjct 137125 TCATCTGTGTCACAC---CTTCATCTGTGTCACAC 137156

Ustilago maydis 521 hypothetical protein (UM04065.1) partial mRNA

Sequence ID: **ref|XM_755119.1|** Length: 4017 Number of Matches: 1
 Range 1: 1612 to 1640

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Plus	

Features:

Query 633 GCGTACACTACGCGCGCTCTCGTCATCCG 661
 Sbjct 1612 GCATACACCACGCGCGCTCTCGTCATCCG 1640

Mus musculus BAC clone RP24-562E3 from chromosome 7, complete sequence

Sequence ID: **gb|AC134534.3|** Length: 185268 Number of Matches: 1
 Range 1: 70541 to 70573

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Minus	

Features:

```

Query   916   TCATCTGTGTCACACACACTACATCTGTGTCAC   948
      |||
Sbjct   70573  TCATCTGTTTCACACACACTACATTTGGGGCAC   70541

```

Mus musculus BAC clone RP24-85I19 from chromosome 7, complete sequence

Sequence ID: **gb|AC154902.2|** Length: 213932 Number of Matches: 1

Range 1: 5009 to 5041

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Plus	

Features:

```

Query   916   TCATCTGTGTCACACACACTACATCTGTGTCAC   948
      |||
Sbjct   5009   TCATCTGTTTCACACACACTACATTTGGGGCAC   5041

```

Human DNA sequence from clone RP11-187L3 on chromosome 13, complete sequence

Sequence ID: **emb|AL161715.24|** Length: 88079 Number of Matches: 1

Range 1: 33297 to 33324

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query   925   TCACACACACTACATCTGTGTCACACAC   952
      |||
Sbjct   33297  TCACACACACCACATGTGTGTCACACAC   33324

```

Homo sapiens BAC clone RP11-319N12 from 4, complete sequence

Sequence ID: **gb|AC093803.3|** Length: 191903 Number of Matches: 1

Range 1: 99269 to 99297

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Minus	

Features:

```

Query   129   ATACGACATGCATGCATGCACGCTAGCATG   158
      |||
Sbjct   99297  ATAC-ACATGCATGCATGCACGCTTGCATG   99269

```

Homo sapiens BAC clone RP11-472F4 from 4, complete sequence

Sequence ID: **gb|AC025821.7|** Length: 178378 Number of Matches: 1

Range 1: 170561 to 170589

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Minus	

Features:

```

Query   129   ATACGACATGCATGCATGCACGCTAGCATG   158
      |||
Sbjct   170589  ATAC-ACATGCATGCATGCACGCTTGCATG   170561

```