

Basic Local Alignment Search Tool

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Nucleotide Sequence (1396 letters)

RID [CN9W6K21015](#) (Expires on 02-23 13:15 pm)

Query ID lcl|Query_47157

Description None

Molecule type nucleic acid

Query Length 1396

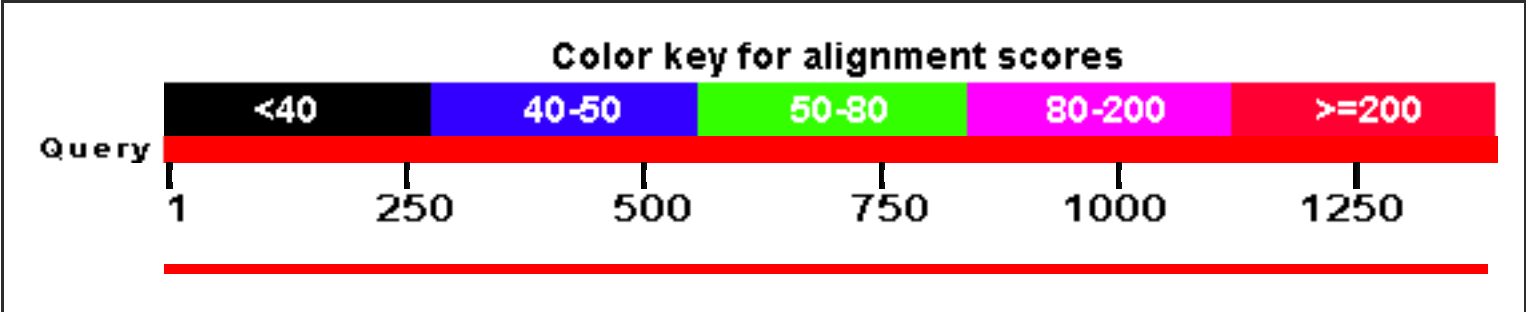
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.3.1+

[Graphic Summary](#)

Distribution of 1 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila x virus polyprotein gene, complete cds	874	874	99%	0.0	78%	U60650.1

Alignments

Drosophila x virus polyprotein gene, complete cds
Sequence ID: **gb|U60650.1|DXU60650** Length: 3360 Number of Matches: 1
Range 1: 1909 to 3295

Score	Expect	Identities	Gaps	Strand	Frame
874 bits(473)	0.0()	1093/1397(78%)	23/1397(1%)	Plus/Minus	
Features:					
Query 2		GGTGTGTTAGTGTAGTTGGCACTACCTCTAAAACTCTCCTCACCTA-TCTTCTCTGTC			60
Sbjct 3295		GGTTTGTAGTGTAGTTGGCACTACCTCTAAAAATTCCTCACCTCCTC-TCTCTGAC			3237
Query 61		GGACCATGAGTCATGAGTTCATGGCTGGATTTATACAATGTTTTCATCCTCTCCTTGAC			120
Sbjct 3236		GGCCCATGAGTCATGAGTTCATGGGTGGACTTATACAATGTCATTGTCTCTCCACGCAC			3177
Query 121		TCCCCGAATTTCGAGAAGTGAAGCCCTCCGACTGGAGGGGA-CAGTTTGGACAGTCTGAG			179
Sbjct 3176		TCTTCGCAATCGGTCAAGTGCGGCCCTCCTTCCGG-GGGGATCAGTTTGAGCAGTCTGAG			3118
Query 180		CTGATACAAGTCGTCGTGGGGGCACCTTAGGTGC--TTGTCTCGGTTGGGTAACAAGTGT			237
Sbjct 3117		CTGATACAATTCGGCGTGGGGGGACTCTAGGAGCAGTTG-C-CGGTTGGTTGACAAGTGA			3060
Query 238		GTGTGAAATTAGTCTGCGTACCGCATGGCTAAGCTCTCGAGCCTGCTCCTGTGATGGCCC			297
Sbjct 3059		GTGCGAAATAAGCCTGCGGACAGCATGACTTAATTCCCGAGCTTGTTCCCTGGGATGGCCC			3000
Query 298		CTTACCTTGATTTCTGTCAATACCTCATCGACGAGATCTCTCACGGCACTTATC-TGAT			356
Sbjct 2999		CTTCCCTTGATTTCTGTCTATATGTCGTGACAAGGTCCTTAACAGCA-TCGGCTTGTT			2941
Query 357		CTTCGCTTGAGATGGTCCAAGCATTAGCGTGTAGCTATCATAATGCCTCCGAATGGATC			416
Sbjct 2940		CTTGCGTTGGTGACGGCCCAAGCATCATAATGTAGCTGTCTAGTGTCTGCTT-TGGA-C			2883
Query 417		TGGGAGGAGG-A--GGTTGTGTCCAGTCCTCATCCCTGAGCCACAAGGCTATTTGGGTGC			473
Sbjct 2882		ACG-AGGTGGTATTGGCTGGGACCAATCGTCACCTTTAACCACATTGCGATTGTATGC			2824
Query 474		CTGTGGGCAACGACTCTTGCTCCATCCAAAAGTCTACAAAGTCATCTTCAGTATATGAAT			533
Sbjct 2823		CAGTAGGCAATGACTCCTGCTCCATCCAATAGGATACAAAGTCATCCACAGTGTACGACT			2764
Query 534		-TGCTAATGGAAGCATTATTTGTGAAGATTCTCCGTAACCTTGCAGCCTTTTGGCTCTTC			592
Sbjct 2763		CTTGG-ATCGAGGCGTTATTGCTATAGATTCTCCGTAACCTTGCATCCTTTTGGTTCTTC			2705
Query 593		CGGGCTTTCCTCATTGCGAGTTCTGTGTCCGCTGTGTGATTTTCCCACTAGTCATTATC			652
Sbjct 2704		CGAGCAATCCTCATTGCTAGTTCCGTGTCTTCTTTCGATATTCTTCCTCTTGACATTATT			2645
Query 653		CTGCTCTCATCAACATAGATTCCCTTGTTTTCTAGGTTCTTATTTTTCTTTCTAGCCTT			712
Sbjct 2644		TTGCTCTCATCAACATATATCCCTTGATTTTCCAAGTTTCGAAGTTTTCGTTCTAGTCTT			2585
Query 713		TGCCTTCTTTTCGTCCGGTGACCTCTTGAGACTGGGTCTGTATGTTGAGTGCGCTTTTCACT			772
Sbjct 2584		TGCCTTCTTTTCGCCGGTGACTTCTCGAGACTGGGTTTCGATGTTTCAGAGCGCTTTTACT			2525
Query 773		ACCATGTTACGAGTGAGCGACCTTTTCCTTGGCTGATTAAGCTGAACATAGCTTCCTCC			832
Sbjct 2524		ACCATGTTGATAAGAGACCGGCTCTCCCTTGGCTTATCAAGCTGAACATTGCCTCCTCT			2465
Query 833		AGATCTTTGTGCTCCAGTATATACTCGTGAATTGTGGCTATCTTCTCCTGGGAGCTCGGG			892
Sbjct 2464		AACTCCTTGTGTTCCAGGAGGTACTCGTGTATTGTGGCAATCTTCTCTTGAGAGCTTGGG			2405

Query	893	ATCGTCTGTCCGTCTGCGAGGAACATGTCGCGGGTATCTTCCGATATTGCCTTCGCTATG	952
Sbjct	2404	ATGGTTTGGACCGTCCGATAGAAACAAATCCCGAGTCTCCTCGGAGATTGGCTTTGCAGCG	2345
Query	953	TTCCCCTGCAGGGGGACGTCTTCGTTCGTTCAAGAATGGGTTCGTTGACAAGAACGGGTTC	1012
Sbjct	2344	TTGCTTGGTATCGGCTGGTCCAACCTCTTCCAGGAATGGGTTCGTGTTTCATGAATGGGTTC	2285
Query	1013	GT--T-GAAGATCCCGCTGTCCAGTGTGGCAATGTCCTTTTTTGGTGTCCCTTCTTTTACG	1069
Sbjct	2284	ATGCTCGCGGACCCGGCTGTCCAGTGCGGGAGGGTCTGTTTTGGGGTTCTTCTCTTTACG	2225
Query	1070	TCGCCCATATCTTTTATTTTCTTGTCCAGAGCTCTTAGGTTTCGTAACCTGGGACCAATCCT	1129
Sbjct	2224	TCTCCCATATCTTTTATCTTTTGTCCAGAGATGTCAGGGTCTTTACTTGAACATAATCCT	2165
Query	1130	GGTGAGTTCCCAAGTAGAGGTATCCCAAGGGAGTCCGTCAGGTGGAGTTTCAGGTTGATT	1189
Sbjct	2164	GGTGAGTTCCCAAGTAGTGGAATCCCAAGAGAGTCCGTCAATTGGAGTTTCAGGTTGATG	2105
Query	1190	CCAAAAACTTCTCCCACCGTTGATCCGACAACGGATCCGGTGAAAGCGGCAAATGGTGCC	1249
Sbjct	2104	CCAAAAACTTCTCCCACACTGGACCCGACAACGGATCCTGTGAAAGCTGCAAATGGTGCC	2045
Query	1250	TTCCCTAGCACTCCATTCTTCTG-AAGATCGTCTGCTGCATATATGGCAAGCTGGTGGGA	1308
Sbjct	2044	TTCCCCAAAACCTCCACTCTTTAGTAAG-TCGTCTGCTGCATAAATGGCAAGCTGGTGGGA	1986
Query	1309	TGTTCCCGTTACTTTGTTTGGAGAAGTTGACGATGCTAGTTTTCCGTCTAATAACTGATA	1368
Sbjct	1985	CGTTCCCGTTACCTTGTTTGGTGATGTCGACGATGCGAGTCTTCCTTCTAATAATTGATA	1926
Query	1369	GCATGGTAGGAGGATGT	1385
Sbjct	1925	GCATGGTAGGAGGATGT	1909