M (1027 bp)

Nature: cRNA

Source: NC_002016.1 Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 7

AGCGAAAGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATC
CCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATC
TTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATT
TGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAAT
GGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACAT
TCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATA
CAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCT
GACTCCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAA
TGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGC
CATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCC
AGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGC
AACGGTTCAAGTGATCCTCTCGCTATTGCCGCAAATATCATTGGGATCTTGCACTTGATATTGTGGATTC
TTGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGCCTTCTACGGA
AGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTGCTGTGGATGCTGACGATGGT
CATTTTGTCAGCATAGAGCTGGAGTAAAAAACTACCTTGTTTCTACT

M1 protein

Source: NP_040978.1 (252 aa)

Sequence: 26 - 784

MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLMEWLKTRPILSPLTKGILGFVFTLTVPS
ERGLQRRRFVQNALNGNGDPNNMDKAVKLYRKLKREITFHGAKEISLSYSAGALASCMGLIYNRMGAVTT
EVAFGLVCATCEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQAR
QMVQAMRTIGTHPSSSAGLKNDLLENLQAYQKRMGVQMQRFK

M2 protein

Source: NP_040979.2 (97 aa)

Sequence: 26 - 1007

MSLLTEVETPIRNEWGCRCNGSSDPLAIAANIIGILHLILWILDRLFFKCIYRRFKYGLKGGPSTEGVPK
SMREEYRKEQQSAVDADDGHFVSIELE

M (1027 bp)

Nature: vRNA

Source: Illumina sequences from virus stocks_RPS2022

NNNNNNNGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCT
CTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCA
GGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACC
TCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGC
AGCGTAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAA
GCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTC
ACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG
CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCC
CAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAG
AATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAG
CAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATT
GGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTA
TCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACTATTGCCGCAAAT
ATCATTGGGATCTTGCACTTGACATTGTGGATTCTTGATCGTCTTTTTTTCAAATGCATTTA
CCGTCGCTTTAAATACGGACTGAAAGGAGGGCCTTCTACGGAAGGAGTGCCAAAGTCTATGA
GGGAAGAATATCGAAAGGAACAGCAGAGTGCTGTGGATGCTGACGATGGTCATTTTGTCAGC
ATAGAGCTGGAGTAAAAAACTACCTTGNNNNNNNN

M (1027 bp)

Nature: cDNA_pHW2000

Source: GATC sequences from Maxiprep_RPS_2023

AGCAAAAGCAGGTAGATATTGAAAG**ATG**AGTCTTCTAACCGAGGTCGAAACGTACGTACTCT
CTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCA
GGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACC
TCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGC
AGCGTAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAA
GCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTC
ACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG
CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCC
CAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAG
AATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAG
CAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATT
GGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTA
TCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACTATTGCCGCAAAT
ATCATTGGGATCTTGCACTTGACATTGTGGATTCTTGATCGTCTTTTTTTCAAATGCATTTA
CCGTCGCTTTAAATACGGACTGAAAGGAGGGCCTTCTACGGAAGGAGTGCCAAAGTCTATGA
GGGAAGAATATCGAAAGGAACAGCAGAGTGCTGTGGATGCTGACGATGGTCATTTTGTCAGC
ATAGAGCTGGAGTAAAAAACTACCTTGTTTCTACT

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CLUSTAL O(1.2.4) multiple sequence alignment


PR8_M_Illumina      NNNNNNNGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACT        60
PR8_M_NCBI          AGCGAAAGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCT        60
PR8_M_pHW2000       AGCAAAAGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACT        60
                           ************************************************ **

PR8_M_Illumina      CTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTT        120
PR8_M_NCBI          CTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTT        120
PR8_M_pHW2000       CTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTT        120
                    ************************************************************

PR8_M_Illumina      TGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCT        180
PR8_M_NCBI          TGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCT        180
PR8_M_pHW2000       TGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCT        180
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PR8_M_Illumina      GTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCG        240
PR8_M_NCBI          GTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCG        240
PR8_M_pHW2000       GTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCG        240
                    ************************************************************

PR8_M_Illumina      AGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAA        300
PR8_M_NCBI          AGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAA        300
PR8_M_pHW2000       AGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAA        300
                    ************************************************************

PR8_M_Illumina      CATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGC        360
PR8_M_NCBI          CATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGC        360
PR8_M_pHW2000       CATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGC        360
                    ************************************************************

PR8_M_Illumina      CAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATA        420
PR8_M_NCBI          CAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATA        420
PR8_M_pHW2000       CAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATA        420
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PR8_M_Illumina      CAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGA        480
PR8_M_NCBI          CAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGA        480
PR8_M_pHW2000       CAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGA        480
                    ************************************************************

PR8_M_Illumina      ACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACT        540
PR8_M_NCBI          ACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACT        540
PR8_M_pHW2000       ACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACT        540
                    ************************************************** *****

PR8_M_Illumina      AATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAT        600
PR8_M_NCBI          AATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAT        600
PR8_M_pHW2000       AATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAT        600
                    ************************************************************

PR8_M_Illumina      GGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAAT        660
PR8_M_NCBI          GGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAAT        660
PR8_M_pHW2000       GGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAAT        660
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PR8_M_Illumina      GGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGA        720
PR8_M_NCBI          GGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGA        720
PR8_M_pHW2000       GGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGA        720
                    ************************************************************

PR8_M_Illumina      TCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAA        780
PR8_M_NCBI          TCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAA        780
PR8_M_pHW2000       TCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAA        780
                    ************************************************************

PR8_M_Illumina      GTGATCCTCTCACTATTGCCGCAAATATCATTGGGATCTTGCACTTGACCATTGTGGATTC        840
PR8_M_NCBI          GTGATCCTCTCGCTATTGCCGCAAATATCATTGGGATCTTGCACTTGATTATTGTGGATTC        840
PR8_M_pHW2000       GTGATCCTCTCACTATTGCCGCAAATATCATTGGGATCTTGCACTTGACCATTGTGGATTC        840
                    *********** ********************************** ***********

PR8_M_Illumina      TTGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGC        900
PR8_M_NCBI          TTGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGC        900
PR8_M_pHW2000       TTGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGC        900
                    ************************************************************

PR8_M_Illumina      CTTCTACGGAAGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTG        960
PR8_M_NCBI          CTTCTACGGAAGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTG        960
PR8_M_pHW2000       CTTCTACGGAAGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTG        960
                    ************************************************************

PR8_M_Illumina      CTGTGGATGCTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAAAAAACTACCTTGN       1020
PR8_M_NCBI          CTGTGGATGCTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAAAAAACTACCTTGT       1020
PR8_M_pHW2000       CTGTGGATGCTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAAAAAACTACCTTGT       1020
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PR8_M_Illumina      NNNNNNN     1027
PR8_M_NCBI          TTCTACT     1027
PR8_M_pHW2000       TTCTACT     1027
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