

Basic Local Alignment Search Tool

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GTAC

RID [Y0UCVZHE01R](#) (Expires on 08-06 13:20 pm)

Query ID lc|233475

Description None

Molecule type nucleic acid

Query Length 952

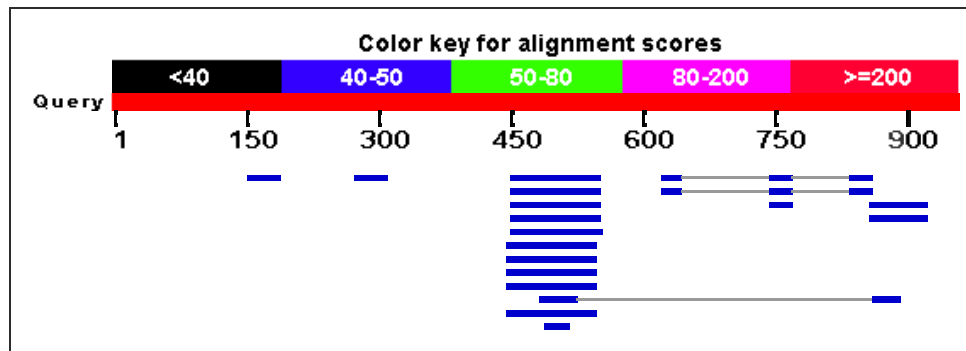
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 26 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Bos taurus liprin-alpha-1-like (LOC781635), transcript variant X1, mRNA	44.6	44.6	10%	2.2	73%	XM_003585571.2
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101902420), partial mRNA	44.6	44.6	10%	2.2	73%	XM_005200548.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101903852), mRNA	44.6	44.6	10%	2.2	73%	XM_005199954.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X2, mRNA	44.6	44.6	10%	2.2	73%	XM_005199772.1
PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X1, mRNA	44.6	44.6	10%	2.2	73%	XM_005199771.1
Homo sapiens BAC clone CH17-277L15 from chromosome 8, complete sequence	44.6	44.6	10%	2.2	71%	AC245121.2
Homo sapiens BAC clone CH17-31A6 from chromosome 8, complete sequence	44.6	44.6	10%	2.2	71%	AC245519.3
Homo sapiens BAC clone CH17-174L20 from chromosome 8, complete sequence	44.6	44.6	10%	2.2	71%	AC245187.1
Homo sapiens FOSMID clone ABC27-926G5 from chromosome 8, complete sequence	44.6	44.6	10%	2.2	72%	AC240557.2
Antheraea pernyi nucleopolyhedrovirus isolate AnpeMNPV-L2, complete genome	44.6	133	7%	2.2	100%	EF207986.1
Antheraea pernyi nucleopolyhedrovirus, complete genome	44.6	133	7%	2.2	100%	DQ486030.3
Mytilus galloprovincialis microsatellite ISSR sequence, clone 16.554	44.6	172	7%	2.2	82%	AJ938115.1
Homo sapiens chromosome 8, clone CTD-2517C5, complete sequence	44.6	44.6	10%	2.2	72%	AC133633.5
PREDICTED: Fragaria vesca subsp. vesca uncharacterized LOC101295560 (LOC101295560), mRNA	42.8	42.8	3%	7.6	83%	XM_004306719.1
Procamburus clarkii myosin light chain 2 mRNA, complete cds	42.8	42.8	2%	7.6	93%	JX013934.1
Cellulomonas fimi ATCC 484, complete genome	42.8	42.8	2%	7.6	93%	CP002666.1
Zebrafish DNA sequence from clone DKEY-159N16 in linkage group 4, complete sequence	42.8	42.8	3%	7.6	90%	BX927318.10
Human DNA sequence from clone RP11-298P3 on chromosome 13, complete sequence	42.8	42.8	6%	7.6	78%	AL137247.14
Human DNA sequence from clone RP1-130N4 on chromosome 13, complete sequence	42.8	42.8	6%	7.6	78%	Z75887.2

Alignments

PREDICTED: Bos taurus liprin-alpha-1-like (LOC781635), transcript variant X1, mRNA

Sequence ID: [ref|XM_003585571.2|](#) Length: 1059 Number of Matches: 1

Range 1: 61 to 157

Score	Expect	Identities	Gaps	Strand	Frame
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Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	77/106(73%)	12/106(11%)	Plus/Minus	
Features:					
Query 449	TCTC	ACTACGACATATACGCGCGCGCAGGCT-CTCTC	ACTAAGCTCTCTC	ACTACTA	507
Sbjct 157	TCTC	ACTACGACACCACTCTC	ACTACTGCTCTC	ACTACTA	101
Query 508	CGACC--TCTC	ACTACGACTCGTAGCTGGCTCTC	ACTACTACGAC		551
Sbjct 100	C-ACCGTTCTC	ACTATGACCACT-----GCTCTC	ACTATGAC		61

PREDICTED: Bos taurus liprin-alpha-1-like (LOC101902420), partial mRNA
Sequence ID: **reflXM_005200548.1** Length: 2749 Number of Matches: 1
Range 1: 1827 to 1923

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	77/106(73%)	12/106(11%)	Plus/Minus	
Features:					
Query 449	TCTC	ACTACGACATATACGCGCGCGCAGGCT-CTCTC	ACTAAGCTCTCTC	ACTACTA	507
Sbjct 1923	TCTC	ACTACGACACCACTCTC	ACTACTGCTCTC	ACTACTA	1867
Query 508	CGACC--TCTC	ACTACGACTCGTAGCTGGCTCTC	ACTACTACGAC		551
Sbjct 1866	C-ACCGTTCTC	ACTATGACCACT-----GCTCTC	ACTATGAC		1827

PREDICTED: Bos taurus liprin-alpha-1-like (LOC101903852), mRNA
Sequence ID: **reflXM_005199954.1** Length: 1680 Number of Matches: 1
Range 1: 132 to 228

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	77/106(73%)	12/106(11%)	Plus/Minus	
Features:					
Query 449	TCTC	ACTACGACATATACGCGCGCGCAGGCT-CTCTC	ACTAAGCTCTCTC	ACTACTA	507
Sbjct 228	TCTC	ACTACGACACCACTCTC	ACTACTGCTCTC	ACTACTA	172
Query 508	CGACC--TCTC	ACTACGACTCGTAGCTGGCTCTC	ACTACTACGAC		551
Sbjct 171	C-ACCGTTCTC	ACTATGACCACT-----GCTCTC	ACTATGAC		132

PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X2, mRNA
Sequence ID: **reflXM_005199772.1** Length: 763 Number of Matches: 1
Range 1: 91 to 187

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	77/106(73%)	12/106(11%)	Plus/Minus	
Features:					
Query 449	TCTC	ACTACGACATATACGCGCGCGCAGGCT-CTCTC	ACTAAGCTCTCTC	ACTACTA	507
Sbjct 187	TCTC	ACTACGACACCACTCTC	ACTACTGCTCTC	ACTACTA	131
Query 508	CGACC--TCTC	ACTACGACTCGTAGCTGGCTCTC	ACTACTACGAC		551
Sbjct 130	C-ACCGTTCTC	ACTATGACCACT-----GCTCTC	ACTATGAC		91

PREDICTED: Bos taurus liprin-alpha-1-like (LOC101909461), transcript variant X1, mRNA
Sequence ID: **reflXM_005199771.1** Length: 859 Number of Matches: 1
Range 1: 91 to 187

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	77/106(73%)	12/106(11%)	Plus/Minus	
Features:					
Query 449	TCTC	ACTACGACATATACGCGCGCGCAGGCT-CTCTC	ACTAAGCTCTCTC	ACTACTA	507
Sbjct 187	TCTC	ACTACGACACCACTCTC	ACTACTGCTCTC	ACTACTA	131
Query 508	CGACC--TCTC	ACTACGACTCGTAGCTGGCTCTC	ACTACTACGAC		551
Sbjct 130	C-ACCGTTCTC	ACTATGACCACT-----GCTCTC	ACTATGAC		91

Homo sapiens BAC clone CH17-277L15 from chromosome 8, complete sequence

Sequence ID: **gb|AC245121.2|** Length: 201829 Number of Matches: 1

Range 1: 162524 to 162623

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	75/105(71%)	9/105(8%)	Plus/Plus	

Features:

```
Query 445      GCTCTCTCACACTACGACATATACGCGCGCGCAGGCTCTCTCACAC---TAAGCTCTCTC 501
               |||
Sbjct 162524   GCTCTCTCACACTCACACACACATACTCTCCCATGCTCTCTCACACACACATGCTCTCTC 162583
               |||
Query 502      ACACTACGACCTCTCACACTACGACTCGTA-GCTGGCTCTCACAC 545
               |||
Sbjct 162584   ---CTAC--ACTCACACACTCACACTCACATGCTGTCTCTCACAC 162623
               |||
```

Homo sapiens BAC clone CH17-31A6 from chromosome 8, complete sequence

Sequence ID: **gb|AC245519.3|** Length: 206677 Number of Matches: 1

Range 1: 66952 to 67051

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	75/105(71%)	9/105(8%)	Plus/Plus	

Features:

```
Query 445      GCTCTCTCACACTACGACATATACGCGCGCGCAGGCTCTCTCACAC---TAAGCTCTCTC 501
               |||
Sbjct 66952    GCTCTCTCACACTCACACACACATACTCTCCCATGCTCTCTCACACACACATGCTCTCTC 67011
               |||
Query 502      ACACTACGACCTCTCACACTACGACTCGTA-GCTGGCTCTCACAC 545
               |||
Sbjct 67012    ---CTAC--ACTCACACACTCACACTCACATGCTGTCTCTCACAC 67051
               |||
```

Homo sapiens BAC clone CH17-174L20 from chromosome 8, complete sequence

Sequence ID: **gb|AC245187.1|** Length: 212712 Number of Matches: 1

Range 1: 192699 to 192798

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	75/105(71%)	9/105(8%)	Plus/Minus	

Features:

```
Query 445      GCTCTCTCACACTACGACATATACGCGCGCGCAGGCTCTCTCACAC---TAAGCTCTCTC 501
               |||
Sbjct 192798   GCTCTCTCACACTCACACACACATACTCTCCCATGCTCTCTCACACACACATGCTCTCTC 192739
               |||
Query 502      ACACTACGACCTCTCACACTACGACTCGTA-GCTGGCTCTCACAC 545
               |||
Sbjct 192738   ---CTAC--ACTCACACACTCACACTCACATGCTGTCTCTCACAC 192699
               |||
```

Homo sapiens FOSMID clone ABC27-926G5 from chromosome 8, complete sequence

Sequence ID: **gb|AC240557.2|** Length: 37415 Number of Matches: 1

Range 1: 1168 to 1265

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	74/103(72%)	7/103(6%)	Plus/Minus	

Features:

```
Query 445      GCTCTCTCACACTACGACATATACGCGCGCGCAGGCTCTCTCACAC-TAAGCTCTCTCAC 503
               |||
Sbjct 1265     GCTCTCTCACACTCACACACACATACTCTCCCATGCTCTCACACACACATGCTCTCTC-- 1208
               |||
Query 504      ACTACGACCTCTCACACTACGACTCGTA-GCTGGCTCTCACAC 545
               |||
Sbjct 1207     -CTAC--ACTCACACACTCACACTCACATGCTGTCTCTCACAC 1168
               |||
```

Antheraea pernyi nucleopolyhedrovirus isolate AnpeMNPV-L2, complete genome

Sequence ID: **gb|EF207986.1|** Length: 126246 Number of Matches: 3

Range 1: 90878 to 90901

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 830 CGCGCGCAGCCGCGCATCTAGCGC 853
 Sbjct 90901 CGCGCGCAGCCGCGCATCTAGCGC 90878

Range 2: 90878 to 90901

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 740 CGCGCGCAGCCGCGCATCTAGCGC 763
 Sbjct 90901 CGCGCGCAGCCGCGCATCTAGCGC 90878

Range 3: 90878 to 90901

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 617 CGCGCGCAGCCGCGCATCTAGCGC 640
 Sbjct 90901 CGCGCGCAGCCGCGCATCTAGCGC 90878

Antheraea pernyi nucleopolyhedrovirus, complete genome

Sequence ID: **gb|DQ486030.3|** Length: 126629 Number of Matches: 3

Range 1: 36178 to 36201

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 617 CGCGCGCAGCCGCGCATCTAGCGC 640
 Sbjct 36178 CGCGCGCAGCCGCGCATCTAGCGC 36201

Range 2: 36178 to 36201

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 740 CGCGCGCAGCCGCGCATCTAGCGC 763
 Sbjct 36178 CGCGCGCAGCCGCGCATCTAGCGC 36201

Range 3: 36178 to 36201

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 830 CGCGCGCAGCCGCGCATCTAGCGC 853
 Sbjct 36178 CGCGCGCAGCCGCGCATCTAGCGC 36201

Mytilus galloprovincialis microsatellite ISSR sequence, clone 16.554

Sequence ID: **emb|AJ938115.1|** Length: 554 Number of Matches: 4

Range 1: 141 to 189

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	40/49(82%)	6/49(12%)	Plus/Minus	

Features:

Query 480 CTCTCTCACAATAA---GCTCTCTCACAACGAC---CTCTCACAATA 522
 Sbjct 189 CTCTCTCACAATAATATCCTCTCTCACAACGACCCCTCTCTCACAATA 141

Range 2: 141 to 171

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Minus	
Features:					
Query	856	CTCTCTCACACTACGACGCTCTCTCACACTA	886		
Sbjct	171	CTCTCTCACACTAGCACCTCTCTCACACTA	141		

Range 3: 177 to 207

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Minus	
Features:					
Query	856	CTCTCTCACACTACGACGCTCTCTCACACTA	886		
Sbjct	207	CTCTCTCACACTAGTACCTCTCTCACACTA	177		

Range 4: 195 to 225

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Minus	
Features:					
Query	856	CTCTCTCACACTACGACGCTCTCTCACACTA	886		
Sbjct	225	CTCTCTCACACTAGTACCTCTCTCACACTA	195		

Homo sapiens chromosome 8, clone CTD-2517C5, complete sequence

Sequence ID: **gb|AC133633.5|** Length: 94195 Number of Matches: 1

Range 1: 8683 to 8780

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	74/103(72%)	7/103(6%)	Plus/Minus	
Features:					
Query	445	GCTCTCTCACACTACGACATATACGCGCGCAGGCTCTCTCACAC-TAAGCTCTCTCAC	503		
Sbjct	8780	GCTCTCTCACACTCACACACACATACTCTCCCATGCTCTCACACACACATGCTCTCTC--	8723		
Query	504	ACTACGACCTCTCACACTACGACTCGTA-GCTGGCTCTCACAC	545		
Sbjct	8722	-CTAC--ACTCACACACTCACACTCACATGCTGTCTCTCTCACAC	8683		

PREDICTED: *Fragaria vesca* subsp. *vesca* uncharacterized LOC101295560 (LOC101295560), mRNA

Sequence ID: **ref|XM_004306719.1|** Length: 1475 Number of Matches: 1

Range 1: 229 to 269

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	4/41(9%)	Plus/Plus	
Features:					
Query	154	TGCATGCAGTCGTCTGCGATAG----GGAGAGAGCTCTCTC	190		
Sbjct	229	TGCATGGAGTCATCTGTGATAGCTGCGGAGAGAGCTCTCTC	269		

Procambarus clarkii myosin light chain 2 mRNA, complete cds

Sequence ID: **gb|JX013934.1|** Length: 1362 Number of Matches: 1

Range 1: 1107 to 1134

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	
Features:					
Query	487	ACACTAAGCTCTCTCACACTACGACCTC	514		
Sbjct	1134	ACACTGAGCTCCCTCACACTACGACCTC	1107		

Cellulomonas fimi ATCC 484, complete genome
Sequence ID: **gb|CP002666.1|** Length: 4266344 Number of Matches: 1
Range 1: 2834762 to 2834789

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

Features:
GCN5-related N-acetyltransferase

```
Query 739      GCGCGCGCAGCCGCGCATCTAGCGCCTC 766
                |||
Sbjct 2834762  GCGCGCGCAGCCGCGCCTCGAGCGCCTC 2834789
```

Zebrafish DNA sequence from clone DKEY-159N16 in linkage group 4, complete sequence
Sequence ID: **emb|BX927318.10|** Length: 149430 Number of Matches: 1
Range 1: 57167 to 57203

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/39(90%)	3/39(7%)	Plus/Minus	

Features:

```
Query 273      CTCTCTCACACTAAGCTCTCTCACAC-TACGACATATAC 310
                |||
Sbjct 57203    CTCTCTCACAC-AAGCTCTCTCACACATAC-ACATACAC 57167
```

Human DNA sequence from clone RP11-298P3 on chromosome 13, complete sequence
Sequence ID: **emb|AL137247.14|** Length: 79506 Number of Matches: 1
Range 1: 73343 to 73401

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/65(78%)	7/65(10%)	Plus/Minus	

Features:

```
Query 852      GCAGCTCTCTCACACTACGACGCTCTCTCACACTACCGCGCATCTAGC-GCAGCTCTCTC 910
                |||
Sbjct 73401    GCAGCTCACTCACACTA----GCTCTCTCAT-CAGCAGCTC-TCTCGCAGCAGCTCTCTC 73348

Query 911      ACACT 915
                |||
Sbjct 73347    ACACT 73343
```

Human DNA sequence from clone RP1-130N4 on chromosome 13, complete sequence
Sequence ID: **emb|Z75887.2|** Length: 84169 Number of Matches: 1
Range 1: 12086 to 12144

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/65(78%)	7/65(10%)	Plus/Minus	

Features:

```
Query 852      GCAGCTCTCTCACACTACGACGCTCTCTCACACTACCGCGCATCTAGC-GCAGCTCTCTC 910
                |||
Sbjct 12144    GCAGCTCACTCACACTA----GCTCTCTCAT-CAGCAGCTC-TCTCGCAGCAGCTCTCTC 12091

Query 911      ACACT 915
                |||
Sbjct 12090    ACACT 12086
```