

Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastn suite/](#) **Formatting Results - CN9VK2FG014**
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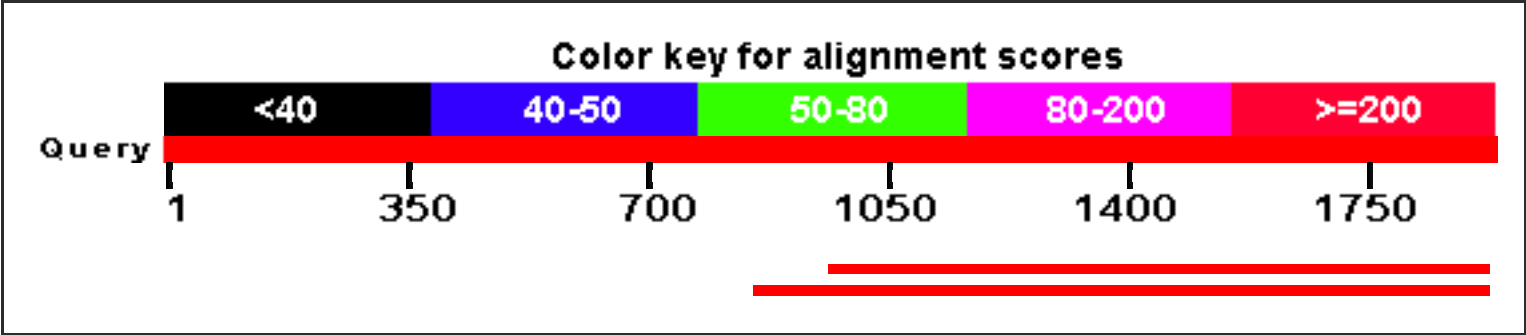
Nucleotide Sequence (1938 letters)

RID [CN9VK2FG014](#) (Expires on 02-23 13:15 pm)

Query ID	lcl Query_108309	Database Name	nr
Description	None	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.3.1+
Query Length	1938		

[Graphic Summary](#)

Distribution of 2 Blast Hits on the Query Sequence



[-] [Descriptions](#)

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Culex Y virus isolate P1-BS2010 segment B, complete sequence	342	342	49%	1e-89	73%	JQ659255.1
Espirito Santo virus segment B, complete sequence	335	335	55%	2e-87	73%	JN589002.1

[-] [Alignments](#)

Culex Y virus isolate P1-BS2010 segment B, complete sequence
Sequence ID: **gb|JQ659255.1|** Length: 3254 Number of Matches: 1
Range 1: 1176 to 2134

Score	Expect	Identities	Gaps	Strand	Frame
342 bits(185)	1e-89()	715/973(73%)	28/973(2%)	Plus/Minus	
Features:					
Query 968		TTGTTTCTAAGCATGGACTGTATCGTGTTCCAGTGGTT-GGTGACATAGCTCTCCACTGT			1026
Sbjct 2134		TTGTTTCGAAGCATAGAATCAATTGTGTTCCAATGGTTCAGGG-CGTATCCTTCGATGGT			2076
Query 1027		TTGTGCTATGCATGGGTACGCCCAGGCACCCACGTACAGTAGGGCAACGTTTTGAATGTA			1086
Sbjct 2075		CTGGGCTATACAGGGGTATGCCACCCACCCACGTATAACAGTGCAGACGTTCTGTATGTA			2016
Query 1087		TTTGTGCACCTGCTTCGCTATGTTCTGA-CTGGAATGTGCTGCTTGGGGGTGTGGGCATG			1145
Sbjct 2015		CCTGTGGACTTGTTTGGCTATGTGGGAGCT-GAAGGTGCTACTAGGAGGTGTGGGCAGG			1957
Query 1146		CAATTGATTTGAACA-TCCTCTCTTTAGAGAGTACTGGAGTGTAACCATATTCCGTGTGT			1204
Sbjct 1956		CTATTGACTTAAACAATCGTTCCTTTGCCAAG-ACTGGGGTGAAACCATACTGAGTGTGT			1898
Query 1205		GTTACATCCCATCCTAACATATCCATTTCAACAATTGTTCTGGGTTGCACCCTATTGTTT			1264
Sbjct 1897		GTTACATCCCACCCCAACATGTCCATGGAAACAATCGTTCCTAGGCCTAATCCTATCCTCA			1838
Query 1265		GTTGGTATAGAGTGGTTGGAAGCCTCAATTAGTTTTTCCCTGAAGTTGTGAACGACCAGT			1324
Sbjct 1837		ACAGGGAGCGAGTGCTCCCTTGCTCCAGTAGTTTCTTCTTGAATTCAGGCACCACTAGC			1778
Query 1325		TCAACTTTGAAGTCTATGCCTGTCATTGTTGCTAGTTTCTCTATAACTTCTGGG--GTTG			1382
Sbjct 1777		TCAACTTTGAAGTCTATAACCAGTTTCTGAGGAAAGCTTCTCAATAAC--CTGGGCTGTAG			1720
Query 1383		GTTGTGGTTTGCCAATCTCAGCCCATCTGTTCAATTAAGATGGTGGTTAGTACATGGTTGT			1442
Sbjct 1719		GTTTTGGTCGGCCCATGGCTCTCCACTTGTTCAATTAGTATGGTTGTCAATACATGATTGT			1660
Query 1443		TTAGGAATGTCCAGGGGTTTCCACTTCCTTGTCAGGGTTCTTTATCTGGAAGTTTTTTA			1502
Sbjct 1659		TTAGGAAAGTCCATGGGTTGCCACTCCCCTGACCTGGATTTTAAATCTGGAAGTTCTTCA			1600
Query 1503		GGATGCTTATTGAGTCCACTGTCATGTATGGTATAGCATA-A-AGGGATAGGTATGCCCA			1560
Sbjct 1599		AAATGCTTATAGAGTCCACAGTTGTGTAGGGTAT--CATATAGAGGGCCAGGTAAGCCCA			1542
Query 1561		CGTGTAATTGTATAGCGGGGTGCCCTGTGTTGAT-GTCCAACCTCTTGTCAGCAAGTACA			1619
Sbjct 1541		CGTATAGTTGTATAG-TGGTACCCCTTCGTTGCTCGTCCACCCCTAGTTAGCAAGTACA			1483
Query 1620		TGGCCATTGTCATCGCTACATCACGTGTGCAGTTGGCTTCACCCTTTGTTAAATCTATGC			1679
Sbjct 1482		TTGCTGTTGTCATTGCAATGTCCCTGGTACAGTTGGCTTCACCCTTGGTGAGGTCTATAC			1423
Query 1680		TATACCATATGTC-T-TCGTTCCGATAGTATATGTAGGCATTGTCTGCGTATACTAGTTC			1737
Sbjct 1422		TATACCAGACATCCTCTC-TAGGGA-AGTACATATAGGCGTTATCTGCATACACCAGTTC			1365
Query 1738		CACAGTTTCTGTTGCATTGAGGATTATATTAATAAGAGCGTCCATCCCTCCCTGTGTTGG			1797
Sbjct 1364		TGTGATGTCGGTGGCTTCGAGAATGCGATTAAACAAGAGCATCCATCCCCCTTGAGTTGG			1305

Query	1798	AGAAAAC	TTTGATAGGGATGGGGT	CCTGGTTT	--T-GCAGTTCAGGACGTT	CAGCATA	ACG	1854
Sbjct	1304	AGAAAAC	TTTGATAGGGATGGGGT	A--GGTTCGCTAGAA	GTG-AGA	ACATTGAGCAT	GCG	1248
Query	1855	CTTAGCTGGCTGGTCCGATATTGTAGA-CCCGATAAGGTGTGTGACATAGCTGGCACTCC						1913
Sbjct	1247	CTTTGCTGGTTGGTCCGAGATAATTGATCCCAAT-AGATGCGTCACATAGCTTGCACTCC						1189
Query	1914	AAATGTTCC	TAGT	1926				
Sbjct	1188	AAATGTTCC	TAGT	1176				

Espirito Santo virus segment B, complete sequence
Sequence ID: **gb|JN589002.1|** Length: 3250 Number of Matches: 1
Range 1: 1171 to 2241

Score	Expect	Identities	Gaps	Strand	Frame	
335 bits(181)	2e-87()	791/1087(73%)	35/1087(3%)	Plus/Minus		
Features:						
Query	859	TGCATAGTCCTGTT	CATGCATTGGTTTCTCT-AGGCTTAGCAGGCT-CATTACCTCACTG		916	
Sbjct	2241	TGCATAATTTT	GCTCGTGCATTGGTTTC-CTGATG-TTAATTAGCTCCATGACCTCACGG		2184	
Query	917	AACGGGCTAGTCTCGACCGCTTTGCTGATGGCTTTGTCCAGGTTGTA-CT--CTTTGTTT			973	
Sbjct	2183	AATGGGCTCGTGTCAACAGCCTTCGTTAAGGCTTTCTCTAGGTCATAATTAGGGTTGTTT			2124	
Query	974	CTAAGCATGGACTGTATCGTGTTCAGTGGTT-GGTGACATAGCTCTCCACTGTTTGTGC			1032	
Sbjct	2123	CGAAGCATAGAATCAATTGTGTTCCAATGGTTCAGGG-CGTATCCTTCGATGGTTTGGGC			2065	
Query	1033	TATGCATGGGTACGCCCAGGCACCCACGTACAGTAGGGCAACGTTTTGAATGTATTTGTG			1092	
Sbjct	2064	TATACAGGGGTATGCCCACCCACCCACGTATAACAGTGCGACGTCCTGTATGTACTTGTG			2005	
Query	1093	CACCTGCTTCGCTATGTT	CGA-CTGGAATGTGCTGCTTGGGGGTTGTGGGCATGCAATTG		1151	
Sbjct	2004	GACTTGTTTGGCTACGTGGGAGCT-GAAGGTGCTACTAGGAGGTTGTGGACAGGCTATTG			1946	
Query	1152	ATTTGAACA-TCCTCTCTTTAGAGAGTACTGGAGTGTAACCATAATCCGTGTGTGTTACA			1210	
Sbjct	1945	ACTTAAACAATCGTTCCTTTGCCAAG-ACTGGGGTGAAACCATACTGAGTGTGTGTTACA			1887	
Query	1211	TCCCATCCTAACATATCCATTTCAACAATTGTTCTGGGTTTCGACCC	TATTGTTTGTGTTGGT		1270	
Sbjct	1886	TCCCACCCCAACATGTCCATGGAAACAATCGTTCTAGGCCTAATCCTATCCTCAACAGGG			1827	
Query	1271	ATAGAGTGGTTGGAAGCCTCAATTAGTTTTTCCCTGAAGTTGTGAACGACCAGTTCAACT			1330	
Sbjct	1826	AGCGAGTGCTCCCTTGCTCCAGTAGTTTCTTCTTGAATTCAGGCACCACTAGCTCAACT			1767	
Query	1331	TTGAAGTCTATGCCTGT	CATTGTTGCTAGTTTCTCTATAACTTCTGGG--GTTGGTTGTG		1388	
Sbjct	1766	TTGAAGTCTATA	CCAGTTTCTGAGGAAAGCTTCTCAATAAC--CTGGGCTGTAGGTTTTG		1709	
Query	1389	GTTTGCCAATCTCAGCCCATCTGTT	CATTAAGATGGTGGTTAGTACATGGTTGTTTAGGA		1448	
Sbjct	1708	GTCGGCCCATGGCTCTCCACTTGTTCATTAGTATGGTTGTCAATACATGATTGTTTAGGA			1649	
Query	1449	ATGTCCAGGGGTTTCCACTTCCTTGTCAGGGTTCCTTATCTGGAAGTTTTTTAGGATGC			1508	
Sbjct	1648	AAGTCCATGGGTGCCACTCCCCTGACCTGGATTTT	TAAATCTGGAAGTTCTTCAAAATGC		1589	
Query	1509	TTATTGAGTCCACTGT	CATGTATGGTATAGCATA-A-AGGGATAGGTATGCCCACGTGTA		1566	
Sbjct	1588	TTATAGAGTCCACAGTTGTGTAGGGTAT--CATATAGAGGGCCAGGTAAGCCCACGTATA			1531	
Query	1567	ATTGTATAGCGGGGTGCCCTGTGTTGAT-GTCCAACCTCTTGTCAGCAAGTACATGGCCA			1625	
Sbjct	1530	GTTGTATAG-TGGTACCCCTTCGTTGCTCGTCCACCCCCTAGTTAGCAAGTACATTGCTG			1472	
Query	1626	TTGTCATCGCTACATCACGTGTGCAGTTGGCTTCACCCTTTGTTAAATCTATGCTATACC			1685	
Sbjct	1471	TTGTCATTGCAATGTCCCTGGTACAGTTGGCTTCACCCTTGGTGAGGTCTATACTATACC			1412	
Query	1686	ATATGTC-T-TCGTT	CGGATAGTATATGTAGGCATTGTCTGCGTATACTAGTTCCACAGT		1743	
Sbjct	1411	AGACATCCTCTC-TAGGGA-AGTACATATAGGCGTTATCTGCATACACCAGTTCTGTGAT			1354	
Query	1744	TTCTGTTGCATTGAGGATTATATTAATAAGAGCGTCCATCCCTCCCTGTGTTGGAGAAAA			1803	
Sbjct	1353	GTCGGTGGCTTCGAGAATGCGATTAAACAAGAGCATCCATCCCCCCTTGAGTTGGAGAAAA			1294	
Query	1804	CTTTGATAGGGATGGGGT	CCTGGTTT--T-GCAGTTCAGGACGTT	CAGCATA	CGCTTAGC	1860
Sbjct	1293	CTTTGATAGGGATGGGGT	A--GGTTCGCTAGAAGTG-AGA	ACATTGAGCATGCGCTTTGC	1237	

Query	1861	TGGCTGGTCCGATATTGTAGA-CCCGATAAGGTGTGTGACATAGCTGGCACTCCAAATGT	1919
Sbjct	1236	TGGTTGGTCCGAAACGATTGATCCCAAT-AGATGCGTCACATAGCTTGCACTCCAAATGT	1178
Query	1920	TCCTAGT	1926
Sbjct	1177	TCCTAGT	1171