BLAST®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CN9XZ4UY014

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Blast report description

Nucleotide Sequence (375 letters)

RID <u>CN9XZ4UY014</u> (Expires on 02-23 13:16 pm)

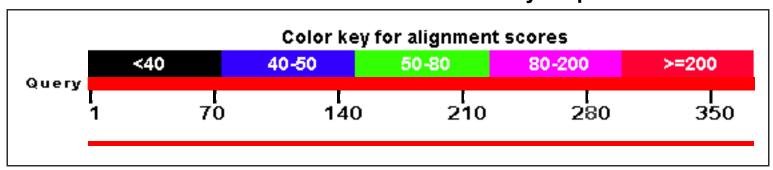
Description None **Description** Nucleotide collection (nt)

Molecule type nucleic acid Program BLASTN 2.3.1+

Query Length 375

□ 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 segment B putative RNA- dependent RNA polymerase VP1 (Vp1) gene, complete cds	292	292	99%	3e-75	81%	AF196645.2

□ <u>Alignments</u>

Drosophila x virus segment B putative RNA-dependent RNA polymerase VP1 (Vp1) gene, complete cds Sequence ID: **gb|AF196645.2|** Length: 3243 Number of Matches: 1

Range 1: 302 to 675

		Identities	Gaps	Strand	Frame	
(158)	3e-75()	305/377(81%)	6/377(1%)	Plus/Plus		
S :						
1	GCCGTATGATGA	GTTGGTTAATATTCC	CCTTTAGGGAAGCCGC	CATGTCCTAGAAT	GATGGC	60
302	dccdtatdatda	attddttaatattdd	cctttatagaggccgc	catctcctagaat	rgatggc	361
61	CCTCTATGGGGA	ACTGTTGGACACCAA	AAGACGTTTCATTGCC	TGTTGGCTCCGA	CCTGCA	120
362	CCTGTACGGGGA	ACTGTTGGATTCCAA	AAGACGTTTCACTGCC	ctgttggctctg	SCCTGCA	421
121	AATTCCAACCTA	TAAACCAGGTCACGA	AGGTCTCGCCACCCCT	TTTAACCCTGCC	C-AA-AC	178
422	cataccaaccta	TAAGCCAGGCCATGA	AGGTCACCCCACCCCT	CCTCACTTTACC	CTAACTC	481
179	GCTCTCGCATAT	GAATACATGCACTAC	CATCTCAAAGTCATCA	AATGATGCCTGG	GATGAG	238
482	GCTTTC-C-TAT	GAGTACATGCATTAC	catagetaacteaget	TAATGACACGTGG	GACAAG	539
239	-AGAGTGTACGA	GACCCTTCGAGAACT	TTCTGGTGGCTCAAGC	CACCACACGGTT	CTCAAC	297
540	CAGA-TTTATGA	GACCCTTAAAGAAC1	TACTTGTAGCTCAAGC	CTACAAATAGGTI	CTCTAC	598
298	AGGGTCTCTTTT	GGGACAGGTTAAGAG	GGTTGCAGCCGGACA	AGACGTAGCATA	TGGAAG	357
599	TGGTTCCCTACT	TGGTCAAGTGAAGAG	eggttgcggcca	AGATGTGGCATA	TGGAAG	658
358	AAAAGGTCACCA	TAAGA 374				
659	AAAAGGTCACCA	TAAGA 675				
	302 61 362 121 422 179 482 239 540 298 599 358	1 GCCGTATGATGA 302 GCCGTATGATGA 302 GCCGTATGATGA 61 CCTCTATGGGGA 362 CCTGTACGGGGA 121 AATTCCAACCTA 422 CATACCAACCTA 179 GCTCTCGCATAT 482 GCTTTC-C-TAT 239 -AGAGTGTACGA 540 CAGA-TTTATGA 298 AGGGTCTCTTTT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCCGTATGATGAGTTGGTTAATATTCC 302 GCCGTATGATGAATTGGTTAATATTCC 61 CCTCTATGGGGAACTGTTGGACACCAA 362 CCTGTACGGGGAACTGTTGGATTCCAA 121 AATTCCAACCTATAAACCAGGTCACGA 422 CATACCAACCTATAAACCAGGTCACGAACTATAAACCAGCCATGAA 482 GCTTTC-C-TATGAGTACATGCACTAC 482 GCTTTC-C-TATGAGTACATGCATTAC 239 -AGAGTGTACGAGACCCTTCGAGAACT 540 CAGA-TTTATGAGACCCTTAAAGAACT 298 AGGGTCTCTTTTGGGACAGGTTAAGACC 359 TGGTTCCCTACTTGGTCAAGTGAAGACC 358 AAAAGGTCACCATAAGA 374	GCCGTATGATGAGTTGGTTAATATTCCCTTTAGGGAAGCCGC 302 GCCGTATGATGAATTGGTTAATATTCCCTTTATAGAGGCCGC 61 CCTCTATGGGGAACTGTTGGACACCAAAGACGTTTCACTGCC 362 CCTGTACGGGGAACTGTTGGATTCCAAAGACGTTTCACTGCC 121 AATTCCAACCTATAAACCAGGTCACGAGGTCTCGCCACCCCT 422 CATACCAACCTATAAACCAGGCCATGAGGTCACCCCACCCCT 179 GCTCTCGCATATGAATACATGCACTACATCTCAAAGTCATCA 482 GCTTTC-C-TATGAGTACATGCACTTCTGGTGGCTCAAGC 239 -AGAGTGTACGAGACCCTTCGAGAACTTCTGGTGGCTCAAGC 540 CAGA-TTTATGAGACCCTTAAAGAACTACTTGTAGCTCAAGC 298 AGGGTCTCTTTTGGGACAGGTTAAGAGGGTTGCAGCCGGACA 599 TGGTTCCCTACTTGGTCAAGTGAAGAGGGTTGCGGCCGGC	GCCGTATGATGAGTTGGTTAATATTCCCTTTAGGGAAGCCGCATGTCCTAGAAT GCCGTATGATGAATTGGTTAATATTCCCTTTATAGAGGCCGCATCTCCTAGAAT CCTCTATGGGGAACTGTTGGACACCAAAGACGTTTCATTGCCTGTTGGCTCCGA CCTGTACGGGGAACTGTTGGATTCCAAAGACGTTTCACTGCCTGTTGGCTCTGGC 121 AATTCCAACCTATAAACCAGGTCACGAGGTCTCGCCACCCCTTTTAACCCTGCC 422 CATACCAACCTATAAGCCAGGCCATGAGGTCACCCCACCCCTCCTCACTTTACC 179 GCTCTCGCATATGAATACATGCACTACATCTCAAAGTCATCAAATGATGCCTGGC 482 GCTTTC-C-TATGAGTACATGCATTACATAGCTAACTCAGCTAATGACACGTGGC 239 -AGAGTGTACGAGACCCTTCGAGAACTTCTGGTGGCTCAAGCCACCACCGGTT 540 CAGA-TTTATGAGACCCTTCGAGAACTTCTGGTGGCTCAAGCCACACAGGTT 298 AGGGTCTCTTTTGGGACAGGTTAAGAGAGCTTGCAGCCGGACAAGATGTGGCATA 599 TGGTTCCCTACTTGGTCAAGTGAAGAGGGTTGCGGCCGGC	1 GCCGTATGATGAGTTGGTTAATATTCCCTTTAGGGAAGCCGCATGTCCTAGAATGATGGC 302 GCCGTATGATGATTAGTTAATATTCCCTTTATAGAGGCCGCATCTCCTAGAATGATGGC 61 CCTCTATGGGGAACTGTTGGACACCAAAGACGTTTCATTGCCTGTTGGCTCCGACCTGCA 362 CCTGTACGGGGAACTGTTGGATTCCAAAGACGTTTCACTGCCTGTTGGCTCCGCCACCCAC