

HA (1762 bp)

Nature: cRNA

Source: DQ487341.1 Influenza A virus (A/Moscow/10/99(H3N2)) segment 4

```
AGCAAAAGCAGGGGAGAATTCTATTAACCATGAAGACTATCATTGCTTTGAGCTACATTTTATGTCTGGT
TTTCGCTCAAAAACCTTCCCGGAAATGACAACAGCACGGCAACGCTGTGCCTGGGACACCATGCAGTGCCA
AACGGAACGCTAGTGAAAACAATCACGAATGACCAAATTGAAGTGACTAATGCTACTGAGCTGGTTCAGA
GTTCTCAACAGGTAGAATATGCGACAGTCCTCACCAAATCCTTGATGGAGAAAACTGCACACTGATAGA
TGCTCTATTGGGAGACCCACATTGTGATGGCTTCCAAAATAAGGAATGGGACCTTTTTTGTGTAACGCAGC
AAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGATTATGCCTCCCTTAGGTCACTAGTTGCCTCAT
CCGGCACCCCTGGAGTTTAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAACAAGCTCTGC
TTGCAAAAGGAGATCTATTAAGTTTCTTTAGTAGATTGAATTGGTTGCACCAATTAGAAAACAGATAT
CCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTGACAAATTGTACATTTGGGGGGTTCCACCACC
CGAGTACGGACAGTGTCCAAACCAGCGTATATGTCCAAGCATCAGGGAGAGTCCAGTCTCTACCAAAAG
AAGCCAACAACTGTAATCCCGAATATCGGATCCAGACCCTGGGTAAGGGGTGTCTCCAGCAGAATAAGC
ATCTATTGGACAATAGTAAAACCGGGAGACATACTTTTGATTAAACAGCACAGGGAACTAATTGCTCCTC
GGGGTTACTTCAAAATACGAAGTGGGAAAAGCTCAATAATGAGGTCAGATGCACCCATTGGCAAATGCAA
TTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTTCAAAATGTAAACAGGATCACA
TATGGGGCCTGTCCCAGATATGTTAAGCAAAACACTCTGAAATTGGCAACAGGGATGCGGAATGTACCAG
AGAAACAACTAGAGGCATATTCGGCGCAATCGCGGGTTTCATAGAAAATGGTTGGGAGGGAATGATGGA
CGGTTGGTACGGTTTTCAGGCATCAAAATTTCTGAGGGCACAGGACAAGCAGCAGATCTTAAAAGCACTCAA
GCAGCAATCAACCAAAATCAACGGGAAAACCTGAATAGGTTAATCGAGAAAACGAACGAGAAAATTCATCAAA
TTGAAAAAGAATTCTCAGAAGTAGAAGGGAGAATTCAGGACCTCGAGAAAATATGTTGAGGACACTAAAAT
AGATCTCTGGTCGTACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCTAACTGAC
TCAGAAATGAACAACTGTTTGAAAGAACAAGGAAGCAACTGAGAGAAAATGCTGAGGATATGGGCAATG
GTTGTTTCAAAATATACCACAAATGTGACAATGCCTGCATAGGGTCAATCAGAAATGGAACCTTATGACCA
TGATGTATACAGAGACGAAGCATTAACAACCGGTTCCAGATCAAAGGTGTTGAGCTGAAGTCAGGATAC
AAAGATTGGATCCTATGGATTTCTTTGCCATATCATGTTTTTGTCTTGTGTTGTTTTGCTGGGGTTCA
TTATGTGGGCCTGCCAAAAGGCAACATTAGGTGCAACATTTGCATTTGAGTGCATTAATTAACAAACACC
CTTGTTTCTACT
```

HA protein

Source: ABE73115.1 (566 aa) polymerase PB2

Sequence: 29- 521

MKTIIALS YILCLVFAQKLP GNDNSTATLCLGHHAVP NGTLVKTITNDQIEVTNATELVQSSSTGRICDS
PHQILDGENCTLIDALLGDPHCDGFQNK EWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNES
FNWTGVAQNGTSSACKRRS IKSFFSRLNWLHQLENRYPALNVTMPNNDKFDKLYIWGVHHPSTDSVQTSV
YVQASGRVTVSTKRSQQTVIPNIGSRPWVRGVSSRISYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGA
IAGFIENGWEGMMDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRLIEKTNEKFHQIEKEFSEVEG
RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMKNL FERTRKQLRENAEDMGN GCFKIYHKCD
NACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQK GNI
RCNICI

HA (1759 bp)

Nature: vRNA

Source: Illumina sequences from virus stocks_RPS2022

NNNNNNNGCAGGGGATAATTCTATTAACCATGAAGACTATCATTGCTTTGAGCTACATTTTA
TGTCTGGTTTTTCGCTCAAAAACCTCCCGGAAATGACAACAGCACGGCAACGCTGTGCCTGGG
ACACCATGCAGTGCCAAACGGAACGCTAGTGAAAACAATCACGAATGACCAAATTGAAGTGA
CTAATGCTACTGAGCTGGTTCAGAGTTCCTCAACAGGTAGAATATGCGACAGTCCTCACCAA
ATCCTTGATGGAGAAAACCTGCACACTGATAGATGCTCTATTGGGAGACCCACATTGTGATGG
CTTCCAAAATAAGGAATGGGACCTTTTTTGTTGAACGCAGCAAAGCCTACAGCAACTGTTACC
CTTATGATGTGCCGGATTATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACCCCTGGAG
TTTAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAACAAGCTCTGCTTGCAA
AAGGAGATCTATTAACAGTTTCTTTAGTAGATTGAATTGGTTGCACCAATTAATAACAGAT
ATCCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTGACAAATTGTACATTTGGGGG
GTTCAACACCCGAGTACGGACAGTGACCAAACCAGCCTATATACCCCATCAGGGAGAGTCAC
AGTCTCTACCAAAAGAAGCCAACAACTGTAATCCCGAATATCGGATCCAGACCCTGGGTAA
GGGGTATCTCCAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGGGAGACATACTTTTG
ATTAACAGCACAGGGAATCTAATTGCTCCTCGGGGTACTTCAAAATACGAAGTGGGAAAAG
CTCAATAATGAGGTGAGATGCACCCATTGACAAATGCAATTCTGAATGCATCACTCCAAATG
GAAGCATTCCCAATGACAAACCATTTCAAAATGTAAACAGGATCACATATGGGGCCTGTCCC
AGATATGTTAAGCAAAACACTCTGAAATTGGCAACAGGGATGCGGAATGTACCAGAGAAACA
AACTAGAGGCATATTCGGCGCAATCGCGGGTTTCATAGAAAATGGTTGGGAGGGAATGATGG
ACGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGCACAGGACAAGCAGCAGATCTTAAA
AGCACTCAAGCAGCAATCAACCAAATCAACGGGAACTGAATAGGTTAATCGAGAAAACGAA
CGAGAAATTCCATCAAATTGAAAAAGAATTCTCAGAAGTAGAAGGGAGAATTCAGGACCTCG
AGAAATATGTTGAGGACACTAAAATAGATCTCTGGTCGTACAACGCGGAGCTTCTTGTTGCC
CTGGAGAACCAACATACAATTGATCTAACTGACTCAGAAATGAACAACTGTTTGAAAGAAC
AAGGAAGCAACTGAGAGAAAATGCTGAGGATATGGGCAATGGTTGTTTCAAATATACCACA
AATGTGACAATGCCTGCATAGGGTCAATCAGAAATGGAACCTATGACCATGATGTATACAGA
GACGAAGCATTAACAACCGGTTCCAGATCAAAGGTGTTGAGCTGAAGTCAGGATACAAAGA
TTGGATCCTATGGATTTCTTTGCCATATCATGTTATTTGCTTTGTGTTGTTTTGCTGGGGT
TCATTATGTGGGCCTGCCAAAAGGCAACATTAGGTGCAACATTTGCATTTGAGTGCATTAA
TTAAAAACACCNNNNNNNNNNNN

HA (1759 bp)

Nature: cDNA_pHW2000

Source: GATC sequences from Maxiprep_RPS_2023

AGCAAAAGCAGGGGATAATTCTATTAACC**ATGA**AAGACTATCATTGCTTTGAGCTACATTTTA
TGTCTGGTTTTTCGCTCAAAAACCTTCCCGGAAATGACAACAGCACGGCAACGCTGTGCCTGGG
ACACCATGCAGTGCCAAACGGAACGCTAGTGAAAACAATCACGAATGACCAAATTGAAGTGA
CTAATGCTACTGAGCTGGTTCAGAGTTCCTCAACAGGTAGAATATGCGACAGTCCTCACCAA
ATCCTTGATGGAGAAAACCTGCACACTGATAGATGCTCTATTGGGAGACCCACATTGTGATGG
CTTCCAAAATAAGGAATGGGACCTTTTTTGTTGAACGCAGCAAAGCCTACAGCAACTGTTACC
CTTATGATGTGCCGGATTATGCCTCCCTTAGGTCAGTTGCCTCATCCGGCACCCCTGGAG
TTTAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAACAAGCTCTGCTTGCAA
AAGGAGATCTATTAACAGTTTCTTTAGTAGATTGAATTGGTTGCACCAATTAATAACAGAT
ATCCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTGACAAATTGTACATTTGGGGG
GTTCAACACCCGAGTACGGACAGTG**A**CCAAACCAGCCTATATACCCCATCAGGGAGAGTCAC
AGTCTCTACCAAAAGAAGCCAACAACTGTAATCCCGAATATCGGATCCAGACCCTGGGTAA
GGGGTATCTCCAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGGGAGACATACTTTTG
ATTAACAGCACAGGGAATCTAATTGCTCCTCGGGGTACTTCAAAATACGAAGTGGGAAAAG
CTCAATAATGAGGTGAGATGCACCCATTG**A**CAAATGCAATTCTGAATGCATCACTCCAAATG
GAAGCATTCCCAATGACAAACCATTTCAAAATGTAAACAGGATCACATATGGGGCCTGTCCC
AGATATGTTAAGCAAAACACTCTGAAATTGGCAACAGGGATGCGGAATGTACCAGAGAAACA
AACTAGAGGCATATTCGGCGCAATCGCGGGTTTCATAGAAAATGGTTGGGAGGGAATGATGG
ACGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGCACAGGACAAGCAGCAGATCTTAAA
AGCACTCAAGCAGCAATCAACCAAATCAACGGGAACTGAATAGGTTAATCGAGAAAACGAA
CGAGAAATTCCATCAAATTGAAAAAGAATTCTCAGAAGTAGAAGGGAGAATTCAGGACCTCG
AGAAATATGTTGAGGACACTAAAATAGATCTCTGGTCGTACAACGCGGAGCTTCTTGTTGCC
CTGGAGAACCAACATACAATTGATCTAACTGACTCAGAAATGAACAACTGTTTGAAAGAAC
AAGGAAGCACTGAGAGAAAATGCTGAGGATATGGGCAATGGTTGTTTCAAAATATAACCACA
AATGTGACAATGCCTGCATAGGGTCAATCAGAAATGGAACCTATGACCATGATGTATACAGA
GACGAAGCATTAACAACCGGTTCCAGATCAAAGGTGTTGAGCTGAAGTCAGGATACAAAGA
TTGGATCCTATGGATTTCTTTGCCATATCATGTT**A**TTTGCTTTGTGT**T**GTTTTGCTGGGGT
TCATTATGTGGGCCTGCCAAAAGGCAACATTAGGTGCAACATTTGCATT**TGA**GTGCATTAA
TTAAAAACACCCCTTGTTTCTACT

MO_HA_Virus	NNNNNNNGCAGGGGA	AATTCTATTAA	CCATGAAGACTATCATTGCTTTGAGCTACATTT	60
MO_HA_NCB1	AGCAAAAGCAGGGGA	AATTCTATTAA	CCATGAAGACTATCATTGCTTTGAGCTACATTT	60
MO_HA_pHW2000	AGCAAAAGCAGGGGA	AATTCTATTAA	CCATGAAGACTATCATTGCTTTGAGCTACATTT	60

MO_HA_Virus	TATGTCTGGTTTTCGCTCA	AAAACTTCCCGGAAATGACAACAGCACGGCAACGCTGTGCC	120	
MO_HA_NCB1	TATGTCTGGTTTTCGCTCA	AAAACTTCCCGGAAATGACAACAGCACGGCAACGCTGTGCC	120	
MO_HA_pHW2000	TATGTCTGGTTTTCGCTCA	AAAACTTCCCGGAAATGACAACAGCACGGCAACGCTGTGCC	120	

MO_HA_Virus	TGGGACACCATGCGAGTG	CCAAACGGAACGCTAGTGA	AAACAATCACGAATGACCAAAATTG	180
MO_HA_NCB1	TGGGACACCATGCGAGTG	CCAAACGGAACGCTAGTGA	AAACAATCACGAATGACCAAAATTG	180
MO_HA_pHW2000	TGGGACACCATGCGAGTG	CCAAACGGAACGCTAGTGA	AAACAATCACGAATGACCAAAATTG	180

MO_HA_Virus	AAGTGACTAATGCTACTG	AGCTGGTTCAGAGTTCCTCAACAGGTAGAATATGCGACAGTC	240	
MO_HA_NCB1	AAGTGACTAATGCTACTG	AGCTGGTTCAGAGTTCCTCAACAGGTAGAATATGCGACAGTC	240	
MO_HA_pHW2000	AAGTGACTAATGCTACTG	AGCTGGTTCAGAGTTCCTCAACAGGTAGAATATGCGACAGTC	240	

MO_HA_Virus	CTCACCAAATCCTTGATG	GAGAAAACTGCACACTGATAGATGCTCTATTGGGAGACCCAC	300	
MO_HA_NCB1	CTCACCAAATCCTTGATG	GAGAAAACTGCACACTGATAGATGCTCTATTGGGAGACCCAC	300	
MO_HA_pHW2000	CTCACCAAATCCTTGATG	GAGAAAACTGCACACTGATAGATGCTCTATTGGGAGACCCAC	300	

MO_HA_Virus	ATTGTGATGGCTTCCAAA	ATAAGGAATGGGACCTTTTGTGAACGCAGCAAAAGCCTACA	360	
MO_HA_NCB1	ATTGTGATGGCTTCCAAA	ATAAGGAATGGGACCTTTTGTGAACGCAGCAAAAGCCTACA	360	
MO_HA_pHW2000	ATTGTGATGGCTTCCAAA	ATAAGGAATGGGACCTTTTGTGAACGCAGCAAAAGCCTACA	360	

MO_HA_Virus	GCAACTGTTACCCCTTAT	GATGTGCCGGATTATGCCTCCCTTAGGTC	ACTAGTTGCCCTCAT	420
MO_HA_NCB1	GCAACTGTTACCCCTTAT	GATGTGCCGGATTATGCCTCCCTTAGGTC	ACTAGTTGCCCTCAT	420
MO_HA_pHW2000	GCAACTGTTACCCCTTAT	GATGTGCCGGATTATGCCTCCCTTAGGTC	ACTAGTTGCCCTCAT	420

MO_HA_Virus	CCGGCACCCCTGGAGTTT	AAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAA	480	
MO_HA_NCB1	CCGGCACCCCTGGAGTTT	AAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAA	480	
MO_HA_pHW2000	CCGGCACCCCTGGAGTTT	AAACAATGAAAGCTTCAATTGGACTGGAGTCGCTCAGAATGGAA	480	

MO_HA_Virus	CAAGCTCTGCTTGCAAA	AGGAGATCTATTAA	CAGTTTCTTTAGTAGATTGAATTGGTTGC	540
MO_HA_NCB1	CAAGCTCTGCTTGCAAA	AGGAGATCTATTAA	CAGTTTCTTTAGTAGATTGAATTGGTTGC	540
MO_HA_pHW2000	CAAGCTCTGCTTGCAAA	AGGAGATCTATTAA	CAGTTTCTTTAGTAGATTGAATTGGTTGC	540

MO_HA_Virus	ACCAATTAA	AAATACAGATATCCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTG	600	
MO_HA_NCB1	ACCAATTAG	AAATACAGATATCCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTG	600	
MO_HA_pHW2000	ACCAATTAA	AAATACAGATATCCAGCACTGAACGTGACTATGCCAAACAATGACAAATTTG	600	

MO_HA_Virus	ACAAATTGTACATTTTGG	GGGGTTTACCACCCGAGTACGGACAGTG	ACCAAACCGAGCTAT	660
MO_HA_NCB1	ACAAATTGTACATTTTGG	GGGGTTTACCACCCGAGTACGGACAGTG	ACCAAACCGAGCTAT	660
MO_HA_pHW2000	ACAAATTGTACATTTTGG	GGGGTTTACCACCCGAGTACGGACAGTG	ACCAAACCGAGCTAT	660

MO_HA_Virus	AT	CCC---CATCAGGGAGAGTCA	CAGTCTCTACCAAAAGAAGCCAACAACTGTAATCC	717
MO_HA_NCB1	AT	CCGCAAGCTCAGGGAGAGTCA	CAGTCTCTACCAAAAGAAGCCAACAACTGTAATCC	720
MO_HA_pHW2000	AT	CCC---CATCAGGGAGAGTCA	CAGTCTCTACCAAAAGAAGCCAACAACTGTAATCC	717
	**	*		
MO_HA_Virus	CGAATATCGGATCCGAT	CCAGACCCCTGGGTAAAGGGGT	ATCTCCAGCAGAATAAGCATCTATTGGA	777
MO_HA_NCB1	CGAATATCGGATCCGAT	CCAGACCCCTGGGTAAAGGGGT	ATCTCCAGCAGAATAAGCATCTATTGGA	780
MO_HA_pHW2000	CGAATATCGGATCCGAT	CCAGACCCCTGGGTAAAGGGGT	ATCTCCAGCAGAATAAGCATCTATTGGA	777

MO_HA_Virus	CAATAGTAAAACCGGAG	ACATAC	TTTGGATTAAACAGCACAGGGAATCTAATTGCTCCTC	837
MO_HA_NCB1	CAATAGTAAAACCGGAG	ACATAC	TTTGGATTAAACAGCACAGGGAATCTAATTGCTCCTC	840
MO_HA_pHW2000	CAATAGTAAAACCGGAG	ACATAC	TTTGGATTAAACAGCACAGGGAATCTAATTGCTCCTC	837

MO_HA_Virus	GGGGTTACTTCAAAAT	ACGAAGTGGGAAAAGCTCAATAATGAGGT	CAGATGCACCCATTG	897
MO_HA_NCB1	GGGGTTACTTCAAAAT	ACGAAGTGGGAAAAGCTCAATAATGAGGT	CAGATGCACCCATTG	900
MO_HA_pHW2000	GGGGTTACTTCAAAAT	ACGAAGTGGGAAAAGCTCAATAATGAGGT	CAGATGCACCCATTG	897

MO_HA_Virus	ACAAATGCAATTCTGA	ATGATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTTTC	957	
MO_HA_NCB1	ACAAATGCAATTCTGA	ATGATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTTTC	960	
MO_HA_pHW2000	ACAAATGCAATTCTGA	ATGATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTTTC	957	

MO_HA_Virus	AAAAATGTAACAGGAT	CACATATGGGGCCTGTCC	CAGATATGTTAAGCAAAACACTCTGA	1017
MO_HA_NCB1	AAAAATGTAACAGGAT	CACATATGGGGCCTGTCC	CAGATATGTTAAGCAAAACACTCTGA	1020
MO_HA_pHW2000	AAAAATGTAACAGGAT	CACATATGGGGCCTGTCC	CAGATATGTTAAGCAAAACACTCTGA	1017

MO_HA_Virus	AATTGGCAACAGGGAT	GCGGAATGTACCAGAGAAACAAACTAGAGGCATATT	CGGCGCAA	1077
MO_HA_NCB1	AATTGGCAACAGGGAT	GCGGAATGTACCAGAGAAACAAACTAGAGGCATATT	CGGCGCAA	1080
MO_HA_pHW2000	AATTGGCAACAGGGAT	GCGGAATGTACCAGAGAAACAAACTAGAGGCATATT	CGGCGCAA	1077

MO_HA_Virus	TCGCGGGTTTCATAGA	AAATGGTTGGGAGGGAATGATGGACGGTTGGTACGGTTTCAGGC	1137	
MO_HA_NCB1	TCGCGGGTTTCATAGA	AAATGGTTGGGAGGGAATGATGGACGGTTGGTACGGTTTCAGGC	1140	
MO_HA_pHW2000	TCGCGGGTTTCATAGA	AAATGGTTGGGAGGGAATGATGGACGGTTGGTACGGTTTCAGGC	1137	

MO_HA_Virus	ATCAAAATTTCTGAGG	GCGACAGGACAAGCAGCAGATCTTAAAGCACTCAAGCAGCAATCA	1197	
MO_HA_NCB1	ATCAAAATTTCTGAGG	GCGACAGGACAAGCAGCAGATCTTAAAGCACTCAAGCAGCAATCA	1200	
MO_HA_pHW2000	ATCAAAATTTCTGAGG	GCGACAGGACAAGCAGCAGATCTTAAAGCACTCAAGCAGCAATCA	1197	

MO_HA_Virus	ACCAAAATCAACGGGA	AACTGAATAGGTTAATCGAGAAAACGAACGAGAAAT	TCCATCAAA	1257
MO_HA_NCB1	ACCAAAATCAACGGGA	AACTGAATAGGTTAATCGAGAAAACGAACGAGAAAT	TCCATCAAA	1260
MO_HA_pHW2000	ACCAAAATCAACGGGA	AACTGAATAGGTTAATCGAGAAAACGAACGAGAAAT	TCCATCAAA	1257

MO_HA_Virus	TTGAAAAAGAATTCTC	AGAAGTAGAAGGGAGAATT	CAGGACCTCGAGAAATATGTTGAGG	1317
MO_HA_NCB1	TTGAAAAAGAATTCTC	AGAAGTAGAAGGGAGAATT	CAGGACCTCGAGAAATATGTTGAGG	1320
MO_HA_pHW2000	TTGAAAAAGAATTCTC	AGAAGTAGAAGGGAGAATT	CAGGACCTCGAGAAATATGTTGAGG	1317

MO_HA_Virus	ACACTAAAAATAGAT	CTCTGGTCTACAACGCGGAGCTTCTTGTG	CCCTGGAGAACCAAC	1377
MO_HA_NCB1	ACACTAAAAATAGAT	CTCTGGTCTACAACGCGGAGCTTCTTGTG	CCCTGGAGAACCAAC	1380
MO_HA_pHW2000	ACACTAAAAATAGAT	CTCTGGTCTACAACGCGGAGCTTCTTGTG	CCCTGGAGAACCAAC	1377

MO_HA_Virus	ATACAATTGATCTA	ACTGACTCAGAAATGAACAAACTGTTTGAAAGAACAAAGGAAGCAAC	1437	
MO_HA_NCB1	ATACAATTGATCTA	ACTGACTCAGAAATGAACAAACTGTTTGAAAGAACAAAGGAAGCAAC	1440	
MO_HA_pHW2000	ATACAATTGATCTA	ACTGACTCAGAAATGAACAAACTGTTTGAAAGAACAAAGGAAGCAAC	1437	

MO_HA_Virus	TGAGAGAAAATGCTG	AGGATATGGGCAATGGTTGTTTCAAAATATACCACAAATGTGACA	1497	
MO_HA_NCB1	TGAGAGAAAATGCTG	AGGATATGGGCAATGGTTGTTTCAAAATATACCACAAATGTGACA	1500	
MO_HA_pHW2000	TGAGAGAAAATGCTG	AGGATATGGGCAATGGTTGTTTCAAAATATACCACAAATGTGACA	1497	

MO_HA_Virus	ATGCTTGCATAGGGT	CAATCAGAAATGGA	ACTTATGACCATGATGTATACAGAGACGAAG	1557
MO_HA_NCB1	ATGCTTGCATAGGGT	CAATCAGAAATGGA	ACTTATGACCATGATGTATACAGAGACGAAG	1560
MO_HA_pHW2000	ATGCTTGCATAGGGT	CAATCAGAAATGGA	ACTTATGACCATGATGTATACAGAGACGAAG	1557

MO_HA_Virus	CATTAAACAACCGGT	TCCAGATCAAAGGTGTTGAGCTGAAGT	CAGGATACAAAGATTGGA	1617
MO_HA_NCB1	CATTAAACAACCGGT	TCCAGATCAAAGGTGTTGAGCTGAAGT	CAGGATACAAAGATTGGA	1620
MO_HA_pHW2000	CATTAAACAACCGGT	TCCAGATCAAAGGTGTTGAGCTGAAGT	CAGGATACAAAGATTGGA	1617

MO_HA_Virus	TCCTATGGATTTCCT	TTGCCATATCATGTTA	TTTGCTTTGTGTTGTTTGTCTGGGGTTCA	1677
MO_HA_NCB1	TCCTATGGATTTCCT	TTGCCATATCATGTTA	TTTGCTTTGTGTTGTTTGTCTGGGGTTCA	1680
MO_HA_pHW2000	TCCTATGGATTTCCT	TTGCCATATCATGTTA	TTTGCTTTGTGTTGTTTGTCTGGGGTTCA	1677

MO_HA_Virus	TTATGTGGGCTGCCA	AAAAAGGCAACATTAGGTGCAACATTTG	CATTGAGTGCATTAAT	1737
MO_HA_NCB1	TTATGTGGGCTGCCA	AAAAAGGCAACATTAGGTGCAACATTTG	CATTGAGTGCATTAAT	1740
MO_HA_pHW2000	TTATGTGGGCTGCCA	AAAAAGGCAACATTAGGTGCAACATTTG	CATTGAGTGCATTAAT	1737

MO_HA_Virus	TAAAAACACCCNNNN	NNNNNNNN	1759	
MO_HA_NCB1	TAAAAACACCCCTGT	TCTACT	1762	
MO_HA_pHW2000	TAAAAACACCCCTGT	TCTACT	1759	

CLUSTAL O(1.2.4) multiple sequence alignment

HA_NCBI	MKTIILSYILCLVFAQKLPGNDNSTATLCLGHHAVPNGTLVKTITNDQIEVTNATELVQ	60
HA_pHW2000	-----	0
HA_NCBI	SSSTGRICDSPHQILDGENCTLIDALLGDPHCDGFQNKEDLFFVERSKAYSNCYPYDVPD	120
HA_pHW2000	SKSRG*FY*P*R-----LSLL*-----ATFYVW---FSLKN	24
	.* * : : **: : . * : : :	
HA_NCBI	YASLRSLVASSGTLEFNNESEFNWTGVAQNGTSSAC-KRRSIKSFSSRLNWLHQLEN-RYP	178
HA_pHW2000	FPE-----MTTARQRCAWDTMQCQTER**KQSRMTKLK*LMLLSWFRVPQQVEYA	71
	: . : .: * : : . * : . : *.*: : : .*	
HA_NCBI	-ALNVTMPNNDKFDKLYIWGVHHPSTDSVQTSVYVQASGRVTVSTKRSQQTVIPNIG---	234
HA_pHW2000	TVLTKSLMEKTAH**MLYWETHIVMASKIRNGTFLLNAAKPTATVTLMMCRIMPPLGH*L	128
	.*. : : : . : * .* : : : : : : : * : : : : *	
HA_NCBI	--SRPWVRGVSS-----	244
HA_pHW2000	PHPAPWSLTMKASIGLESLRMEQALLAKGDLLTVSLVD*IGCTN*NTDIQH*T*LCQTM	184
	** : :	
HA_NCBI	-----	244
HA_pHW2000	NLTNCTFGGFTTRVRTVTKPAYIPHQGESQSLPKEANKL*SRISDPDPG*GVSPA*ASI	241
HA_NCBI	---RISYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITP	300
HA_pHW2000	GQ**NRETYF*LTAQGI*LLLGVTISKY-----EVGKAQ**GQMHLPTNAILNASLQ	286
	. . *: : . * **: . *: : . *: : . *	
HA_NCBI	NGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIA----GFI	355
HA_pHW2000	MEAFPMTNHFKM*TGSHMGVPDMLSKTL*NWQQCGMYQRNK-LEAYSAQSRVS*KMVG	342
	:* : * : . * * : : : : * : : : * : :	
HA_NCBI	ENGWE-GMMDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRL--IEKTNEKFHQIE	412
HA_pHW2000	RE*WTVGTVSGIKILRAQDKQILKALKQQSTKSTGN*IG*SRKTRNSIKLKKNSQK*K	398
	. : * * : . * * : : : * . : : : : * * . : * : : : : :	
HA_NCBI	KEFSEVEGRIQDLEK---YVEDTKIDLWSYNAELLVALENQH-TIDLTDSE---MNKLFE	465
HA_pHW2000	GEFRTSRNMLRTLK*ISGRTTTSFLLPWRTNIQLI*LTQK*TNCLKEQGSN*EKMLRIWA	454
	** .. : : * : . : : * * :* : : : . . .* : * : :	
HA_NCBI	RTRKQLRENA--EDMGNGCF---KiyHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIK	519
HA_pHW2000	MVVSkyTTNVTMPA*GQSEMELMTMMYTETKH*TTG-----SRSKVL	494
	. . : * . * : . : : * : : : *	
HA_NCBI	GVELKSGYKDWILWISFAISCFLLCVLLGF-----IMWACQKGNIRCNI	564
HA_pHW2000	S*SQDTKIGSYGFPLPYHVICF---VLFCWGSLSLCPAKKATLGATFAFECIN*KHPCFY	548
	. . . : . : : : : ** **: : : : * : : *	
HA_NCBI	CI	566
HA_pHW2000	--	548