

# Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastn suite/](#) **Formatting Results - CN9ZKP0W014**

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## Nucleotide Sequence (1285 letters)

**RID**    [CN9ZKP0W014](#) (Expires on 02-23 13:17 pm)

**Query ID**    lcl|Query\_140179

**Description**    None

**Molecule type**    nucleic acid

**Query Length**    1285

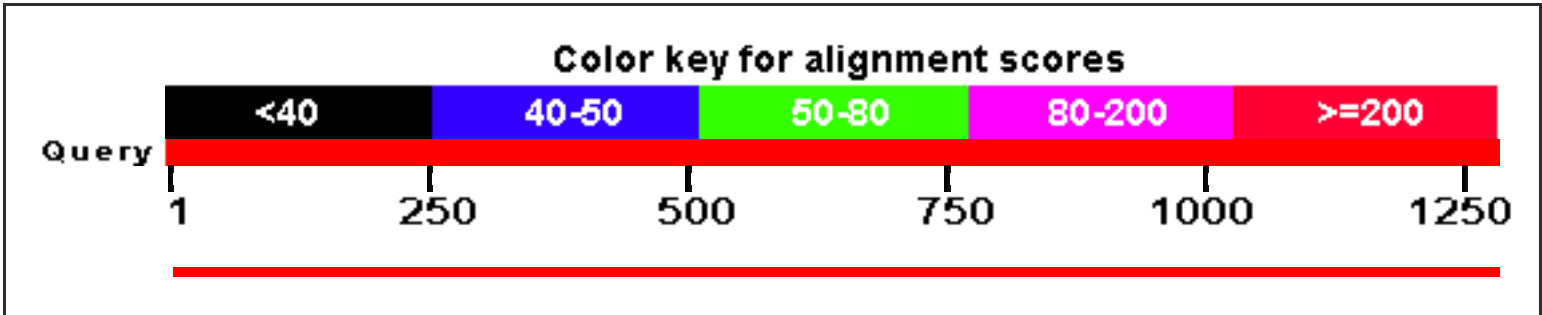
**Database Name**    nr

**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	771	771	99%	0.0	78%	<a href="#">U60650.1</a>

Alignments

Drosophila x virus polyprotein gene, complete cds  
Sequence ID: **gb|U60650.1|DXU60650** Length: 3360 Number of Matches: 1  
Range 1: 448 to 1725

Score	Expect	Identities	Gaps	Strand	Frame
771 bits(417)	0.0()	996/1283(78%)	10/1283(0%)	Plus/Plus	
Features:					
Query 8		TGAACGGAAC	TTTCAATGCAGTTTGGTTCCAGGGTACACTCAGCG-AG-GTCAGTGATTA	65	
Sbjct 448		TGAATGGCACATTCAATGCAGTCTGGTTCCAAGGGACCTTGAGTGAAGTGTC--TGACTA	505		
Query 66		CTCATATGATAGGATCCTTTCAATCACGTCAAATCCTCTTGACAAGGTTGGTAATGTACT	125		
Sbjct 506		CTCTTACGATAGGATCCTGTCAATAACATCCAATCCTCTGGATAAGGTTGGAAATGTGTT	565		
Query 126		CGTTGGTGACGGGCTAGAGATTCTGAGCCTTCCACAAGGGTTCAACAACCCATATGTGAG	185		
Sbjct 566		GGTTGGAGACGGCATAGAGGTTCTAAGCCTGCCGCAGGGGTTCAACAACCCCTACGTTAG	625		
Query 186		GCTCGGTGATAAATCCCCATCAACTCTGCAATCACCAACGCACATCACCAACACATCACG	245		
Sbjct 626		GCTGGGTGACAAGTCACCGTCCACTCTATCCTCTCCAACCCACATAACCAACACTTCCCA	685		
Query 246		AAACCTTGGCTA-TGGTGGAGCCTACAAGATCCCATCAACCACGATCCCTGGACAAGGTA	304		
Sbjct 686		GAA-CTTGGCTACGGGAGGTGCATACATGATCCCAGTAACCACAGTTCCTGGGCAAGGAT	744		
Query 305		TCCACACAAAAGAGTTCAGCATCAACGTTGACTCAGTGGGTCCAATTGATATTATGTGGT	364		
Sbjct 745		TCCATAACAAGGAATTCAGCATTAATGTGGACTCCGTAGGGCCAGTTGACATCTTGTGGT	804		
Query 365		CTGGTCAAATGACCATGGTAGACGAATGGACTGTGACGGCCAACCTACCAACCACTTAACA	424		
Sbjct 805		CTGGTCAAATGACTATGCAGGACGAATGGACTGTAAGTCAAAATTATCAACCATTGAACA	864		
Query 425		TCTCAGGGACTTTGATTGCTGGCAG-CATGAAGACTCTAGTATGGTCAAACACAGGAGTG	483		
Sbjct 865		TCTCTGGCACGCTAATTGCAAACAGTCA-GCGAACCCTAACATGGTCCAACACTGGTGTA	923		
Query 484		GCCAACGGCAATCACTATATGAACATGAATGAACTAAACGTATCCCTCTTCCATGAAAAT	543		
Sbjct 924		TCCAATGGCAGCCACTACATGAACATGAACAACCTTAATGTCTCCCTTTTCCATGAGAAT	983		
Query 544		CCACCTCCCGAACCCGTCGCAGCATTGAAGGTTCAATAACCTATGGCAACAACACCAAC	603		
Sbjct 984		CCACCACCTGAACCCGTTGCCGCCATAAAAATAAACATCAATTATGGAAACAACACCAAT	1043		
Query 604		GGTGACAGTGACTTTAGTGTAGACTCGTCTTTCACTATCAACGTCATCGGTGGAGCAACC	663		
Sbjct 1044		GGTGACAGCTCGTTCAGTGTGGACTCATCATTTACCATCAATGTCATTGGGGGCGCCACC	1103		
Query 664		ATTGGCGTCAATTACCAACAGTAGTTGTTGGATAACCAGGCTGTGGCTGAAGGCACCGCT	723		
Sbjct 1104		ATTGGCGTCAACTCTCCAACAGTCGGTGTGTTGGTTACCAAGGAGTAGCTGAGGGCACCGCC	1163		
Query 724		ATCACAATTAGCGGAATCAACAACCTACGAGCTGGTACCGAACCTGACCTACAGAAAAAC	783		
Sbjct 1164		ATTACAATTAGCGGTATCAACAACCTATGAGCTGGTACCCAATCCGGACTTGCAAAAGAAC	1223		
Query 784		TTGCCTATGTCTTATGGAAAATGCGACCCCCAGGACCTGAACTACATCAAGTACATTTTA	843		
Sbjct 1224		CTGCCAATGACATATGGCACTTGTGATCCACATGATTTGACTTACATCAAGTACATACTG	1283		
Query 844		TCAAACCGAGAAAAACTCGGACTGCGCTCTGTAATGACACTAGCAGAATACAACCGTATG	903		
Sbjct 1284		TCAAACCGAGAACAGTTGGGACTTAGGTCAGTGATGACCTTGGCCGACTACAATAGGATG	1343		

Query	904	AAAATGTACATGCATGTACTGACCAACTACAACGTGGATGAGAAAGAGGCGGCAAGCTTC	963
Sbjct	1344	AAGATGTACATGCATGTACTGACGAACATATCATGTCGATGAGAGGGAAGCATCGAGCTTC	1403
Query	964	GACTTCTGGCACCTTCTAAAGCAGATAAAAAAGGTTGCTGTGCCCTTGGCAGCTACACTT	1023
Sbjct	1404	GATTTCTGGCAACTACTGAAACAGATAAAAAATGTTGCCGTGCCCTTGGCAGCTACACTT	1463
Query	1024	GCCCCCAATATGCTCCAATAATCGGAGCCGC-AAGCGGCTTGGCAGATGCTGTATTGGG	1082
Sbjct	1464	GCCCCCAGTTTCGCACCAATAATCGGTGCTGCCGATGGGTTAGCCA-ATGCAATATTGGG	1522
Query	1083	TGATAGTGCCAGTGGACGGCCAGTAGGCAATTCAGCCAGTGGTATGCCAATATCACTGAG	1142
Sbjct	1523	TGATAGCGCCAGCGGAAGGCCTGTTGGCAATTCGCTAGCGGTATGCCCATTTCAATGAG	1582
Query	1143	TAGGAGATTGAGAAATGCCTACTCAGCTGACTCCCCACTCGGGGAAGAGCATTGGAAGCC	1202
Sbjct	1583	TAGGCGTCTTAGAAACGCTTACTCAGCTGACTCCCCCTTAGGTGAAGAGCATTGGCTGCC	1642
Query	1203	GAACGAAAGCGAAGAGTTCAACAAATTTGACATCATCTACGACGTATCCTACTCATCCAT	1262
Sbjct	1643	AAACGAGAATGAGAACTTCAATAAATTTGACATCATCTATGACGTATCACATTCATCCAT	1702
Query	1263	GGCTTTATTTCCAGTCATAATGA	1285
Sbjct	1703	GGCTTTATTTCCAGTCATAATGA	1725