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BLAST Results

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Job title: Nucleotide Sequence

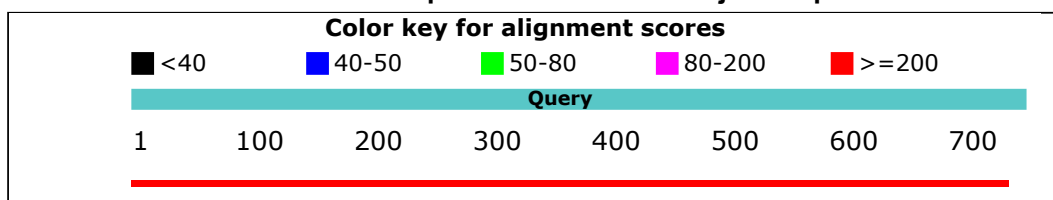
RID [9J53XE0K015](#) (Expires on 03-27 01:48 am)

Query ID lcl|Query_156449
Description None
Molecule type nucleic acid
Query Length 734

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.9.0+

[Graphic Summary](#)

Distribution of the top 1 Blast Hits on 1 subject sequences



Descriptions

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Perc. ident | Accession |
|---|-----------|-------------|-------------|---------|-------------|----------------------------|
| Influenza A virus (A/Shanghai/02/2013(H7N9)) segment 8 nuclear export protein (NEP) and nonstructural protein 1 (NS1) genes, complete cds | 619 | 619 | 100% | 4e-180 | 81.90% | KF021601.1 |

Alignments

Influenza A virus (A/Shanghai/02/2013(H7N9)) segment 8 nuclear export protein (NEP) and nonstructural protein 1 (NS1) genes, complete cds

Sequence ID: **KF021601.1** Length: 841 Number of Matches: 1
Range 1: 1 to 734

| Score | Expect | Identities | Gaps | Strand | Frame |
|---------------|---|--------------|-----------|-----------|-------|
| 619 bits(335) | 4e-180() | 602/735(82%) | 2/735(0%) | Plus/Plus | |
| Features: | | | | | |
| Query 1 | ATGGATTCCAACACTGTGTCAAGTTTCCAGGTAGATTGCTTTCTTTGGCATATCCGGA | 60 | | | |
| Sbjct 1 | ATGGATTCCAATACTGTGTCAAGCTTCCAGGTAGACTGCTTTCTTTGGCATGTCCGCAA | 60 | | | |
| Query 61 | CAAGTTAAAGACCAAGAACTGAGTGATGCCCCATTCTTGATCGGCTTCGCCGAGATCAG | 120 | | | |
| Sbjct 61 | CGATTTCGAGACCAAGAAATGGGTGATGCCCCATTCTTAGACCGGCTTCGCCGAGATCAG | 120 | | | |
| Query 121 | AGGTCCTAAGGGGAAGAGGCAATACTCTCGGTCTAGACATCAAAGCAGCCACCATGTT | 180 | | | |
| Sbjct 121 | AAGTCCCTGAGAGGAAGAAGCAGCACTCTTGGTCTGGACATCAGAAGTCCACGCGTGAA | 180 | | | |
| Query 181 | GGAAAGCAAATTGTAGAAAAGATTCTGAAAGAAGAATCTGATGAGGCACTTAAAAATGACC | 240 | | | |
| Sbjct 181 | GGAAAGCATATAGTGGAGCGGATTTTAGAGGAAGAGTCAGATGAAGCATTTAAAAATGAGT | 240 | | | |
| Query 241 | ATGGTCTCCA-CACCTGCTTCGCATACATAAAGTACATGACTATTGAGGAATTGTCAAG | 299 | | | |
| Sbjct 241 | ATTG-CTTCAGTGCCAGCTCCACGCTATCTAACTGACATGACTCTTGAAGAAATGTCAAG | 299 | | | |
| Query 300 | AAACTGGTTCATGCTAATGCCCAAGCAGAAAGTGAAGGACCTCTTTGCATCAGAATGGA | 359 | | | |
| Sbjct 300 | AGATTGGTTAATGCTCATTCCTCCAAACAGAAAATAACAGGGTCCCTATGCATTAGAAATGGA | 359 | | | |
| Query 360 | CCAGGCAATCATGGAGAAAAACATCATGTTGAAAGCGAATTTTCAGTGTGATTTTTGACCG | 419 | | | |
| Sbjct 360 | CCAAGCAATAGTGGACAAAAACATCACATTGAAAGCAAATTTTCAGTGTGATTTTCAATCG | 419 | | | |
| Query 420 | ACTAGAGACCATAGTATTACTAAGGGCTTTACCGAAGAGGGAGCAATTGTTGGCGAAAT | 479 | | | |
| Sbjct 420 | GCTTGAAGCCCTGATACTACTTAGAGCTTTTACGGAAGAAGGAGCAATTGTAGGCGAAAT | 479 | | | |
| Query 480 | CTCACCATTGCCTTCTTTTCCAGGACATACTATTGAGGATGTCAAAAATGCAATTGGGGT | 539 | | | |
| Sbjct 480 | CTCACCATTACCTTCTCTTCCAGGACATACTGACAAGGATGTCAAAAATGCAATTGAGAT | 539 | | | |
| Query 540 | CCTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTAAAAATCTACAGAG | 599 | | | |
| Sbjct 540 | CCTCATCGGAGGATTGGAATGGAATGATAACACAGTTCGAGTCTCTGAAACTCTACAGAG | 599 | | | |
| Query 600 | ATTTCGTTGGAGAAGCAGTAATGAGAATGGGGACCTCCACTTACTCCAAAACAGAAACG | 659 | | | |
| Sbjct 600 | ATTTCGTTGGAGAAGCAGCGATGAGGATGGGAGATCTCCACTCTCTACAAAGTAGAAACG | 659 | | | |
| Query 660 | GAAAAATGGCGAGAACAGCTAGGTCAAAAGTTTGAAGAGATAAGATGGCTGATTGAAGAAG | 719 | | | |
| Sbjct 660 | GGAAATGGAGAGAACAGTTAAGCCAGAAGTTCGAAGAAATAAGATGGTTGATTGAAGAAG | 719 | | | |
| Query 720 | TGAGACACAGACTAA | 734 | | | |
| Sbjct 720 | TACGACATAGATTAA | 734 | | | |

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