

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ Formatting Results - Y0TTZM1M014

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CTAG

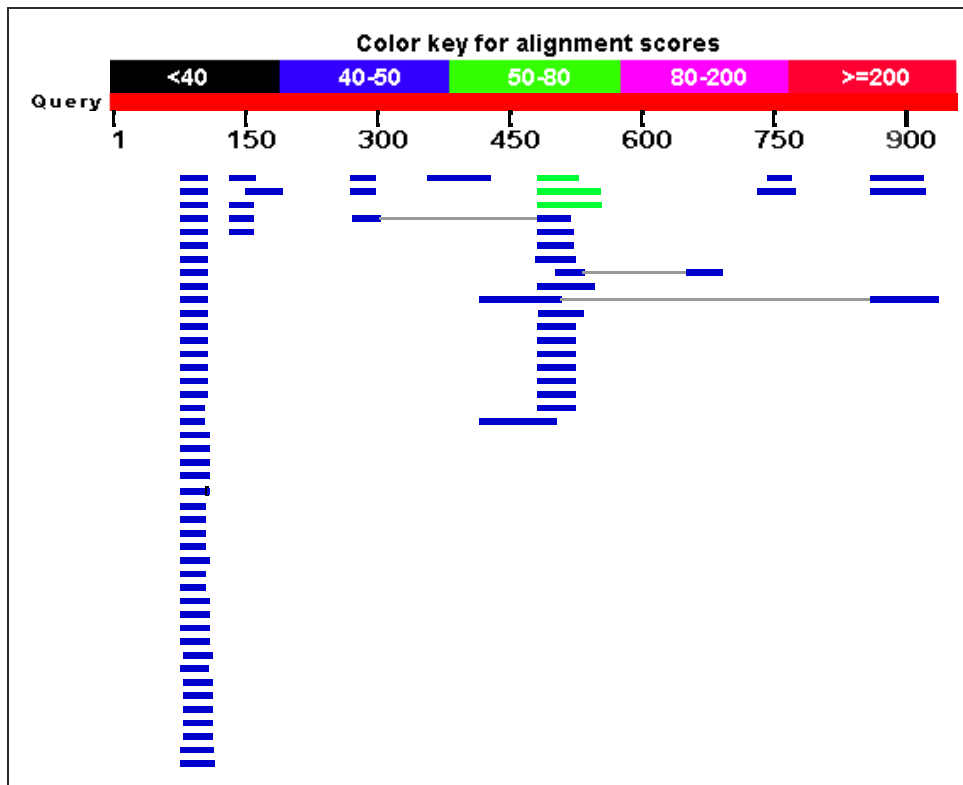
RID [Y0TTZM1M014](#) (Expires on 08-06 13:10 pm)

Query ID lc|22501
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 124 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pan troglodytes BAC clone CH251-63H1 from chromosome 4, complete sequence	53.6	53.6	5%	0.004	88%	AC192394.3
Human DNA sequence from clone RP3-513G18 on chromosome 4, complete sequence	51.8	140	7%	0.015	79%	AL109760.3
Human DNA sequence from clone LA04NC01-17A9 on chromosome 4, complete sequence	51.8	140	7%	0.015	79%	Z54335.1
Homo sapiens FOSMID clone ABC11-47249900G10 from chromosome unknown, complete sequence	50.0	92.7	6%	0.051	80%	AC229891.2
Pongo abelii BAC clone CH276-449G9 from chromosome unknown, complete sequence	46.4	90.9	7%	0.62	89%	AC207086.4
Mus musculus BAC clone RP23-14N12 from chromosome 8, complete sequence	46.4	46.4	4%	0.62	88%	AC182458.2
Mus musculus BAC clone RP23-76C13 from chromosome 8, complete sequence	46.4	46.4	4%	0.62	88%	AC122205.6
Klebsiella pneumoniae subsp. pneumoniae PittNDM01, complete genome	44.6	44.6	3%	2.2	91%	CP006798.1
Klebsiella pneumoniae subsp. pneumoniae KPR0928, complete sequence	44.6	44.6	3%	2.2	91%	CP008831.1
Klebsiella pneumoniae subsp. pneumoniae KPNIH1, complete genome	44.6	44.6	3%	2.2	91%	CP008827.1
Klebsiella pneumoniae subsp. pneumoniae KPNIH24, complete genome	44.6	44.6	3%	2.2	91%	CP008797.1
Klebsiella pneumoniae subsp. pneumoniae KP5-1, complete genome	44.6	44.6	3%	2.2	91%	CP008700.1
Klebsiella pneumoniae strain KG1 large virulence fragment VF1 genomic sequence	44.6	44.6	3%	2.2	91%	KJ719250.1
Serratia sp. FS14, complete genome	44.6	44.6	3%	2.2	91%	CP005927.1
Klebsiella pneumoniae subsp. pneumoniae KPNIH27, complete genome	44.6	44.6	3%	2.2	91%	CP007731.1
Klebsiella pneumoniae subsp. pneumoniae KPNIH10, complete genome	44.6	44.6	3%	2.2	91%	CP007727.1
PREDICTED: Cricetulus griseus hyphally regulated cell wall protein 3-like (LOC103162938), mRNA	44.6	1827	4%	2.2	82%	XM_007634121.1
Klebsiella pneumoniae str. Kp52.145, chromosome, complete genome	44.6	44.6	3%	2.2	91%	FO834906.1
Klebsiella pneumoniae 30660/NJST258_1, complete genome	44.6	44.6	3%	2.2	91%	CP006923.1
Klebsiella pneumoniae 30684/NJST258_2, complete genome	44.6	44.6	3%	2.2	91%	CP006918.1
PREDICTED: Neolamprologus brichardi gap junction alpha-8 protein-like (LOC102786875), mRNA	44.6	44.6	3%	2.2	93%	XM_006795174.1
Klebsiella pneumoniae ATCC BAA-2146, complete genome	44.6	44.6	3%	2.2	91%	CP006659.1

Serratia marcescens SM39 DNA, complete genome	44.6	44.6	3%	2.2	91%	AP013063.1
Klebsiella pneumoniae subsp. pneumoniae Kp13, complete genome	44.6	44.6	3%	2.2	91%	CP003999.1
Serratia marcescens subsp. marcescens Db11, complete genome	44.6	44.6	3%	2.2	91%	HG326223.1
Klebsiella pneumoniae CG43, complete genome	44.6	44.6	3%	2.2	91%	CP006648.1
Streptomyces ansochromogenes clone nik metabolite biosynthetic gene cluster, complete sequence	44.6	44.6	3%	2.2	93%	KF170355.1
Streptomyces ansochromogenes clone nrps3 metabolite biosynthetic gene cluster, complete sequence	44.6	44.6	3%	2.2	93%	KF170331.1
Klebsiella pneumoniae JM45, complete genome	44.6	44.6	3%	2.2	91%	CP006656.1
Capsaspora owczarzaki ATCC 30864 integral membrane sensor hybrid histidine kinase (CAOG_02681) mRNA, complete cds	44.6	44.6	4%	2.2	85%	XM_004349381.1
Klebsiella pneumoniae subsp. pneumoniae 1084, complete genome	44.6	44.6	3%	2.2	91%	CP003785.1
Klebsiella pneumoniae subsp. pneumoniae HS11286, complete genome	44.6	44.6	3%	2.2	91%	CP003200.1
Klebsiella pneumoniae KCTC 2242, complete genome	44.6	44.6	3%	2.2	91%	CP002910.1
Burkholderia gladioli BSR3 chromosome 2, complete sequence	44.6	89.1	3%	2.2	93%	CP002600.1
Erwinia amylovora ATCC BAA-2158, whole genome shotgun sequence, contig 12	44.6	44.6	3%	2.2	93%	FR1719192.1
Erwinia sp. Ejp617, complete genome	44.6	44.6	3%	2.2	93%	CP002124.1
Erwinia amylovora CFBP1430 complete genome	44.6	44.6	3%	2.2	93%	FN434113.1
Erwinia amylovora ATCC 49946 chromosomal sequence	44.6	44.6	3%	2.2	93%	FN666575.1
Klebsiella variicola At-22, complete genome	44.6	44.6	3%	2.2	91%	CP001891.1
Erwinia pyrifoliae DSM 12163 complete genome, culture collection DSM:12163	44.6	44.6	3%	2.2	93%	FN392235.1
Haliangium ochraceum DSM 14365, complete genome	44.6	44.6	3%	2.2	93%	CP001804.1
Erwinia pyrifoliae strain Ep1/96 complete chromosome	44.6	44.6	3%	2.2	93%	FP236842.1
Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044 DNA, complete genome	44.6	44.6	3%	2.2	91%	AP006725.1
Klebsiella pneumoniae 342, complete genome	44.6	44.6	3%	2.2	91%	CP000964.1
Drosophila ananassae GF22237 (Dana\GF22237), mRNA	44.6	87.3	7%	2.2	85%	XM_001966520.1
Citrobacter koseri ATCC BAA-895, complete genome	44.6	44.6	3%	2.2	91%	CP000822.1
Pan troglodytes BAC clone CH251-322P12 from chromosome 4, complete sequence	44.6	44.6	6%	2.2	76%	AC193930.3
Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	44.6	44.6	3%	2.2	91%	CP000647.1
Zebrafish DNA sequence from clone CH211-271G18 in linkage group 4, complete sequence	44.6	87.3	17%	2.2	73%	BX323072.9
PREDICTED: Callorhinchus milii homer homolog 3 (Drosophila) (homer3), mRNA	42.8	42.8	5%	7.6	82%	XM_007898909.1

PREDICTED: Haplochromis burtoni gap junction alpha-8 protein-like (LOC102306072), transcript variant X3, mRNA	42.8	42.8	2%	7.6	93%	XM_005946580.1
PREDICTED: Haplochromis burtoni gap junction alpha-8 protein-like (LOC102306072), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_005946579.1
PREDICTED: Haplochromis burtoni gap junction alpha-8 protein-like (LOC102306072), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_005946578.1
PREDICTED: Bos taurus uncharacterized LOC101905650 (LOC101905650), misc_RNA	42.8	42.8	4%	7.6	83%	XR_239055.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101903852), transcript variant X1, mRNA	42.8	42.8	4%	7.6	83%	XM_005200981.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC781635), transcript variant X1, mRNA	42.8	42.8	4%	7.6	83%	XM_003585571.2
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101902420), partial mRNA	42.8	42.8	4%	7.6	83%	XM_005200548.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101903852), mRNA	42.8	42.8	4%	7.6	83%	XM_005199954.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X2, mRNA	42.8	42.8	4%	7.6	83%	XM_005199772.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X1, mRNA	42.8	42.8	4%	7.6	83%	XM_005199771.1
Mycobacterium sp. 05-1390, complete genome	42.8	42.8	3%	7.6	88%	CP003347.1
Pseudomonas sp. UW4, complete genome	42.8	42.8	3%	7.6	90%	CP003880.1
Mycobacterium indicus pranii MTCC 9506, complete genome	42.8	42.8	3%	7.6	88%	CP002275.1
PREDICTED: Strongylocentrotus purpuratus dynamin 1-like, transcript variant 8 (dnm1l), mRNA	42.8	42.8	4%	7.6	81%	XM_796968.3
Mycobacterium sp. MOTT36Y, complete genome	42.8	42.8	3%	7.6	88%	CP003491.1
Mycobacterium intracellulare MOTT-64, complete genome	42.8	42.8	3%	7.6	88%	CP003324.1
Mycobacterium intracellulare MOTT-02, complete genome	42.8	42.8	3%	7.6	88%	CP003323.1
Mycobacterium intracellulare ATCC 13950, complete genome	42.8	42.8	3%	7.6	88%	CP003322.1
Gordonia polyisoprenivorans VH2, complete genome	42.8	42.8	3%	7.6	86%	CP003119.1
Cyprinus carpio clone 763136 microsatellite sequence	42.8	42.8	2%	7.6	93%	JN767833.1
Cyprinus carpio clone 195990 microsatellite sequence	42.8	42.8	2%	7.6	93%	JN722478.1
Mus musculus chromosome 3, clone RP23-112A11, complete sequence	42.8	42.8	6%	7.6	80%	AC110544.13
Pan troglodytes chromosome 22 clone:PTB-109H19, map 22, complete sequences	42.8	42.8	7%	7.6	74%	BS000047.1
Trifolium repens microsatellite agr1036 sequence	42.8	42.8	9%	7.6	73%	AY178321.1
Amycolatopsis orientalis cosmid PCZA363	42.8	42.8	3%	7.6	84%	AJ223999.1

Pan troglodytes BAC clone CH251-63H1 from chromosome 4, complete sequence

Sequence ID: **gb|AC192394.3|** Length: 173860 Number of Matches: 1
Range 1: 75549 to 75596

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	44/50(88%)	3/50(6%)	Plus/Plus	

Features:

```
Query  480      GTGTGTGAGAGTAACGTGTGTGAGAGTAGCAG-GTGTGAGAGTAGCAGTG  528
      |||
Sbjct  75549    GTGTGTGAGAGTGTAGTGTGTGAGAGT-GCAGTGTGTGAGAGT-GCAGTG  75596
```

Human DNA sequence from clone RP3-513G18 on chromosome 4, complete sequence

Sequence ID: **emb|AL109760.3|** Length: 112560 Number of Matches: 3
Range 1: 88504 to 88568

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	59/75(79%)	11/75(14%)	Plus/Minus	

Features:

```
Query  480      GTGTGTGAGAGTAACGTGTGTGAGAGTAGCAG-GTGTGAGAGTAGCAGTGCTACGTCCGT  538
      |||
Sbjct  88568    GTGTGTGAGAGTGTAGTGTGTGAGAGT-GCAGTGTGTGTGAGT-GCAGTG-----TGT  88518

Query  539      GTGAGAGTAGCAGTG  553
      |||
Sbjct  88517    GTGAGAGT-GCAGTG  88504
```

Range 2: 88536 to 88585

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	44/52(85%)	5/52(9%)	Plus/Minus	

Features:

```
Query  480      GTGTGTGAGA--GTAACGTGTGTGAGAGTAGCAG-GTGTGAGAGTAGCAGTG  528
      |||
Sbjct  88585    GTGTGTGAGAATGTAGTGTGTGTGAGAGT-GTAGTGTGTGAGAGT-GCAGTG  88536
```

Range 3: 88877 to 88929

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	44/54(81%)	5/54(9%)	Plus/Minus	

Features:

```
Query  480      GTGTGTGAGA--GTAACGTGTGTGAGA--GTAGCAGGTGTGAGAGTAGCAGTGC  529
      |||
Sbjct  88929    GTGTGTGAGAGTGTAGTGTGTGTGAGAATGTAGTGTGTGTGAGAGT-GCAGTGC  88877
```

Human DNA sequence from clone LA04NC01-17A9 on chromosome 4, complete sequence

Sequence ID: **emb|Z54335.1|** Length: 38013 Number of Matches: 3
Range 1: 14958 to 15022

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	59/75(79%)	11/75(14%)	Plus/Minus	

Features:

```
Query  480      GTGTGTGAGAGTAACGTGTGTGAGAGTAGCAG-GTGTGAGAGTAGCAGTGCTACGTCCGT  538
      |||
Sbjct  15022    GTGTGTGAGAGTGTAGTGTGTGAGAGT-GCAGTGTGTGTGAGT-GCAGTG-----TGT  14972

Query  539      GTGAGAGTAGCAGTG  553
      |||
Sbjct  14971    GTGAGAGT-GCAGTG  14958
```

Range 2: 14990 to 15039

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	44/52(85%)	5/52(9%)	Plus/Minus	

Features:

```
Query  480      GTGTGTGAGA--GTAACGTGTGTGAGAGTAGCAG-GTGTGAGAGTAGCAGTG  528
      |||
```

Sbjct 15039 GTGTGTGAGAATGTAGTGTGTGTGAGAGT-GTAGTGTGTGAGAGT-GCAGTG 14990

Range 3: 15331 to 15383

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	44/54(81%)	5/54(9%)	Plus/Minus	
Features:					
Query 480	GTGTGTGAGA--GTAACGTGTGTGAGA--GTAGCAGGTGTGAGAGTAGCAGTGC	529			
Sbjct 15383	GTGTGTGAGAGTGTAGTGTGTGTGAGAATGTAGTGTGTGTGAGAGT-GCAGTGC	15331			

Homo sapiens FOSMID clone ABC11-47249900G10 from chromosome unknown, complete sequence

Sequence ID: **gb|AC229891.2|** Length: 40586 Number of Matches: 2

Range 1: 75 to 134

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	49/61(80%)	2/61(3%)	Plus/Minus	
Features:					
Query 855	CGTGTGTGAGAGTAGCAGCGTGTGTGAGAGTAG-GCGCGATGTACGCGACGTGTGTGAGA	913			
Sbjct 134	CGTGTGTGAGAGTGGGGGCGTGTGTGAGAGGGGCGTGAGAGGTA-GGGGCGTGTGTGAGA	76			
Query 914	G 914				
Sbjct 75	G 75				

Range 2: 94 to 152

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	46/60(77%)	1/60(1%)	Plus/Minus	
Features:					
Query 855	CGTGTGTGAGAGTAGCAGCGTGTGTGAGAGTAGGCGCGATGTACGCGACGTGTGTGAGAG	914			
Sbjct 152	CGTGTGTGAAGGGAGGGGCGTGTGTGAGAGTGGGGGCG-TGTGTGAGAGGGGCGTGAGAG	94			

Pongo abelii BAC clone CH276-449G9 from chromosome unknown, complete sequence

Sequence ID: **gb|AC207086.4|** Length: 215640 Number of Matches: 2

Range 1: 123725 to 123760

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	33/37(89%)	1/37(2%)	Plus/Minus	
Features:					
Query 480	GTGTGTGAGAGTAACGTGTGTGAGAGTAGCAGGTGTG	516			
Sbjct 123760	GTGTGTGAGAGTGA-GTGTGTGAGAGTAGCAAGTATG	123725			

Range 2: 123731 to 123760

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Minus	
Features:					
Query 273	GTGTGTGAGAGTAACGTGTGTGAGAGTAGCA	303			
Sbjct 123760	GTGTGTGAGAGTGA-GTGTGTGAGAGTAGCA	123731			