BLAST ®

Basic Local Alignment Search Tool

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Blast report description

Nucleotide Sequence (318 letters)

RID	CNA206AF014 (Expires on 02-23 13:18 pm)		
Query ID	lcl|Query_85697	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	318		
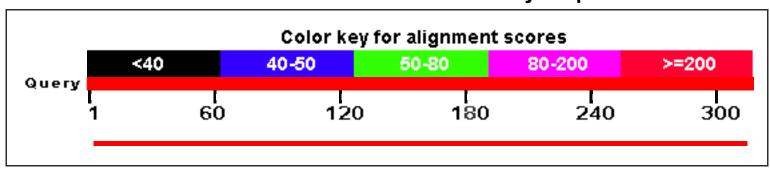
⊟ Graphic Summary

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 melanogaster birnavirus SW-2009a strain DBV segment A, complete sequence	322	322	98%	3e-84	85%	GQ342962.1

Alignments

Drosophila melanogaster birnavirus SW-2009a strain DBV segment A, complete sequence

Sequence ID: gb|GQ342962.1| Length: 3260 Number of Matches: 1

Range 1: 1381 to 1692

Score	Expect	Identities	Gaps	Strand	Frame
322 bits(174)	3e-84()	266/312(85%)	0/312(0%)	Plus/Plus	

Features:

```
Query  4     AAAGCCAGATTCCCATTATTCGAGGAATTAGGGCTGATGCAGTCTGATGCCAGCATTACT  63
             |||||||| |||||||||||||||||| |||| |||||||||||| ||||| ||||| ||
Sbjct  1381  AAAGCCAGGTTCCCATTATTCGAGGAACTTGGCCTCATGCAGTCAGACGCCAGTATCACA  1440

Query  64    GAAGCAATGGCCTTTGGCATTCATGATGTTATATCGTGGATCAGAGGCCTTGTACCAGCA  123
             || ||||||||||||| |  ||||||||||||||||| ||||| ||||||| |||||||||
Sbjct  1441  GAGGCCATGGCTTTCGGTATACATGATGTTATATCATGGATACGTGGCCTAGTACCAGCA  1500

Query  124   GCTTCAGATTGGGCCAATCGTATGCTGCCAGGAACTGGAGACGTGATCAAAGGAATCAAC  183
             || ||||| |||||||||||||||||| ||||| |||| ||||||| ||| |||||||||
Sbjct  1501  GCCTCAGACTGGGCCAATCGTATGCTACCAGGTTCAGGGGATGTGATTAAAGGAATCAAC  1560

Query  184   CGAACTGCAGGGCACCTATTGTACGGTGAAGCTGCATCTGGGAGGTTGATAGCGCAATCC  243
              ||||| |||||||||| | || ||||||||||||| ||||| ||||||||||| ||||||
Sbjct  1561  AGAACCGCAGGGCACCTTCTTTATGGAGAAGCTGCCTCAGGCCGGTTGATAGCACAATCC  1620

Query  244   GCGAGCGGATCACTCATAGGTAGGCTGGGGCACCGGGATGCTTTGGCTTGTGATGTAGAC  303
             ||||||||||||||| ||||||| ||||||||||||||||||| |||||||||||||||||
Sbjct  1621  GCGAGCGGATCACTAATAGGTCAGCTGGGGCACCGGGATGCCTTGGCTTGTGATGTAGAC  1680

Query  304   CCAACGCTCATG  315
             ||||||||||||
Sbjct  1681  CCAACGCTCATG  1692
```