

# Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastx/](#) **Formatting Results - B8BTN925014**

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## Nucleotide Sequence (318 letters)

**RID** [B8BTN925014](#) (Expires on 02-06 12:12 pm)

**Query ID** lcl|Query\_195908

**Description** None

**Molecule type** nucleic acid

**Query Length** 318

**Database Name** nr

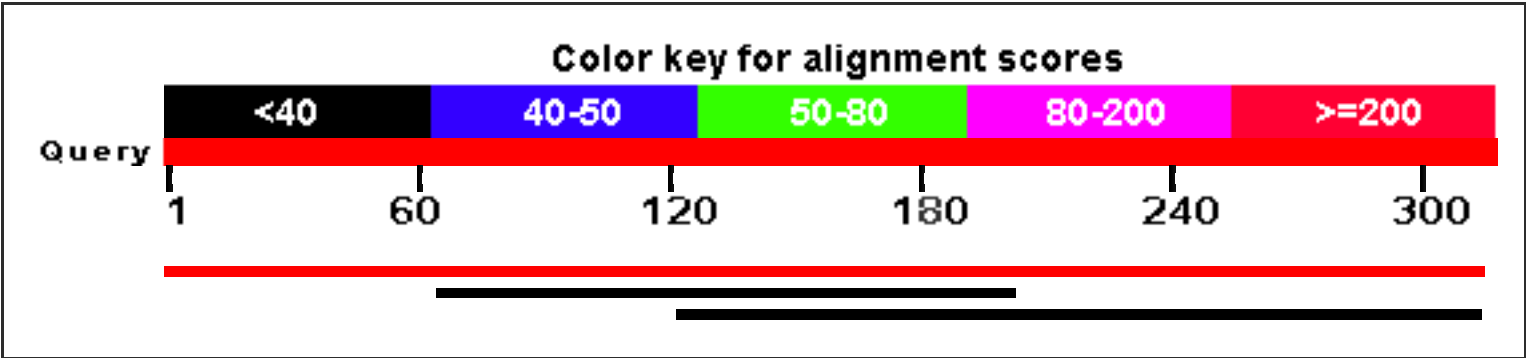
**Description** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

**Program** BLASTX 2.3.1+

## [Graphic Summary](#)

No putative conserved domains have been detected

### Distribution of 3 Blast Hits on the Query Sequence



☐ [Descriptions](#)

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
polyprotein [Drosophila melanogaster birnavirus SW-2009a]	220	220	99%	2e-64	98%	<a href="#">ACU32790.1</a>
PREDICTED: uncharacterized protein LOC106639518 [Copidosoma floridanum]	36.2	36.2	43%	5.3	39%	<a href="#">XP_014208652.1</a>
RNA polymerase sigma factor RpoS [Cupriavidus basilensis]	35.0	35.0	60%	9.7	33%	<a href="#">WP_043347474.1</a>

☐ [Alignments](#)

polyprotein [Drosophila melanogaster birnavirus SW-2009a]  
Sequence ID: **gb|ACU32790.1|** Length: 979 Number of Matches: 1  
Range 1: 396 to 500

Score	Expect	Method	Identities	Positives	Gaps	Frame
220 bits(561)	2e-64()	Composition-based stats.	103/105(98%)	105/105(100%)	0/105(0%)	+1
Features:						
Query	1	YKARFPLFEELGLMQSDASITEAMAFGIHDVISWIRGLVPAASDWANRMLPGTGDVIKGI				180
Sbjct	396	YKARFPLFEELGLMQSDASITEAMAFGIHDVISWIRGLVPAASDWANRMLPG+GDVIKGI				455
Query	181	NRTAGHLLYGEAASGRLIAQSASGSLIGRLGHRDALACDVDPTLM		315		
Sbjct	456	NRTAGHLLYGEAASGRLIAQSASGSLIGQLGHRDALACDVDPTLM		500		

PREDICTED: uncharacterized protein LOC106639518 [Copidosoma floridanum]  
Sequence ID: **ref|XP\_014208652.1|** Length: 1375 Number of Matches: 1  
Range 1: 1325 to 1364

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.2 bits(82)	5.3()	Composition-based stats.	18/46(39%)	26/46(56%)	6/46(13%)	+3
Features:						
Query	66	SNGLWHS*CYIVDQRPCTSSFRLGQSYAARNWRRDQRNQPNCRAPI		203		
Sbjct	1325	TNQVKRSNCYTLD---CRHSF---HYHCAKSWFKTQRTCPNCRAPV		1364		

RNA polymerase sigma factor RpoS [Cupriavidus basilensis]  
Sequence ID: **ref|WP\_043347474.1|** Length: 392 Number of Matches: 1

▶ **See 1 more title(s)**  
Range 1: 7 to 68

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(79)	9.7()	Composition-based stats.	21/64(33%)	31/64(48%)	2/64(3%)	-2
Features:						
Query	314	MSVGSTSQAKASRCPSLPMSDPLADCAINLPDAASPYNRCPAVRLIPLITSPVPGSIRLA		135		
Sbjct	7	VSTGSTSRARHPKQPELPQSTGVAQADADADSEA--YGQDPAADLVPLTDEPITTGTAVG		64		

Query	134	QSEA	123
		EA	
Sbjct	65	LREA	68