BLAST ®

Basic Local Alignment Search Tool

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Blast report description

Nucleotide Sequence (7037 letters)

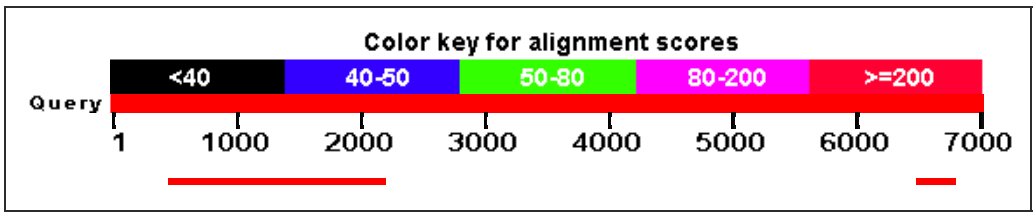
RID CF61S751014 (Expires on 02-21 05:33 am)

Query ID lcl|Query_58665
Description None
Molecule type nucleic acid
Query Length 7037

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Nematostella vectensis predicted protein (NEMVEDRAFT_v1g165346) partial mRNA	3225	3225	24%	0.0	99%	XM_001634356.1
Nematostella vectensis predicted protein (NEMVEDRAFT_v1g232574) partial mRNA	571	571	4%	6e-158	99%	XM_001634355.1

Alignments

Nematostella vectensis predicted protein (NEMVEDRAFT_v1g165346) partial mRNA

Sequence ID: **ref|XM_001634356.1|** Length: 1758 Number of Matches: 1

Range 1: 1 to 1758

Score	Expect	Identities	Gaps	Strand	Frame
3225 bits(1746)	0.0()	1754/1758(99%)	0/1758(0%)	Plus/Minus	

Features:

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Query  472   GGCTGGGGTACTGGTAGCGAATTTGTCAGCCGAGTATCTTGGCGGGGGGTGAGGCGGACTT  531
Sbjct  1758  GGCTGGGGTACTGGTAGCGAATTTGTCAGCCGAGTATCTTGGCGGGGGGTGAGGCGGACTT  1699
Query  532   TGGGCGGATCGATCCGTAAGACCCATCCACAAGGGACTCTTCGAGTTTCTGCGACTCGCG  591
Sbjct  1698  TGGGCGGATCGATCCGTAAGACCCATCCACAAGGGACTCTTCGAGTTTCTGCGACTCGCG  1639
Query  592   GTCAAGCACCGTGGGCTCATAGATAGTGTCACGTGCCACGATGTTCAGGGAATCCTCAAG  651
Sbjct  1638  ATCAAGCACCGTGGGCTCATAGATAGTGTCACGTGCCACGATGTTCAGGGAATCCTCAAG  1579
Query  652   CTTACTGCGCAGGTCCTTGATCTCGTCGGATTTCTGAGCAGTGCGGGTTAGGTACGACTG  711
Sbjct  1578  CTTACTGCGCAGGTCCTTGATCTCGTCGGATTTCTGAGCAGTGCGGGTTAGGTACGACTG  1519
Query  712   CTTCTTCTGTAATTCTTTGGCGAGCTGGTCTTTCAGTGTGGCCACCTGCTCCTCCAAACC  771
Sbjct  1518  CTTCTTCTGTAATTCTTTGGCGAGCTGGTCTTTCAGTGTGGCCACCTGCTCCTCCAAACC  1459
Query  772   CTTGACTCTTTGCTTGTGTGCACGCTCGCGAGCCATTTGAGTCTTCTCTAGTTGGCCCTG  831
Sbjct  1458  CTTGACTCTTTGCTTGTGTGCACGCTCGCGAGCCATTTGAGTCTTCTCTAGTTGGCCCTG  1399
Query  832   AGACTGACGCGCGCGATCGCCCTCCATCTCGATCTCCTGACGGTGGCGTGACGTCACTTC  891
Sbjct  1398  AGACTGACGCGCGCGATCGCCCTCCATCTCGATCTCCTGACGGTGGCGTGACGTCACTTC  1339
Query  892   CACGAGTTTACGCGCGTGGGACTGCTCTGTCTCGGCCAGCTGCTGCTGTAGTATCTGAAT  951
Sbjct  1338  CACGAGTTTACGCGCGTGGGACTGCTCTGTCTCGGCCAGCTGCTGCTGTAGTATCTGAAT  1279
Query  952   CTGGCGATGCAGCTCTTGGTTCTCGTGCTCGAAGTTCGCGCTGGATCGATCAAGACGCTC  1011
Sbjct  1278  CTGGCGATGCAGCTCTTGGTTCTCGTGCTCGAAGTTCGCGCTGGATCGATCAAGACGCTC  1219
Query  1012  GCGGTCATCGCGCAGACGCGTGTTCGTCTCGTCCGTCTCGAGCTTTTCGCGTTCAATCTT  1071
Sbjct  1218  GCGGTCATCGCGCAGACGCGTGTTCGTCTCGTCCGTCTCGAGCTTTTCGCGTTCAATCTT  1159
Query  1072  GTCGAGGGTGTTACGAAGAGCCTTCTTATCCTTCTCCAGACGCACATGAGCTCGCTCCAG  1131
Sbjct  1158  GTCGAGGGTGTTACGAAGAGCCTTCTTATCCTTCTCCAGACGCACATGAGCTCGCTCCAG  1099
Query  1132  TTCCCTTTTCTCCTGCTCGGCCGCGGCCACCGAGCGTTGGAATTTCGCCAGGCGTTCCTG  1191
Sbjct  1098  TTCCCTTTTCTCCTGCTCGGCCGCGGCAACCGAGCGCTGGAATTTCGCCAGGCGTTCCTG  1039
Query  1192  GAGCTCACGCTTCTCCTCTTGTAGCTTGCCAATCCTCGCTACCAGTTCCTCCTCGGCCTC  1251
Sbjct  1038  GAGCTCACGCTTCTCCTCTTGTAGCTTGCCAATCCTCGCTACCAGTTCCTCCTCGGCCTC  979
Query  1252  CTTCTGTTGTCGCAGCATCTGCTGCAGCTGGCGGATCTGGCCTTCAAGTTCCATGCGTCG  1311
Sbjct  978   CTTCTGTTGTCGCAGTATCTGCTGCAGCTGGCGGATCTGGCCTTCAAGTTCCATGCGTCG  919
Query  1312  CACATCGGCATCAGCCTGTTCGTTCTTCATCTGTTGCATGCGGTCCTGTAGCATATTGTT  1371
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Sbjct  918   CACATCGGCATCAGCCTGTTCGTTCTTCATCTGTTGCATGCGGTCCTGTAGCATATTGTT  859
Query  1372  ACGGCCCTTGGCCTCCTGCTGGGCGTTCTTGAGCGCCTCCAGGCGCTCCTGCATGATCTT  1431
Sbjct  858   ACGGCCCTTGGCCTCCTGCTGGGCGTTCTTGAGCGCCTCCAGGCGCTCCTGCATGATCTT  799
Query  1432  GCGGTCGTGCTCGCTATTGGTCAGGGCACGCTGGAGCTGCTGGATCCTCTCCTGTAGCGA  1491
Sbjct  798   GCGGTCGTGCTCGCTATTGGTCAGGGCACGCTGGAGCTGCTGGATCCTCTCCTGTAGCGA  739
Query  1492  CTGCGAGGTGCTGTTGCTGTCATTCAGGGACATGGACAGCTCTGTCACCTTGTTCTTGAA  1551
Sbjct  738   CTGCGAGGTGCTGTTGCTGTCATTCAGGGACATGGACAGCTCTGTCACCTTGTTCTTGAA  679
Query  1552  TGCCATCTCCTCTTCCTCGGTCTTGGCGAGCGCCAGGGTCAGCCTATCCACCGTCAGCTG  1611
Sbjct  678   TGCCATCTCCTCTTCCTCGGTCTTGGCGAGCGCCAGGGTCAGCCTATCCACCGTCAGCTG  619
Query  1612  AAGAGAAGTCGCGCGTGACTCCAGCTCTTGCTGAGATTTAAGCATCTGGTCAATTCGCTC  1671
Sbjct  618   AAGAGAAGTCGCGCGTGACTCCAGCTCTTGCTGAGATTTAAGCATCTGGTCAATTCGCTC  559
Query  1672  CTGAAGAGCGATCTTCTCCGCCTCATTCTCCGAGTTCAGCATTCGCAGTCGCTCAATGTC  1731
Sbjct  558   CTGAAGAGCGATCTTCTCCGCCTCATTCTCCGAGTTCAGCATTCGCAGTCGCTCAATGTC  499
Query  1732  ACCCTCCACGGACCTCTTCTTCAGTTCCACCTTCGTAAGCCTCGACTCCGTATTCTCAAT  1791
Sbjct  498   ACCCTCCACGGACCTCTTCTTCAGTTCCACCTTCGTAAGCCTCGACTCCGTATTCTCAAT  439
Query  1792  CTGCGCGCGCATCGCCTCTTTCTCCTGGTCGCTCTTACTCTCGCTCTGTTGCAAGTTCGC  1851
Sbjct  438   CTGCGCGCGCATCGCCTCTTTCTCCTGGTCGCTCTTACTCTCGCTCTGTTGCAAGTTCGC  379
Query  1852  CACCTTGTCTCTCAGCTGTCGGCGGTCACCCTCTGCCTGCGCGAGACTGGAGTCGAGTGC  1911
Sbjct  378   CACCTTGTCTCTCAGCTGTCGGCGGTCACCCTCTGCCTGCGCGAGACTGGAGTCGAGTGC  319
Query  1912  GGTGATCTTCTCGTTGAGAGCCTTGCGCTCTCGTTCAAGTCTCCTTATGGTCTCTTCTTG  1971
Sbjct  318   GGTGATCTTCTCGTTGAGAGCCTTGCGCTCTCGTTCAAGTCTCCTTATGGTCTCTTCTTG  259
Query  1972  AAGCATGAGCGCAGTCTGGGCACTACTCAGGCGGCCATCAGCACCGCGGCGCTCTTCTTC  2031
Sbjct  258   AAGCATGAGCGCAGTCTGGGCACTACTCAGGCGGCCATCAGCACCGCGGCGCTCTTCTTC  199
Query  2032  AGACTCACCAAGGGATTTCTGGATGCTCTGCATACGCTGGTCCATACGAGTCCGCTCTTC  2091
Sbjct  198   AGACTCACCAAGGGATTTCTGGATGCTCTGCATACGCTGGTCCATACGAGTCCGCTCTTC  139
Query  2092  TTCCAACTCGGCAAGCGCGCGCTGCAAGTTATTAGCGCGTGTCACAGCCTCGTCCCGCTC  2151
Sbjct  138   TTCCAACTCGGCAAGCGCGCGCTGCAAGTTATTAGCGCGTGTCACAGCCTCGTCCCGCTC  79
Query  2152  TCTCTCGGCCTCCTTCATGCTCTGGGCGAAGTCCCGCAGCGCGACCCGCACGGTCTCGGG  2211
Sbjct  78    TCTCTCGGCCTCCTTCATGCTCTGGGCGAAGTCCCGCAGCGCGACCCGCACGGTCTCGGG  19
Query  2212  ATCGATCTCGCCAGACAT  2229
Sbjct  18    ATCGATCTCGCCAGACAT  1
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Nematostella vectensis predicted protein (NEMVEDRAFT_v1g232574) partial mRNA

Sequence ID: **ref|XM_001634355.1|** Length: 411 Number of Matches: 1

Range 1: 1 to 312

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	6e-158()	311/312(99%)	0/312(0%)	Plus/Minus	

Features:

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Query  6505  CCTCTCGCTAACGGCCATGTATTTAGAACCAACTTCATCTCTTTCAGCTCTTGTAGCCGC  6564
Sbjct  312   CCTCTCGCTTACGGCCATGTATTTAGAACCAACTTCATCTCTTTCAGCTCTTGTAGCCGC  253
Query  6565  TAGAAGGTCTTCCAGTCGGCTTATTTCAGACTGGTACATGCGAGACTCATCTCCGAGGCT  6624
Sbjct  252   TAGAAGGTCTTCCAGTCGGCTTATTTCAGACTGGTACATGCGAGACTCATCTCCGAGGCT  193
Query  6625  ACTACCGGCCATTTTATGTTCAACAGGGGAGATGCTTTTGGTGACGATATCTCGAATTTT  6684
Sbjct  192   ACTACCGGCCATTTTATGTTCAACAGGGGAGATGCTTTTGGTGACGATATCTCGAATTTT  133
Query  6685  AGTAGGAACTGTTGGGCTTCTTGAGCCAGGATCACCGTTCAGATGTTGATCTTCCAATCT  6744
Sbjct  132   AGTAGGAACTGTTGGGCTTCTTGAGCCAGGATCACCGTTCAGATGTTGATCTTCCAATCT  73
Query  6745  CTTTATAACAGAACTTAAACCAGGTTCTGGGGAACCGCCATAGTAAGAGGTTTTAGATTC  6804
Sbjct  72    CTTTATAACAGAACTTAAACCAGGTTCTGGGGAACCGCCATAGTAAGAGGTTTTAGATTC  13
Query  6805  TTGGTAACTCAT  6816
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Sbjct  12    TTGGTAACTCAT  1
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