NS (890 bp)

Nature: cRNA

Source: NC_002020.1 Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 8

AGCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGATTGCTTTCT
TTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGTGATGCCCCATTCCTTGATCGGCTTCGCCGA
GATCAGAAATCCCTAAGAGGAAGGGGCAGCACTCTTGGTCTGGACATCGAGACAGCCACACGTGCTGGAA
AGCAGATAGTGGAGCGGATTCTGAAAGAAGAATCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACC
TGCGTCGCGTTACCTAACCGACATGACTCTTGAGGAAATGTCAAGGGAATGGTCCATGCTCATACCCAAG
CAGAAAGTGGCAGGCCCTCTTTGTATCAGAATGGACCAGGCGATCATGGATAAAAACATCATACTGAAAG
CGAACTTCAGTGTGATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGAGGGAGC
AATTGTTGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTGAGGATGTCAAAAATGCAGTT
GGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTGAAACTCTACAGAGATTCG
CTTGGAGAAGCAGTAATGAGAATGGGAGACCTCCACTCACTCCAAAACAGAAACGAGAAATGGCGGGAAC
AATTAGGTCAGAAGTTTGAAGAAATAAGATGGTTGATTGAAGAAGTGAGACACAAACTGAAGGTAACAGA
GAATAGTTTTGAGCAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGA
ACTTTCTCATTTCAGCTTATTTAATAATAAAAAACACCCTTGTTTCTACT

NS1 protein

Source: NP_040984.1 (230 aa)

Sequence: 27 - 719

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILK
EESDEALKMTMASVPASRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIMDKNIILKANFSVIFDR
LETLILLRAFTEEGAIVGEISPLPSLPGHTAEDVKNAVGVLIGGLEWNDNTVRVSETLQRFAWRSSNENG
RPPLTPKQKREMAGTIRSEV

NS1/NEP protein

Source: NP_040983.1 (121 aa)

Sequence: 27 - 864

MDPNTVSSFQDILLRMSKMQLESSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNEKWREQLG
QKFEEIRWLIEEVRHKLKVTENSFEQITFMQALHLLLEVEQEIRTFSFQLI

NS (890 bp)

Nature: vRNA

Source: Illumina sequences from virus stocks_RPS2022

NNNNNNAGCAGGGTGACAAAAACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGAT
TGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGCGATGCCCCATTCCT
TGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGTACTCTCGGTCTGGACA
TCAAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAATCCGAT
GAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACTGACATGACTCT
TGAGGAAATGTCAAGGGACTGGTCCATGCTCATACCCAAGCAGAAAGTGGCAGGCCCTCTTT
GTATCAGAATGGACCAGGCGATCATGGATAAGAACATCATACTGAAAGCGAACTTCAGTGTG
ATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGAGGGAGCAATTGT
TGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTGAGGATGTCAAAAATGCAG
TTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTGAAACTCTA
CAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGACCTCCACTCACTCCAAAACAGAA
ACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAAGAAATAAGATGGTTGATTGAAGAA
GTGAGACACAAACTGAAGATAACAGAGAATAGTTTTGAGCAAATAACATTTATGCAAGCCTT
ACATCTATTGCTTGAAGTGGAGCAAGAGATAAGAACTTTCTCGTTTCAGCTTATTTAGTACT
AAAAAACACCCTTGNNNNNNNN

NS (890 bp)

Nature: cDNA_pHW2000

Source: GATC sequences from Maxiprep_RPS_2023

AGCAAAAGCAGGGTGACAAAAACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGAT
TGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGCGATGCCCCATTCCT
TGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGTACTCTCGGTCTGGACA
TCAAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAATCCGAT
GAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACTGACATGACTCT
TGAGGAAATGTCAAGGGACTGGTCCATGCTCATACCCAAGCAGAAAGTGGCAGGCCCTCTTT
GTATCAGAATGGACCAGGCGATCATGGATAAGAACATCATACTGAAAGCGAACTTCAGTGTG
ATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGAGGGAGCAATTGT
TGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTGAGGATGTCAAAAATGCAG
TTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTGAAACTCTA
CAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGACCTCCACTCACTCCAAAACAGAA
ACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAAGAAATAAGATGGTTGATTGAAGAA
GTGAGACACAAACTGAAGATAACAGAGAATAGTTTTGAGCAAATAACATTTATGCAAGCCTT
ACATCTATTGCTTGAAGTGGAGCAAGAGATAAGAACTTTCTCGTTTCAGCTTATTTAGTACT
AAAAAACACCCTTGTTTCTACT

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CLUSTAL O(1.2.4) multiple sequence alignment


PR8_NS_Illumina      NNNNNNAGCAGGGTGACAAAAACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAG      60
PR8_NS_NCBI          AGCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAG      60
PR8_NS_pHW2000       AGCAAAAGCAGGGTGACAAAAACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAG      60
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PR8_NS_Illumina      ATTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGCGATGCCCCAT      120
PR8_NS_NCBI          ATTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGTGATGCCCCAT      120
PR8_NS_pHW2000       ATTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGCGATGCCCCAT      120
                     ********************************************** **********

PR8_NS_Illumina      TCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGTACTCTCGGTC      180
PR8_NS_NCBI          TCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGCACTCTTGGTC      180
PR8_NS_pHW2000       TCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGTACTCTCGGTC      180
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PR8_NS_Illumina      TGGACATCAAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAG      240
PR8_NS_NCBI          TGGACATCGAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAG      240
PR8_NS_pHW2000       TGGACATCAAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAG      240
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PR8_NS_Illumina      AATCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACTG      300
PR8_NS_NCBI          AATCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACCG      300
PR8_NS_pHW2000       AATCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACTG      300
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PR8_NS_Illumina      ACATGACTCTTGAGGAAATGTCAAGGGACTGGTCCATGCTCATACCCAAGCAGAAAGTGG      360
PR8_NS_NCBI          ACATGACTCTTGAGGAAATGTCAAGGGAATGGTCCATGCTCATACCCAAGCAGAAAGTGG      360
PR8_NS_pHW2000       ACATGACTCTTGAGGAAATGTCAAGGGACTGGTCCATGCTCATACCCAAGCAGAAAGTGG      360
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PR8_NS_Illumina      CAGGCCCTCTTTGTATCAGAATGGACCAGGCGATCATGGATAAGAACATCATACTGAAAG      420
PR8_NS_NCBI          CAGGCCCTCTTTGTATCAGAATGGACCAGGCGATCATGGATAAAAACATCATACTGAAAG      420
PR8_NS_pHW2000       CAGGCCCTCTTTGTATCAGAATGGACCAGGCGATCATGGATAAGAACATCATACTGAAAG      420
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PR8_NS_Illumina      CGAACTTCAGTGTGATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCG      480
PR8_NS_NCBI          CGAACTTCAGTGTGATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCG      480
PR8_NS_pHW2000       CGAACTTCAGTGTGATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCG      480
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PR8_NS_Illumina      AAGAGGGAGCAATTGTTGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTG      540
PR8_NS_NCBI          AAGAGGGAGCAATTGTTGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTG      540
PR8_NS_pHW2000       AAGAGGGAGCAATTGTTGGCGAAATTTCACCATTGCCTTCTCTTCCAGGACATACTGCTG      540
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PR8_NS_Illumina      AGGATGTCAAAAATGCAGTTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAG      600
PR8_NS_NCBI          AGGATGTCAAAAATGCAGTTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAG      600
PR8_NS_pHW2000       AGGATGTCAAAAATGCAGTTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAG      600
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PR8_NS_Illumina      TTCGAGTCTCTGAAACTCTACAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGAC      660
PR8_NS_NCBI          TTCGAGTCTCTGAAACTCTACAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGAC      660
PR8_NS_pHW2000       TTCGAGTCTCTGAAACTCTACAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGAC      660
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PR8_NS_Illumina      CTCCACTCACTCCAAAACAGAAACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAA      720
PR8_NS_NCBI          CTCCACTCACTCCAAAACAGAAACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAA      720
PR8_NS_pHW2000       CTCCACTCACTCCAAAACAGAAACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAA      720
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PR8_NS_Illumina      GAAATAAGATGGTTGATTGAAGAAGTGAGACACAAACTGAAGATAACAGAGAATAGTTTT      780
PR8_NS_NCBI          GAAATAAGATGGTTGATTGAAGAAGTGAGACACAAACTGAAGGTAACAGAGAATAGTTTT      780
PR8_NS_pHW2000       GAAATAAGATGGTTGATTGAAGAAGTGAGACACAAACTGAAGATAACAGAGAATAGTTTT      780
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PR8_NS_Illumina      GAGCAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGA      840
PR8_NS_NCBI          GAGCAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGA      840
PR8_NS_pHW2000       GAGCAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGA      840
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PR8_NS_Illumina      ACTTTCTCGTTTCAGCTTATTTAGTACTAAAAAACACCCTTGNNNNNNNN 890
PR8_NS_NCBI          ACTTTCTCATTTCAGCTTATTTAATAATAAAAAACACCCTTGTTTCTACT 890
PR8_NS_pHW2000       ACTTTCTCGTTTCAGCTTATTTAGTACTAAAAAACACCCTTGTTTCTACT 890
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