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(54) **CANINE INFLUENZA VIRUS AND RELATED COMPOSITIONS AND METHODS OF USE**

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(52) **U.S. Cl.**

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 424/206.1; 424/210.1; 435/236; 435/320.1;  
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(58) **Field of Classification Search**

None  
 See application file for complete search history.

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(57) **ABSTRACT**

The present invention provides an isolated canine influenza virus of subtype H3N8 comprising an HA having SEQ ID NO: 4 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, with the proviso that the amino acids at positions 94 and 233 are identical to SEQ ID NO: 4; a composition comprising attenuated or inactivated virus; isolated or purified HA, NM, NP, M1, NS1, PA, PB1, and PB2 proteins and fragments thereof and compositions comprising same or nucleic acids, optionally as part of a vector, encoding same; and a method of inducing an immune response to canine influenza virus in an animal comprising administering to the animal an aforementioned composition.

**15 Claims, 14 Drawing Sheets**

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NM

AGTTTAAAATGAATCCAAATCAAAGATAATAGCAATTGGATTTGCATCATTGGG  
GATATTAATCATTAAATGTCATTCTCCATGTAGTCAGCATTATAGTAACAGTACTG  
GTCCTCAATAACAATAGAACAGATCTGAACTGCAAAGGGACGATCATAAGAGAA  
TACAATGAAACAGTAAGAGTAGAAAACTTACTCAATGGTATAATACCAGTACA  
ATTAAGTACATAGAGAGACCTTCAAATGAATACTACATGAATAACACTGAACCA  
CTTTGTGAGGCCCAAGGCTTTGCACCATTTTCCAAAGATAATGGAATACGAATTG  
GGTCGAGAGGCCATGTTTTTGTGATAAGAGAACCTTTTGTATCATGTTCCGCCCTC  
AGAATGTAGAACCCTTTTCTCACACAGGGCTCATTACTCAATGACAAACATTCT  
AACGGCACAATAAAGGATCGAAGCCCGTATAGGACTTTGATGAGTGTCAAATA  
GGGCAATCACCCAATGTATATCAAGCTAGGTTTGAATCGGTGGCATGGTCAGCA  
ACAGCATGCCATGATGGAAAAAATGGATGACAGTTGGAGTACAGGGCCCGAC  
AATCAAGCAATTGCAGTAGTGAACACTATGGAGGTGTTCCGGTTGATACTATTAATT  
CATGGGCAGGGGATATTTTAAGAACCCAAGAATCATCATGCACCTGCAITAAAG  
GAGACTGTTATTGGGTAATGACTGATGGACCGGCAAATAGGCAAGCTAAATATA  
GGATATTCAAAGCAAAGATGGAAGAGTAATTGGACAAACTGATATAAGTTTCA  
ATGGGGGACACATAGAGGAGTGTCTTGTACCCCAATGAAGGGAAGGTGGAAT  
GCATATGCAGGGACAATTGGACTGGAACAATATAGACCAATTCTGGTAATATCTTC  
TGATCTATCGTACACAGTTGGATATTTGTGTGCTGGCATTCCCCTGACACTCCTA  
GGGGAGAGGATAGTCAATTCACAGGCTCATGTACAAAGTCCTTTGGGAAATAAAG  
GATACGGTGTAAAAGGCTTCGGGTTTCGACAAGGAAGTACGATGGGGCCGGAA  
GGACAATTAGTAGGACTTCAAGATCAGGATTCGAAATAATAAAAATCAGGAATG  
GTTGGACACAGAACAGTAAGGACCAAATCAGGAGGCAAGTGATTATCGATGACC  
CAAATTGGTCAGGATATAGCGGTTCTTTCACATTGCCGGTTGAACTGACAAAAA  
GGGATGTTTGGTCCCCTGTTTCTGGGTTGAAATGATTAGAGGTAAACCTGAAGAA  
ACAACAATATGGACCTCTAGCAGCTCCATTGTGATGTGTGGAGTAGATCATAAAA  
TTGCCAGTTGGTCATGGCACGATGGAGCTATTCTTCCCTTTGACATCGATAAGAT  
GTAATTTACGAAAAAACTCCTTGTCTTCTACTA (SEQ ID NO: 1)

FIG. 1

NM - Amino

MNPNQKIIAIGFASLGILIIINVILHVVSIIIVTVLVLNNRRTDLNCKGTIIREYNETVRVEK  
LTQWYNTSTIKYIERPSNEYMNNTEPLCEAQGFAPFSKDNIGIRIGSRGHV FVIREPFV  
SCSPSECR TFFLTQGSLNDKHSNGTIKDRSPYRTLMSVKIGQSPNVYQARFESVAWS  
ATACHDGKKWMTVGVTGPDNQAIAVVNYGGVPVDTINSWAGDILRTQESSCTCIKG  
DCYWVMTDGPANRQAKYRIFKAKDGRVIGQTDISFNGGHIEECSCYPNEGKVECICR  
DNWTGTNRPII.VISSDI.SYTVGYLCAGIPTDTPRGEDSQFTGSCTSPLGNKGYGVKGF  
GFRQGTDVWAGRTISRTSRSGFEIIRNGWTQNSKDQIRRQVIIDDPNWSGYSGSFTL  
PYELTKKGCLVPCFWVEMIRGKPEETTIWTSSSSIVMCGVDHKIASWSWIIDGAILPF  
DIDKM (SEQ ID NO: 2)

FIG. 2

HA:

AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTAATACT  
ACTGACCCATTGGGCCTACAGTCAAAACCCAATCAGTGGCAATAACACAGCCAC  
ACTGTGTCTGGGACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATGAG  
TGATGATCAAATTGAGGTGACAAATGCTACAGAATTAGTTCAGAGCATTTCATG  
GGGAAAATATGCAACAAATCATATAGAATTCTAGATGGAAAGAAATTGCACATTA  
ATAGATGCAATGCTAGGAGACCCCCACTGTGACGCCCTTCAGTATGAGAGTTGG  
GACCTCTTTATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCC  
CTGACTATGCATCGCTCCGATCCATTGTAGCATCCTCAGGAACAGTTGAATTCAC  
AGCAGAGGGATTACATGGACAGGTGTAACCTCAAAACGGAAGAAGTGGAGCCTG  
CaaAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCT  
GGAAGCTCTTACCCACATTGAATGTGACAATGCCTAACAAATAAAAATTTGACA  
AGCTATACATCTGGGGGATTCATCACCCGAGCTCAAATCAAGAGCAGACAAAAT  
TGTACATCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAA  
CAATAATCCCTAACATCGAATCTAGACCGTTGGTCAGAGGTCAATCAGGCAGGA  
TAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTA  
ATGGCAACTTAGTTGCACCCGCGGGGATATTTTAAATTGAACACAGGGAAAAGCT  
CTGTAAATGAGATCCGATGTACCCATAGACATTTGTGTGTCTGAAATGTATTACACC  
AAATGGAAGCATCTCCAACGACAAGCCATTCAAAATGTGAACAAAAGTTACATA  
TGGAAAATGCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGAT  
GAGGAATGTACCAGAAAAGCAAACCAGAGGAATCTTTGGAGCAATAGCGGGATT  
CATCGAAAACGGCTGGGAAGGAATGGTTGATGGGTGGTATGGGTTCCGATATCA  
AAACTCTGAAGGAACAGGGCAAGCTGCAGATCTAAAGAGCACTCAAGCAGCCAT  
TGACCAGATTAATGGAAAGTTAAACAGAGTGATTGAAAGAACCAATGAGAAATT  
CCATCAAAATAGAGAAGGAATTCTCAGAAAGTAGAAGGAAGGAATTCAGGACTTGGA  
GAAATATGTAGAAGACACCAAAATAGACCTATGGTCCTACAATGCAGAATTGCT  
GGTGGCTCTAGAAAATCAACATACAATTGACTTAACAGATGCAGAAATGAATAA  
ATTATTTGAGAAGACTAGACGCCAGTTAAGAGAAAACGCAGAAGACATGGGAGG  
TGGATGTTTCAAGATTTACCACAAATGTGATAATGCATGCATTGAATCAATAAGA  
ACTGGGACATATGACCATTACATATACAGAGATGAAGCATTAAACAACCGATTT  
CAGATCAAAGGTGTAGAGTTGAAATCAGGCTACAAAGATTGGATACTGTGGATT  
TCATTCGCCATATCATGCTTCTTAATTTGCGTTGTTCTATTGGGTTTCATTATGTGG  
GCTTGCCAAAAGGCAACATCAGATGCAACATTTGCATTTGAGTAAACTGATAGT  
TAAAAACACCCCTTGTTTCTACT (SEQ ID NO:3)

FIG. 3

HA - Amino

MKTTIILILLTHWAYSQNPISGNNTATLCLGHHAVANGTLVKTMSDDQIEVTNATEL  
VQSISMGKICNKSYRILDGRNCTLIDAMLGDPHCDALQYESWDLFIERSSAFNSCY  
DIPDYASLRISIVASSGIVEFTAEFTWTGVTQNGRSGACKRGSADSFRLNWLTKS  
GSSYPTLNVTMPNNKNFDKLYIWGIHHPSSNQEQTCLYIQESGRVTVSTKRSQQTIIP  
NIESRPLVRGQSGRISYWTIVKPGDILMINSNGNLVAPRGYFKLNTGKSSVMRSDVPI  
DICVSECITPNGSISNDKPFQNVNKVTYGKCPKYIRQNTLKLATGMRNVPEKQTRGIF  
GAIAGFIENGWEGMVDGWYGFYQNSEGTGQAADLKSTQAAIDQINGKLN RV IERT  
NEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDAEMN  
KLFKTRRQIRENAEDMGGGCFKIYHKCDNACIESIRTGTYDHYIYRDEALNNRFQI  
KGVELKSGYKDWILWISFAISCFLICVLLGFIMWACQKGNIRCNICI (SEQ ID NO: 4)

FIG. 4

NP

CAGGGAGCAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAGTCATGG  
CGTCTCAAGGCACCAAACGATCCTATGAACAGATGGAAACTGATGGGGAAACGCC  
AGAATGCAACTGAAATCAGAGCATCTGTCCGAAGGATGGTGGGAGGAATCGGAC  
GGTTTTATGTCCAGATGTGTACTGAGCTTAAACTAAACGACCATGAAGGGCGGCT  
GATTCAGAACAGCATAACAATAGAAAGGATGGTACTTTCAGCATTTCGACGAAAG  
AAGAAACAAGTATCTCGAGGAGCATCCCAGTGCTGGGAAAGACCCTAAGAAAAC  
GGGAGGCCCGATATACAGAAGAAAAGATGGGAAATGGATGAGGGAACTCATCC  
TCCATGATAAAGAAGAAATCATGAGAATCTGGCGTCAGGCCAACAATGGTGAAG  
ACGCTACTGCTGGTCTTACTCATATGATGATCTGGCACTCCAATCTCAATGACAC  
CACATACCAAAGAACAAGGGCTCTTGTTCCGACTGGGATGGATCCCAGAATGTG  
CTCTCTGATGCAAGGCTCAACCCTCCCACGGAGATCTGGAGCCGCTGGTGTGCA  
GTAAAAGGTGTTGGAACAATGGTAATGGAACCTCATCAGGATGATCAAACGCCGA  
ATAAATGATCGGAATTTCTGGAGAGGTGAAAATGGTCGAAGAACCAGAATTGCT  
TATGAAAGAATGTGCAATATCCTCAAAGGGAAATTTTCAGACAGCAGCACAAACGG  
GCTATGATGGACCAGGTGAGGGAAAGGCCGCAATCCTGGAAACGCTGAGATTGAG  
GATCTCATTTCCTTGGCACGATCAGCACTTATTTTGAGAGGATCAGTAGCCATA  
AATCATGCCTACCTGCCTGTGTTTATGGCCTTGCAGTAACCAGTGGGTATGACTTT  
GAGAAGGAAGGATACTCTCTGGTTGGAATTGATCCTTTCAAACCTACTCCAGAACA  
GTCAAATTTTCAGTCTAATCAGACCAAAGAAAACCCAGCACACAAAAGCCAGT  
TGGTGTGGATGGCATGCCATTCTGCAGCATTGAGGATCTGAGAGTTTTAAATTT  
CATTAGAGGAACCAAAGTAATCCCAAGAGGACAGTTAACAACCAGAGGAGTTCA  
AATTGCTTCAAATGAAAACATGGAGACAATAAATTTCTAGCACACTTGAAGTGAAG  
AAGCAAATATTGGGCAATAAGGACCAGAAGCGGAGGAAACACCAGTCAACAGA  
GAGCATTTCAGGACAGATAAGTGTGCAACCTACTTTCTCAGTACAGAGAAATCT  
TCCCTTTGAGAGAGCAACCATTATGGCTGCATTCACTGGTAACACTGAAGGGAGG  
ACTTCCGACATGAGAACGGAAATCATAAGGATGATGGAAAATGCCAAATCAGAA  
GATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAGCTCTCGGACGAAAAGGCAACG  
AACCCGATCGTGGCTTCCCTTTGACATGAGCAATGAAGGGTCTTATTTCCTTCGGAG  
ACAATGCTGAGGAGTTTGACAGTTAAAGAAAATACCCTTGTTTCTACTAATACG  
AGACGATAT (SEQ ID NO: 5)

FIG. 5

NP - Amino

MASQGTKRSYEQMETDGERQNATEIRASVGRMVGGIGRFYVQMCTELKLNDHEGR  
LIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRKDGKWMRELILHD  
KEEIMRIWRQANNGEDATAGLTHMMIWHSNLNDTTYQRTRALVRTGMDPRMCSL  
MQGSTLPRRSGAAGA AVKGVGTMMELIRMIRKGINDRNFWRGENGRRTRIAYER  
MCNILKGKFQTA AQRAMMDQVREGRNPGNAEIEDLIFLARSALILRGSVAHKSC LPA  
CVYGLAVTSGYDFEKEGYSLVGIDPFKLLQNSQIFSLIRPKENPAHKSQLVWMACHS  
AAFEDLRVLNFIRGTKVIPRGQLTTRGVQIASNENMETINSSTLELRSKYWAIRTRSG  
GNTSQQRAFAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN  
AKSEDVSFQGRGVFELSDEKATNPVPSFDMSNEGSYFFGDNAEEFDS (SEQ ID NO:  
6)

FIG. 6



MI

TATTCGTCTCAGGGAGCAAAAGCAGGTAGATATTTAAAGATGAGTCTTCTAACCG  
AGGTTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAAGCCGAGAT  
CGCGCAGAGACTTGAAGATGTCTTTGCGGGAAAGAACACCGATCTTGAGGCACT  
CATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA  
GGATTTGTATTCACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTAGACGCT  
TTGTCCAAAATGCCCTTAGTGGAACCGGAGATCCAAACAAACATGGACAGAGCAG  
TAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGAGGCAAAAGAGG  
TGGCACTCAGCTATTCCACTGGTGCCTAGCCAGCTGCATGGGACTCATATACAA  
CAGAATGGGAACCTGTTACAACCGAAGTGGCATTGGCCTGGTATGCGCCACATGT  
GAACAGATTGCTGATTCCCAGCATCGATCTCACAGGCAGATGGTGACAACAACC  
AACCCATTAATCAGACATGAAAACAGAATGGTATTAGCCAGTACCACGGCTAAA  
GCCATGGAAACAGATGGCAGGATCGAGTGAGCAGGCAGCAGAGGCCATGGAGGT  
TGCTAGTAGGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACCCACCC  
TAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTACAGGCCTACCAG  
AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATCCTCTCGTTATTGCAGC  
AAGTATCATTGGAATCTTGCCTTGATATTGTGGATTCTTGATCGTCTTTTCTTCA  
AATTCATTTAICGICGCCITAAATACGGGTTGAAAAGAGGGCCTTCTACGGAAGG  
AGTACCIGAGTCTATGAGGGAAGAATAICGGCAGGAACAGCAGAAATGCTGTGGA  
TGTTGACGATGGTCATTTTGTCAACATAGAGCTGGAGTAAAAAACTACCTTGTTT  
CTACTAATACGAGACGATAT (SEQ ID NO: 7)

FIG. 7

MI - Amino

MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKG  
ILGFVFTLTVPSERGLQRRRFVQNALSGNGDPNNMDRAVKLYRKLKREITFHEAKEV  
ALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHRSHRQMVTNTNP  
LIRHENRMVLASTITAKAMEQMAGSSEQAAEAMEVASRARQMVMQAMRTIGTHPSSS  
AGLKDDLLENLQAYQKRMGVQMQRFK (SEQ ID NO: 8)

FIG. 8

NSI

GGAGCAAAGCAGGGTGACAAAACATAATGGATTCCAACACTGTGTCAAGCTT  
TCAGGTAGACTGTTTTCTTTGGCATGTCCGCAAACGATTCGCAGACCAAGAAGCTG  
GGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAGAAGTCCCTAAGGGGA  
AGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCATGCAGGAAAGCAG  
ATAGTGGAGCAGATTCTGGAAAAGGAATCAGATGAGGCACTTAAAATGACCATT  
GCCTCTGTTCCCTGCTTCACGCTACTTAACTGACATGACTCTTGATGAGATGTCAAG  
AGACTGGTTCATGCTCATGCCCAAGCAAAAAGTAACAGGCTCCCTATGTATAAG  
AATGGACCAAGCAATCATGGATAAGAACATCATACTTAAAGCAAACCTTTAGTGT  
GATTTTCGAAAGGCTGGAAACACTAATACTACTTAGAGCCTTCACCGAAGAAGG  
AGCAGTCGTTGGCGAAATTTACCATTACCTTCTCTCCAGGACATACTAATGAG  
GATGTCAAAAATGCAATTGGGGTCCTCATCGGAGGACTTAAATGGAATGATAAT  
ACGGTTAGAACTCTGAAACTCTACAGAGATTCGCTTGGAGAAGCAGTCATGAA  
AATGGGAGACCTTCATTCCCTCAAAGCAGAAACGAAAAATGGAGAGAACAATT  
AAGCCAGAAATTTGAAGAAATAAGATGGTTGATTGAAGAAGTGCGACATAGATT  
GAAAAATACAGAAAATAGTTTTGAACAAATAACATTTATGCAAGCCTTACAACCT  
ATTGCTTGAAGTAGAACAAGAGATAAGAACTTCTCGTTTCAGCTTATTTAATGA  
T (SEQ ID NO: 9)

FIG. 9

NSI - Amino

MDSNTVSSFQVDCFLWIIVRKRFAEQELGDAPFLDRLRRDQKSLRGRGSLGLDIET  
ATHAGKQIVEQILEKESDEALKMTIASVPASRYLTDMTLDEMSTRDWFMLMPKQKVI  
GSLCIRMDQAIMDKNIILKANFSVIFERLETLILLRAFTEEGAVVGEISPLPSLPGHTNE  
DVKNAIGVLIGGLKWNDNTVRISETLQRFAWRSSHENGRPSFSPKQKRKMERTIKPEI  
(SEQ ID NO: 10)

FIG. 10

PA

TAAATGGAAGACTTTGTGCGACAGTGCTTCAATCCAATGATCGTCGAGCTTGCGG  
AAAAGGCAATGAAAGAATATGGAGAGAACCCGAAAATCGAAACAAACAAATTT  
GCAGCAATATGCACTCACTTGGAAAGTCTGCTTCATGTACTCGGATTTCCACTTTAT  
AAATGAACTGGGTGAGTCAGTGGTCATAGAGTCTGGTGACCCAAATGCTCTTTTG  
AAACACAGATTTGAAATCATTGAGGGGAGAGATCGAACAATGGCATGGACAGTA  
GTAAACAGCATCTGCAACACCACAAGAGCTGAAAAACCTAAATTTCTTCCAGATT  
TATACGACTATAAGGAGAACAGATTTGTTGAAATTGGTGTGACAAGGAGAGAAG  
TTCACATATACTACCTGGAGAAAGCCAACAAAATAAAGTCTGAGAAAACACATA  
TCCACATTTTCTCATTTACAGGAGAAGAAATGGCTACAAAAGCGGACTATACTCT  
TGATGAAGAGAGTAGAGCCAGGATCAAGACCAGACTATTCCTATAAGACAAGA  
AATGGCCAGTAGAGGCCTCTGGGATTCCTTTTCGTCAGTCCGAGAGAGGCGAAGA  
GACAATTGAAGAAAGATTTGAAATCACAGGAACGATGCGCAAGCTTGCCAATTA  
CAGTCTCCACCGAACTTCTCCAGCCTTGAAAATTTTAGAGTCTATATAGATGGA  
TTCGAACCGAACGGCTGCATTGAGAGTAAGCTTTCTCAAATGTCCAAGAAGTA  
AATGCCAAAATCGAACCATTTTCAAAGACAACACCCCGACCACTCAAATGCCA  
GGTGGTCCACCCTGCCATCAGCGATCCAAATTCTTGCAATGGATGCTCTGAAACT  
GAGCATTGAGGACCCAAGTCACGAGGGAGAGGGGATACCACTATATGATGCAAT  
CAAATGCATGAAAACCTTTCTTTGGATGGAAAGAGCCCAGTATTGTTAAACCACAT  
AAAAAGGGTATAAACCCGAACTATCTCCAAACTTGGAAGCAAGTATTAGAAGAA  
ATACAAGACCTTGAGAACGAAGAAAGGACCCCAAGACCAAGAATATGAAAAA  
ACAAGCCAATTGAAATGGGCACTAGGTGAAAATATGGCACCAAGAGAAAGTGG  
ATTTTGAGGATTGTAAAGACATCAATGATTTAAACAATATGACAGTGATGAGCC  
AGAAGCAAGGTCTCTTGCAAGTTGGATTCAAAGTGAGTTCAACAAGGCTTGTGA  
GCTGACAGATTCAAGCTGGATAGAGCTCGATGAAATTGGGGAGGATGTGCGCCC  
AATAGAATACATTGCGAGCATGAGGAGAAATTATTTTACTGCTGAGATTTCCCAT  
TGTAGAGCAACAGAATATATAATGAAAGGAGTATACATCAACACTGCTCTACTC  
AATGCATCCTGTGCTGCGATGGATGAATTTCAATTAATTCCGATGATAAGTAAAT  
GCAGGACCAAGAAGGGAGAAGGAAAACAATTTATATGGATTCATAATAAAG  
GGAAGGTCCCATTTAAGAAATGATACTGACGTGGTGAACCTTTGTAAGTATGGAAT  
TTTCTCTCACTGATCCAAGATTTGAGCCACACAAATGGGAAAAATACTGCGTTCT  
AGAAATTGGAGACATGCTTCTAAGAAGTCTGTAGGTCAAGTGTCAAGACCCAT  
ATTTTGTATGTAAGGACAAATGGAACCTCTAAAATTAATAATGAAATGGGGAAT  
GGAAATGAGACGCTGCCTCCTTCAGTCTCTGCAACAGATTGAAAGCATGATCGA  
AGCTGAGTCCTCAGTCAAAGAAAAGGACATGACCAAAGAATTTTTTGAGAACAA  
ATCAGAGACATGGCCTATAGGAGAGTCCCCCAAAGGAGTGGAAGAGGGCTCAAT  
CGGGAAGGTTTGCAGGACCTTATTAGCAAAAATCTGTGTTTAAACAGTTTATATGCA  
TCTCCACAACCTGGAAGGATTTTCAGCTGAATCTAGGAAATTACTTCTCATTGTTT  
AGGCTCTTAGAGATGACCTGGAACCTGGAACCTTTGATATTGGGGGGTTATATGA  
ATCAATTGAGGAGTGCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGT  
TCAACTCCTTCCTCACACATGCACTGAAGTAGTTCTGGCAATGCTACTATTTGTTA  
TCCATACTGTCCA (SEQ ID NO: 11)

FIG. 11

PA - Amino

MEDFVRQCFNPMIVELAEKAMKEYGENPKIETNKFAAICTHLEVCFMYSDHFHFINEL  
GESVVIESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTRA EKPKFLPDLYDYKEN  
RFVEIGVTRREVHIYYLEKANKIKSEKTHIHIFSFTGEEMATKADYTLDEESRARIKTR  
LFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRKLANYSLPPNFSSLENFRVYI  
DGFEPNGCIESKLSQMSKEVNAKIEPFSKTTTPRPLKMPGGPPCHQRSKFLMDALKLS  
IEDPSHEGEGIPLYDAIKCMKTFFGWKEPSIVKPHKKGINPNYLQTWKQVLEEIQDLE  
NEERTPKTKNMKKTSQLKWALGENMAPEKVD FEDCKDINDLKQYDSDEPEARSLAS  
WIQSEFNKACELTDSSWIELDEIGEDVAPIEYIASMRRNYFTA EISHCRATEYIMKGVY  
INTALLNASCAAMDEFQLIPMISKCRTKEGRRKTNLYGFIKGRSILRNDTDV VNFVS  
MEFSLTDPRFEPHKWEKYCVLEIGDMLLRTAVGQVSRPIFLYVRTNGTSKIKMKWG  
MEMRRCLLQSLQQIESMIEAESSVKEKDMTKEFFENKSETWPIGESPKGVEEGSIGKV  
CRTLLAKSVFNSLYASPQLEGFSAESRKL LLLIVQALRDDLEPGTFDIGGLYESIEECLIN  
DPWVLLNASWFNSFLTHALK (SEQ ID NO: 12)

FIG. 12

PBI

GAAAGCAGGCAAACCATTTGAATGGATGTCAATCCGACTCTACTTTTCTTAAAGG  
TGCCAGCGCAAATGCTATAAGCACAACATTCCCTTATACTGGAGATCCTCCCTA  
CAGTCATGGAACAGGGACAGGATACACCATGGATACTGTCAACAGAACACACCA  
ATATTCAGAAAAAGGGAAATGGACAACAAACACTGAGATTGGAGCACCACAAT  
TAATCCAATCGATGGACCACTTCCCTGAAGACAATGAACCAAGTGGGTACGCCA  
AACAGATTGTGTATTGGAAGCAATGGCTTTCCTTGAAGAATCCCATCCCGGAATC  
TTTGAAAATTCGTGTCTTGAAACGATGGAGGTGATTCAGCAGACAAGAGTGGAC  
AACTAACACAAGGCCGACAACTTATGATTGGACCTTGAATAGGAATCAACCT  
GCCGCAACAGCACTTGCTAATACGATTGAAGTATTCAGATCAAATGGTCTGACTT  
CCAATGAATCGGGGAGATTGATGGACTTCCCTCAAAGATGTCATGGAGTCCATGA  
ACAAGGAGGAAATGGAAATAACAACACACTTCCAAACGGAAGAGAAGAGTAAGA  
GACAACATGACAAAGAGAATGATAACACAGAGAACCATAGGGAAGAAAAACA  
ACGATTAAGCAGAAAGAGCTATCTAATCAGAACATTAACCCTAACACAATGAC  
CAAGGACGCTGAAAGAGGGAAATGAAACGACGAGCAATCGCTACCCAGGGA  
TGCAGATAAGAGGATTTGTATATTTTGTGAAACACTAGCTCGAAGAATATGTGA  
AAAGCTTGAACAATCAGGATTGCCAGTTGGCGGTAATGAGAAAAAGGCCAACT  
GGCTAATGTCGTCAGAAAAATGATGACTAATCCCAAGACACTGAACTCTCCTTC  
ACCATCACTGGGGACAATACCAAATGGAATGAAAATCAGAACCCACGCATATTC  
CTGGCAATGATCACATACTAGAAATCAGCCAGAATGGTTCAGAAATGTT  
CTAAGCATTGCACCGATTATGTTCTCAAATAAAATGGCAAGACTGGGGAAAGGA  
TATATGTTTGAAGCAAAGTATGAAATTGAGAACTCAAATACCAGCAGAAATG  
CTAGCAAGCATTGACCTAAAATATTTCAATGATTCAACAAAAAAGAAAATTGAA  
AAGATACGACCACTCCTGGTTGACGGGACTGCTTCACTGAGTCTGGCATGATGA  
TGGGAATGTTCAACATGTTGAGCACTGTGCTGGGTGTATCCATATTAACCTGGG  
CCAGAGGAAATATACAAAGACCACATACTGGTGGGATGGTCTGCAATCATCCGA  
TGACTTTGCTTTGATAGTGAATGCGCCTAATCATGAAGGAATACAAGCTGGAGTA  
GACAGATTCTATAGAACTTGCAAACCTGGTCGGGATCAACATGAGCAAAAAGAAG  
TCTTACATAAAATAGAACTGGAAACATTCGAATTCACAAGCTTTTCTTACCGGTATG  
GTTTTGTAGCCAATTTAGCATGGAACCTACCCAGTTTTGGGGTTTCCGGAATAAA  
TGAATCTGCAGACATGAGCATTGGAGTGACAGTCATCAAAAACAACATGATAAA  
TAATGATCTCGGTCCCTGCCACGGCACAATGGYACTCCAACCTTTCATTAAGGAT  
TATCGGTACACATACCGGTGCCATAGAGGTGATACCCAGATACAAACCAGAAGA  
TCTTTIGAGTIGAAGAAACIGTGGGAACAGACTCGATCAAAGACTGGTCTACTGG  
TATCAGATGGGGGTCCAAACCTATATAACATCAGAAACCTACACATCCCGGAAG  
TCTGTTTAAAATGGGAGCTAATGGATGAAGATTATAAGGGGAGGCTATGCAATC  
CATTGAATCCTTTCGTTAGTCACAAAGAAATTGAATCAGTCAACAGTGCAGTAGT  
AATGCCTGCGCATGGCCCTGCCAAAAGCATGGAGTATGATGCTGTGCAACAACA  
CATTCTTGGATCCCAAGAGGAACCGGTCCATATTGAACACAAGCCAAAGGGGA  
ATACTAGAAGATGAGCAGATGTATCAGAAATGCTGCAACCTGTTTGAAAAATTCT  
TCCCAGCAGCTCATAACAGAAGACCAGTCGGAATTTCTAGTATGGTTGAGGCCAT  
GGTATCCAGGGCCCGCATTGATGCACGAATTGACTTCGAATCTGGACGGATAAA  
GAAGGATGAGTTCGCTGAGATCATGAAGATCTGTTCCACCATTGAAGAGCTCAG  
ACGGCAAAAATAGTGAA (SEQ ID NO: 13)

FIG. 13

PB1 - Amino

MDVNPTLLFLK VPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEK GKWT  
TNTEIGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHHPGIFENSCLETMEVIQ  
QTRVDKLTQGRQTYDWTLNRNQPAATALANTIEVFRSNGLTSNESGRLMDFLKDV  
MESMNKEEMEITTHFQRKRRVRDNMTKRMITQRTIGKKKQRLSRKSYLIRTLTLNT  
MTKDAERGKLRRAIATPGMQIRGFVYFVETLARRICEKLEQSGLPVGGNEKKAKL  
ANVVRKMMTNSQDTELSFTITGDNTKWNENQNPRIFLAMITYITRNQPEWFRNVLSI  
APIMFSNKMARLGKGYMFESKSMKLRTQIPAEMLASIDLKYFNDSTKKKIEKIRPLL  
DGTASLSPGMMMGMFNMLSTVLGVSILNLGQRKYTKTTYWWDGLQSSDDFALIVN  
APNHEGIQAGVDRFYRTCKLVGINMSKKKSYINRTGTFFETSFFYRYGFVANFSMELP  
SFGVSGINESADMSIGVTVIKNNMINNDLGPATAQMXLQLFIKDYRYTYRCHRGD  
IQTRRSFELKKLWEQTRSKTGLLVSDGGPNLYNIRNLHIPEVCLKWELMDEDYKGR  
CNPLNPFVSHKEIESVNSAVVMPAHGPAKSMEYDAVATTHSWIPKRNR SILNTSQRGI  
LEDEQMYQKCCNLFKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKKDEF  
AEIMKICSTIEELRRQK (SEQ ID NO: 14)

FIG. 14

PB2

TATTGGICTCAGGGAGCGAAAGCAGGTC AAAATATATTCAATATGGAGAGAATAA  
AAGAACTGAGAGATCTGATGTTACAATCCCGCACCCGCGAGATACTAACAAAA  
CTACTGTGGACCACATGGCCATAATCAAGAAATACACATCAGGAAGACAAGAGA  
AGAACCCTGCACTTAGGATGAAATGGATGATGGCAATGAAATACCCAATTACAG  
CAGATAAGAGGATAATGGAGATGATTCCTGAGAGAAATGAACAGGGACAAAACC  
CTTTGGAGCAAAACGAACGATGCTGGCTCAGACCGCGTAATGGTATCACCTCTGG  
CAGTGACATGGTGGAAATAGGAATGGACCAACAACGAACACAATTCAATTATCCGA  
AAGTCTACAAAACCTATTTTAAAAAGGTTGAAAGATTGAAACACGGAACCTTTG  
GCCCCGTTCATTTTAGGAATCAAGTCAAGATAAGACGAAGAGTTGATGTAAACC  
CTGGTCACGCGGACCTCAGTGCTAAAGAAGCACAAGATGTGATCATGGAAGTTG  
TTTTCCCAAATGAAGTGGGAGCCAGAATTCTAACATCAGAATCACAACATAAAT  
AACCAAAGAGAAAAAGGAAGAACTTCAGGACTGC AAAAATTGCTCCCTTIGATGGT  
AGCATAACATGCTAGAAAGAGAGTTGGTCCGAAAAACAAGGTTCCCTCCAGTAGT  
AGGCGGAACAAGCAGTGTATACATTGAAGTGTTCATCTGACTCAGGGAACATG  
CTGGGAGCAAATGTACACCCAGGAGGAGAAGTTAGAAACGATGATATTGATCA  
AAGTTTAATTATTGCAGCCCGGAACATAGTGAGAAGAGCAACAGTATCAGCAGA  
TCCACTAGCATCCCTACTGGAAAATGTGCCACAGTACACAGATGGTGGAAACAAG  
GATGGTAGACATCCTTAAGCAGAACCCAACAGAGGAACAAGCTGTGGATATATG  
CAAAGCAGCAATGGGATTGAGAATTAGCTCATCATTACGCTTTGGTGGATTCACC  
TTCAAAGGACAAGTGGATCATCAGTCAAGAGAGAAGAAGAAATGCTTACGGGC  
AACCTTCAAACATTGAAAATAAGAGTGCATGAGGGCTATGAAGAATTCACAATG  
GTCGGAAGAAGAGCAACAGCCATTATCAGAAAGGCAACCAGAAGATTGATTCAA  
TTGATAGTAAGTGGGAGAGATGAACAATCAATTGCTGAAGCAATAATTGTAGCC  
ATGGTGTTCGCAAGAAGATTGCATGATAAAAAGCAGTTCGAGGCGATTTGAACT  
TTGTTAATAGAGCAAATCAGCGTTTGAACCCCATGCATCAACTCTTGAGGCATTT  
CCAAAAAGATGCAAAAAGTGCCTTTCCAAAAATTGGGGAAITGAACCCATCGACAA  
TGTAATGGGGATGATTGGAATATTGCCTGACATGACCCCAAGCACCGAGATGTC  
ATTGAGAGGAGTGAGAGTCAGCAAAAATGGGAGTGGATGAGTACTCCAGCACTGA  
GAGAGTGGTGGTGGCATTGACCGTTTTTTAAGAGTTCGGGATCAAAGGGGAAA  
CATACTACTGTCCCCTGAAGAAGTCAGTGAAACACAAGGAACGGAAAAGCTGAC  
AATAATTTATTCGTCATCAATGATGTGGGAGATTAATGGTCCCGAATCAGTGTTG  
GTC AATACTTATCAATGGATCATCAGAAACTGGGAAATTGTAAAAATTCAGTGGT  
CACAGGACCCCAACAATGTTATACAATAAGATAGAATTTGAACCATTCCAATCCCT  
GGTCCCTAGGGCCACCAGAAGCCAATACAGCGGTTTCGTAAGAACCCTGTTTCAG  
CAAATGCGAGATGTACTTGGAAACATTTGATACTGCTCAAATAAATAAACTCCTCC  
CTTTTGCCGCTGCTCCTCCGGAACAGAGTAGGATGCAGTTCTCTTCTTTGACTGTT  
AATGTAAGAGGTTTCGGGAATGAGGATACTTGTAAGAGGCAATTCCTCCGTTGTT  
AACTACAATAAAGTCACTAAAAGGCTCACAGTCCCTCGGAAAGGATGCAGGTGCG  
CTTACTGAGGACCCAGATGAAGGTACGGCTGGAGTAGAATCTGCTGTTCTAAGA  
GGGTTTCTCATTTTAGGTAAAGAAAACAAGAGATATGGCCCAGCACTAAGCATC  
AATGAACTTAGCAAACCTTGCAAAAAGGGGAGAAAGCCAATGTACTAATTGGGCAA  
GGGGACGTAGTGTGGTAATGAAACGGAAACGTGACTCTAGCATACTTACTGAC  
AGCCAGACAGCGACCAAAAAGGATTCGGATGGCCATCAATTAGTGTGAAATTGTTT  
AAAAACGACCTTGTCTACTAATACGAGACCATAT (SEQ ID NO: 15)

FIG. 15

PB2 - Amino

MERIKELRDLMLQSRTREILTKTTVDHMAIHKKYTSGRQEKNPALRMKWMMAMKY  
PITADKRIMEMIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWVNRNGPTTNTIHY  
PKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDVNPBGHADLSAKEAQDVIMEVV  
FPNEVGARILTSESQTLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVVGGTS  
SVYIEVLHLTQGTCWEQMYTPGGEVRNDDIDQSLIAARNIVRRATVSADPLASLLE  
MCHSTQIGGTRMVDILKQNPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVVR  
EEEMLTGNLQTLKIRVHEGYEFTMVGRRATAIRKATRRLIQLIVSGRDEQSI AEAI  
VAMVFSQEDCMIKAVRGDLNRFVNRANQRLNPMHQLLRHFQKDAKVLQFNWGIEPI  
DNVMGMIGILPDMTPSTEMSLRGVRYSKMGVDEYSSTERVVVSIDRFILRVRDQRGNI  
LLSPEEVSETQGTEKLTIIYSSSMWEINGPESVLVNTYQWIIRNWEIVKIQWSQDPT  
MLYNKIEFEPFQSLVPRATRSQYSGFVRTLFQQMRDVLGTFDTAQIIKLLPFAAAPPE  
QSRMQFSSLTVNVRGSGMRILVRGNSPVFNKVKRRLTVLGK DAGALTEDPDEGT  
AGVESAVLRGFLILGKENKRYGPALSINELSKLAKGEKANVLIGQGDVVLMKRKR  
DSSILTDSQTATKRIRMAIN (SEQ ID NO: 16)

FIG. 16



## CANINE INFLUENZA VIRUS AND RELATED COMPOSITIONS AND METHODS OF USE

**Matter enclosed in heavy brackets [ ] appears in the original patent but forms no part of this reissue specification; matter printed in italics indicates the additions made by reissue.**

### CROSS-REFERENCE TO RELATED PATENT APPLICATIONS

This application is a divisional of U.S. Non-Provisional patent application Ser. No. 11/539,123, filed Oct. 5, 2006, now issued as U.S. Pat. No. 7,468,187, which claims the benefit of U.S. Provisional Patent Application No. 60/727,808, filed Oct. 18, 2005, the contents of both the applications are incorporated herein by reference in their entirety.

### TECHNICAL FIELD OF THE INVENTION

The present invention relates to the fields of virology, molecular biology, and immunology. In particular, the present invention relates to canine influenza virus, as well as related compositions and methods of use in inducing an immune response in animals.

### BACKGROUND OF THE INVENTION

Influenza virus is an RNA virus belonging to the family Orthomyxoviridae. The viral RNA consists of eight independent segments, which easily recombine among influenza viruses to produce new subtypes.

Nucleoprotein (NP), which is the primary component of the nucleocapsid, is encoded in the fifth segment. The NP and the matrix protein are used to classify the influenza virus into group A, B or C. Since NP is an internal protein, it is not subject to the pressure of selection by a host's immune system. It binds RNA, is part of the transcriptase complex, and is involved in the nuclear-cytoplasmic transport of viral RNA (vRNA).

Neuraminidase (NM), which splits the  $\alpha$ -keto bond that joins a terminal sialic acid and the next sugar residue, thereby allowing the release of viral progeny from infected cells, is encoded by the sixth segment. Nine subtypes (N1-N9) of this enzyme have been identified. All subtypes have two structural regions—a stalk and a head. All N8 proteins have 470 amino acids, the first eight of which are highly conserved. The following region is rich in hydrophobic amino acids and is considered to be the transmembrane domain. The next 51 amino acids make up the stalk region, and the head region begins at Cys91. The last region contains the catalytic site of the enzyme. Cysteine residues in the head and stalk region tend to be highly conserved. There are 6-8 putative N-glycosylation sites.

Hemagglutinin (HA), which is a membrane glycoprotein responsible for the adsorption of the virus into the host cell, is the main antigen to which neutralizing antibodies are directed. Its antigenic variation is the major cause of influenza epidemics. It is encoded by the fourth segment. Sixteen different subtypes (H1-H16) have been identified. HA has a signal peptide of 16 amino acids and two polypeptides (HA1 and HA2) joined by disulfide bridges. HA1 has the amino terminal end, whereas HA2 has the carboxyl terminal end. A hydrophobic region in HA2 anchors HA to the viral membrane. Cysteine residues tend to be highly conserved. There

are six putative glycosylation sites, which enable the virus to mask its antigenic sites (Skehel et al., PNAS USA 81: 1779 (1984)).

Other proteins include matrix (M or M1 and M2), non-structural (NS or NS1 and NS2), PA, PB1, and PB2. The M1 protein is a major component of the virion that binds to the plasma membrane of infected cells by means of two hydrophobic regions at the N-terminus of the protein, whereas M2 is an ion channel and, therefore, an integral membrane protein. The NS1 protein is found in the nucleus and affects cellular RNA transport, splicing, and translation. The NS2 protein is found in the nucleus and cytoplasm and has unknown function. The PA protein is a transcriptase and may have protease activity, whereas the PB1 protein functions in transcription elongation and the PB2 protein functions in transcription cap binding.

Globally, influenza is the most economically significant respiratory disease in humans, pigs, horses and poultry (Wright et al., Orthomyxoviruses. In: Fields Virology. Knipe et al., eds. Lippincott Williams & Wilkins, Philadelphia, 2001. pp. 1533-1579.). Influenza virus is known for its continuous genetic and antigenic changes, which impede effective control of the virus (Wright et al. (2001), supra; Webster et al., Microbiol. Rev. 56: 152-179 (1992)). Of particular concern for prevention of epidemics and pandemics is the emergency of a new subtype of the virus by genetic re-assortment or inter-species transmission (Wright et al. (2001), supra).

Recently, influenza outbreaks have occurred in species, e.g., feline and canine, which historically do not carry influenza virus (Keawcharoen et al., Emerg. Infect. Dis. 10: 2189-2191 (2004); Crawford et al., Science 310: 398-485 (Oct. 21, 2005; published online Sep. 29, 2005); Dubovi et al., Isolation of equine influenza virus from racing greyhounds with fatal hemorrhagic pneumonia. In: Proceedings of the 47th Annual Meeting of American Association of Veterinary Laboratory Diagnosticians, Greensboro, N.C., Oct. 2005. p. 158; and Yoon et al., Emerg. Infect. Dis. 11(12): 1974-1976 (Dec. 2005)). Therefore, the host range of influenza virus is expanding.

Outbreaks of respiratory disease in racing greyhounds caused by infection with influenza virus have occurred in Florida in 2004, in eastern and western Iowa in April 2005, and in Texas in 2005. The disease was characterized by rapid onset of fever and cough, rapid respiration, and hemorrhagic nasal discharge. The morbidity was almost 100% in both race track compounds in Iowa, although the mortality was less than 5%. While a large percentage of affected dogs recovered, many succumbed to hemorrhagic pneumonia. Therapeutic administration of broad-spectrum antibiotics reduced the severity of the disease but could not control it.

In view of the above, it is an object of the present invention to provide the influenza virus that infects canines. It is another object of the present invention to provide materials and methods for inducing an immune response to the influenza virus in canines. These and other objects and advantages, as well as additional inventive features, will become apparent from the detailed description provided herein.

### BRIEF SUMMARY OF THE INVENTION

The present invention provides an isolated canine influenza virus of subtype H3N8 comprising an HA having SEQ ID NO: 4 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, with the proviso that the amino acids at positions 94 and 233 are identical to SEQ ID NO: 4. In particular, the present invention provides an isolated canine

influenza virus of subtype H3N8 deposited with the American Type Culture Collection (Manassas, Va.) on Jun. 29, 2006, as Patent Deposit No. PTA-7694. Accordingly, the present invention also provides a composition comprising attenuated virus as well as a composition comprising inactivated virus.

The present invention also provides isolated or purified proteins. In one embodiment, the present invention provides an isolated or purified HA, which (i) has the amino acid sequence of SEQ ID NO: 4 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 4 at amino acid positions 94 and 233, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 94 or 233 of SEQ ID NO: 4.

In another embodiment, the present invention provides an isolated or purified NM, which (i) comprises the amino acid sequence of SEQ ID NO: 2 or (ii) is derived from an influenza virus and which comprises an amino acid sequence that is greater than 99% identical to SEQ ID NO: 2, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 2 at amino acid positions 68 and 134, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 68 or 134 of SEQ ID NO: 2.

In yet another embodiment, the present invention provides an isolated or purified NP, which (i) has the amino acid sequence of SEQ ID NO: 6 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 6, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 6 at amino acid position 402, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 402 of SEQ ID NO: 6.

In still yet another embodiment, the present invention provides an isolated or purified M1, which (i) has the amino acid sequence of SEQ ID NO: 8 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 8, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 8 at amino acid position 111, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 111 of SEQ ID NO: 8.

Also provided is an isolated or purified NS1, which has the amino acid sequence of SEQ ID NO: 10.

Further provided is an isolated or purified PA protein, which (i) has the amino acid sequence of SEQ ID NO: 12 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 98% (or 99%) identical to SEQ ID NO: 12, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 12 at amino acid positions 233, 256, 327, and 561, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 233, 256, 327, and 561, of SEQ ID NO: 12.

Still further provided is an isolated or purified PB1, which (i) has the amino acid sequence of SEQ ID NO: 14 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 14, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 14 at amino acid positions 200 and 213, or a fragment of (i) or (ii), wherein the fragment comprises at

least nine contiguous amino acids, at least one of which is identical to the amino acid at position 200 or 213 of SEQ ID NO: 14.

Even still further provided is an isolated or purified PB2, which (i) has the amino acid sequence of SEQ ID NO: 16 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 16, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 16 at amino acid positions 107, 221, 292, and 661, or a fragment of (i) or (ii), wherein the fragment comprises at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 107, 221, 292, or 661 of SEQ ID NO: 16.

In view of the above, the present invention further provides a composition comprising an above-described protein, such as HA or NM, or a fragment thereof in an amount sufficient to induce an immune response in an animal and a biologically acceptable carrier.

Also in view of the above, the present invention provides a method of inducing an immune response to canine influenza virus in an animal. The method comprises administering to the animal the composition comprising a protein or fragment thereof.

An isolated or purified nucleic acid encoding above-described protein or fragment thereof, optionally as part of a vector, is also provided, as is a composition comprising the isolated or purified nucleic acid, which expresses the protein, such as HA or NM, or a fragment thereof, in an amount sufficient to induce an immune response in an animal and a biologically acceptable carrier.

Accordingly, the present invention also provides another method of inducing an immune response to canine influenza virus in an animal. The method comprises administering to the animal the composition comprising a nucleic acid.

#### BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is the partial nucleotide sequence (SEQ ID NO: 1; see also GenBank Acc. No. DQ146420) of the coding domain sequence (CDS) of the NM gene from subtype H3N8 of canine influenza virus. In accordance with convention, the sequence is presented from left to right and top to bottom.

FIG. 2 is the amino acid sequence (SEQ ID NO: 2; see also GenBank Acc. No. DQ146420) encoded by SEQ ID NO: 1. In accordance with convention the sequence is presented in single letter format from left to right and top to bottom.

FIG. 3 is the complete nucleotide sequence (SEQ ID NO: 3; see also GenBank Acc. No. DQ146419) of the CDS of the HA gene from subtype H3N8 of canine influenza virus.

FIG. 4 is the amino acid sequence (SEQ ID NO: 4; see also GenBank Acc. No. DQ146419) encoded by SEQ ID NO: 3.

FIG. 5 is the complete nucleotide sequence (SEQ ID NO: 5) of the CDS of the NP gene from subtype H3N8 of canine influenza virus.

FIG. 6 is the deduced amino acid sequence (SEQ ID NO: 6) encoded by SEQ ID NO: 5.

FIG. 7 is the complete nucleotide sequence (SEQ ID NO: 7) of the CDS of the M1 protein gene from subtype H3N8 of canine influenza virus.

FIG. 8 is the deduced amino acid sequence (SEQ ID NO: 8) encoded by SEQ ID NO: 7.

FIG. 9 is the complete nucleotide sequence (SEQ ID NO: 9) of the CDS of the NS1 protein gene from subtype H3N8 of canine influenza virus.

FIG. 10 is the deduced amino acid sequence (SEQ ID NO: 10) encoded by SEQ ID NO: 9.

FIG. 11 is the complete nucleotide sequence (SEQ ID NO: 11) of the CDS of the PA protein gene from subtype H3N8 of canine influenza virus.

FIG. 12 is the deduced amino acid sequence (SEQ ID NO: 12) encoded by SEQ ID NO: 11.

FIG. 13 is the complete nucleotide sequence (SEQ ID NO: 13) of the CDS of the PB1 protein gene from subtype H3N8 of canine influenza virus.

FIG. 14 is the deduced amino acid sequence (SEQ ID NO: 14) encoded by SEQ ID NO: 13.

FIG. 15 is the complete nucleotide sequence (SEQ ID NO: 15) of the CDS of the PB2 protein gene from subtype H3N8 of canine influenza virus.

FIG. 16 is the deduced amino acid sequence (SEQ ID NO: 16) encoded by SEQ ID NO: 15.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention is predicated on the discovery of a strain of influenza virus in canines. The strain was isolated from racing greyhounds in eastern and western Iowa. The strain has been classified as an H3N8 subtype, and has been designated *A/canine/Iowa/13628/2005*. Accordingly, the present invention provides a virus comprising an HA having SEQ ID NO: 4 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, with the proviso that the amino acids at positions 94 and 233 are identical to SEQ ID NO: 4. The virus can further comprise an NM comprising the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 2, with the proviso that the amino acids at positions 68 and 134 are identical to SEQ ID NO: 2. The virus comprising the aforementioned HA, alone or in further combination with the aforementioned NM, can further comprise at least one of the following: an NP having the amino acid sequence of SEQ ID NO: 6 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 6, with the proviso that amino acid 402 is identical to that of SEQ ID NO: 6; an M1 having the amino acid sequence of SEQ ID NO: 8 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 8, with the proviso that amino acid 111 is identical to that of SEQ ID NO: 8; an NS1 having the amino acid sequence of SEQ ID NO: 10; a PA protein having the amino acid sequence of SEQ ID NO: 12 or an amino acid sequence that is greater than 98% (or 99%) identical to SEQ ID NO: 12, with the proviso that amino acids 233, 256, 327, and 561 are identical to SEQ ID NO: 12; a PB1 having the amino acid sequence of SEQ ID NO: 14 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 14, with the proviso that amino acids 200 and 213 are identical to SEQ ID NO: 14; and/or PB2 having the amino acid sequence of SEQ ID NO: 16 or an amino acid sequence that is greater than 99% identical to SEQ ID NO: 16, with the proviso that amino acids 107, 221, 292, and 661 are identical to SEQ ID NO: 16. In particular, the present invention provides an isolated canine influenza virus of subtype H3N8 deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, U.S.A., on Jun. 29, 2006, as Patent Deposit No. PTA-7694.

Influenza virus can be precipitated by subjecting the virus in aqueous medium to one or more insolubilizing steps brought about by the presence of up to 5% by weight of polyethylene glycol (PEG) having a molecular weight between 3,000 and 20,000 or another linear filamentary non-charged polymer in an amount equivalent to the solubilizing power of PEG, separating an insolubilized fraction from a non-insolubilized fraction, and recovering virus from one of

the fractions (see, e.g., U.S. Pat. No. 3,989,818). Preferably, the temperature does not exceed 35° C., the pH is between 6 and 9, and the ionic strength of the aqueous medium is below the salting out point for the virus. The concentration of the virus in the aqueous medium prior to insolubilizing corresponds to a hemagglutination titer of at least 1 in 32. Aggregated viral particles are obtained, which are believed to provide a better antigenic effect due to the slow release of viral particles after vaccination. If, however, non-aggregated or less aggregated particles are desired, they can be dissociated using any suitable method, such as sonication.

The virus can be attenuated by passaging in a cell system until the virus has lost its ability to produce disease, while fully retaining its immunogenic character. For example, the virus can be serially passaged in a culture of cells originating from a canine species or other suitable species at a temperature of about 37° C. At each passage, the virus is harvested from one culture and inoculated into a medium containing a fresh cell culture in accordance with methods known in the art. For example, the virus can be collected from tissue cell culture fluids and/or cells. Optionally, during harvesting, the cell culture can be sonicated to promote release of the virus. See, e.g., U.S. Pat. Nos. 5,698,433 and 6,455,298.

If desired, an influenza strain can be passaged at least once in the allantoic cavity of embryonated eggs, such as chicken eggs, in the presence of serum, to obtain serum-resistant virus (see, e.g., U.S. Pat. No. 3,953,592; Kilbourne et al., *J. Exp. Med.* 111: 387 (1960); Kilbourne, *Science* 160: 74-75 (April 1968); and Layer et al., *Virology* 30: 493-501 (1966)). High potency influenza vaccine with low pyrogenicity and low endotoxicity can be achieved by treating the concentrated allantoic fluid containing an attenuated virus sequentially with butyl acetate and ethyl acetate, followed by flash evaporation (see, e.g., U.S. Pat. No. 4,000,257). Such virus can be administered intranasally as a vaccine.

Once inoculated into the host, the virus multiplies to some extent so that only a small initial inoculum is required. The virus must be innocuous, and infection of susceptible contacts should be kept to a minimum.

Alternatively, the virus can be inactivated by abolishing replication and virulence. This can be done by chemical or physical means. Chemical inactivation can be carried out by treatment of the virus with an enzyme, formaldehyde,  $\beta$ -propiolacton or derivative thereof, ethyleneimine or derivative thereof, an organic solvent (e.g., halogenated hydrocarbon), and/or a detergent (e.g., Tween®, Triton X®, sodium desoxycholate, sulfobetain, or cetyltrimethylammonium salts). If necessary, chemically activated compositions can be neutralized. For example, if formaldehyde is used to deactivate the composition, the composition can be neutralized with thio-sulphate. If required, the pH subsequently can be returned to a value of about 7. Alternatively, the virus can be extracted with a mixture of ether and ethanol, the aqueous and organic phases can be separated, and residual ether can be removed from the viral suspension under reduced pressure (see, e.g., U.S. Pat. No. 4,431,633). Physical inactivation advantageously can be carried by subjecting the virus to energy-rich radiation, such as ultraviolet light,  $\gamma$ -radiation, or X-rays. Inactivated forms require a relatively high amount of inoculum and, therefore, a correspondingly large quantity of antigenic material, which has to be manufactured, tested, and distributed.

In view of the above, the present invention also provides a composition comprising an attenuated or inactivated virus. The virus should be present in an amount sufficient to induce an immune response and, desirably, should provide protection upon challenge. Generally, an adjuvant, such as Tween®,

Span®, Freund's complete adjuvant, saponin, Corynebacterium parvum (Coparvax®), aluminium phosphate, aluminium hydroxide, or a mixture thereof, is added to the composition, particularly if the composition comprises inactivated virus. Protein hydrolysates and/or amino acids can be added to stabilize the composition (see, e.g., U.S. Pat. No. 4,537,769). Alternatively, the composition can be formulated as an oil-in-water emulsion using oils such as Marcol and/or Arlacel.

Recombinant influenza strains also can be prepared, such as from the combination of an "over-attenuated" (i.e., the number of passages for attenuation is substantially greater than what is normally required to remove pathogenicity) influenza A parent strain, e.g., A2, with a virulent influenza strain as provided herein (see, e.g., U.S. Pat. No. 3,991,179; also, see U.S. Pat. Nos. 4,009,258; 4,278,662; 4,318,903; 4,338,296; and 4,693,893). A recombinant strain preferably has the growth characteristics of the over-attenuated strain coupled with the antigenic properties, e.g., the HA and NM proteins, of the virulent strain. The selection of strains of influenza virus for vaccine formulation is described in U.S. Pat. No. 5,162,112. Recombinant strains can be formulated as compositions for inducing an immune response.

Sucrose, arginine monohydrochloride, the monosodium monohydrate of glutamic acid, and gelatin hydrolysate can be used to stabilize an influenza virus composition for storage in a refrigerator. See, e.g., U.S. Pat. App. Pub. No. 2006/0110406.

In view of the above, the present invention also provides an isolated or purified HA. The HA either has the amino acid sequence of SEQ ID NO: 4 or is derived from an influenza virus and has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 4 at amino acid positions 94 and 233. A fragment of HA comprising at least nine (such as 9, 12, 15, 18, 21 or 24) contiguous amino acids, at least one of which is identical to the amino acid at position 94 or 233 of SEQ ID NO: 4, is also provided.

An isolated or purified NM is also provided. The NM comprises the amino acid sequence of SEQ ID NO: 2 or is derived from an influenza virus and comprises an amino acid sequence that is greater than 99% identical to SEQ ID NO: 2, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 2 at amino acid positions 68 and 134. A fragment of NM comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 68 or 134 of SEQ ID NO: 2, is also provided.

Further provided is an isolated or purified NP. The NP has the amino acid sequence of SEQ ID NO: 6 or is derived from an influenza virus and has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 6, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 6 at amino acid position 402. A fragment of NP comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 402 of SEQ ID NO: 6, is also provided.

Still further provided is an isolated or purified M1. The M1 has the amino acid sequence of SEQ ID NO: 8 or is derived from an influenza virus and has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 8, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 8 at amino acid position 111. A fragment of M1 comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 111 of SEQ ID NO: 8, is also provided.

Even still further provided is an isolated or purified NS1, which has the amino acid sequence of SEQ ID NO: 10.

An isolated or purified PA protein is also provided. The PA has the amino acid sequence of SEQ ID NO: 12 or is derived from an influenza virus and has an amino acid sequence that is greater than 98% (or 99%) identical to SEQ ID NO: 12, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 12 at amino acid positions 233, 256, 327, and 561. A fragment of PA comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 233, 256, 327, or 561 of SEQ ID NO: 12, is also provided.

An isolated or purified PB 1 is provided. The PB1 has the amino acid sequence of SEQ ID NO: 14 or is derived from an influenza virus and has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 14, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 14 at amino acid positions 200 and 213. A fragment of PB1 comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 200 or 213 of SEQ ID NO: 14, is also provided.

Provided also is an isolated or purified PB2. The PB2 has the amino acid sequence of SEQ ID NO: 16 or is derived from an influenza virus and has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 16, with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 16 at amino acid positions 107, 221, 292, and 661. A fragment of PB2 comprising at least nine contiguous amino acids, at least one of which is identical to the amino acid at position 107, 221, 292, or 661 of SEQ ID NO: 16, is provided as well.

The above proteins and fragments thereof can be purified (coupled with chemical or physical fragmentation to generate fragments) or synthesized in accordance with methods known in the art. See, e.g., Meienhofer, *Hormonal Proteins and Peptides 2: 46*, Academic Press, NY (1973), for solid phase protein synthesis, and Schroder et al., *The Peptides*, vol. 1, Academic Press, NY (1965), for solution phase protein synthesis. Automated systems can be used to carry out such techniques in accordance with manufacturer's instructions. Therapeutic quantities can be recombinantly produced and purified.

Alternatively, proteins, in particular HA and NM, can be isolated by selective solubilization, while leaving residual subviral particles consisting of the intact lipid/protein membrane enclosing all other non-essential viral components. The difference in size/density of the solubilized proteins and the residual subviral particles allows separation based on differences in physical properties by gradient centrifugation and fractionation, sedimentation, molecular sieve chromatography, or pelleting in an ultracentrifuge. Selective solubilization of HA and NM can be achieved by treatment of the virus with a cationic detergent (see, e.g., U.S. Pat. No. 4,140,762; the '762 patent). The whole virus-containing fluid obtained from cell culture can be treated with a DNA-digesting enzyme followed by addition of a cationic detergent and isolation of surface-antigen proteins (see, e.g., U.S. Pat. No. 5,948,410). The fluid can be subjected to several ultracentrifugation steps, or the virus can be fragmented in the presence of an amphiphilic nonionic detergent followed by filtration to remove undesirable substances (see, e.g., U.S. Pat. No. 6,048,537). Alternatively, membrane filtration and chemical splitting can be used to obtain a viral protein (see, e.g., U.S. Pat. No. 4,327,182). Other procedures are described in U.S. Pat. Nos. 4,064,232 and 4,057,626. Preferably, the virus is multiplied before treatment as exemplified in the '762 patent (col. 2, 11. 10 et seq).

Mapping can be conducted to identify an immune response-inducing epitope of a viral protein, i.e., "epitope

mapping.” Such mapping involves fragmenting of a protein into overlapping peptides (such as peptides comprising 9, 12, 15, 18, 21 or 24 amino acids). The protein can be fragmented with a proteolytic enzyme. The individual peptides are then tested for their ability to bind to an antibody elicited by the native protein or to induce T-cell or B-cell activation. Alternatively, hydrophilic regions of the protein can be selected, since hydrophilic residues are often on the surface of the protein and, therefore, are accessible to the antibody. X-ray crystallographic analysis of the antigen-antibody complex also can be performed. Potential HLA anchor binding motifs, which are peptide sequences that are known to be likely to bind to MHC molecules, can be identified from the amino acid sequence of a protein. Preferably, the epitope selected is one that shares little to no sequence identity with sequences widely found in the animal to which a composition comprising or expressing a protein fragment will be administered.

An isolated or purified nucleic acid encoding an above-described protein or fragment thereof, optionally as part of a vector, is also provided. The nucleic acid encoding the HA can comprise the nucleotide sequence of SEQ ID NO: 3 or a fragment thereof encoding at least nine (9, 12, 15, 18, 21 or 24) contiguous amino acids. If desired, a trivalent vaccine based on HA can be prepared, wherein one of the HAs comprises the amino acid sequence of SEQ ID NO: 4 (see, e.g., U.S. Pat. Nos. 5,762,939 and 6,245,532; see, e.g., U.S. Pat. No. 6,740,325 for a tetravalent vaccine). The nucleic acid encoding the NM can have the nucleotide sequence of SEQ ID NO: 1 or a fragment thereof encoding at least nine contiguous amino acids (see, e.g., U.S. Pat. No. 6,605,457 and U.S. Pat. App. Pub. No. 2003/0129197), whereas the nucleic acid encoding the NP can have the nucleotide sequence of SEQ ID NO: 5 or a fragment thereof encoding at least nine contiguous amino acids, the nucleic acid encoding the M1 protein can have the nucleotide sequence of SEQ ID NO: 7 or a fragment thereof encoding at least nine contiguous amino acids, the nucleic acid encoding the NS1 protein can have the nucleotide sequence of SEQ ID NO: 9, the nucleic acid encoding the PA can have the nucleotide sequence of SEQ ID NO: 11 or a fragment thereof encoding at least nine contiguous amino acids, the nucleic acid encoding the PB1 can have the nucleotide sequence of SEQ ID NO: 13 or a fragment thereof encoding at least nine contiguous amino acids, and the nucleic acid encoding the PB2 can have the nucleotide sequence of SEQ ID NO: 15 or a fragment thereof encoding at least nine contiguous amino acids. One of ordinary skill in the art will appreciate, however, that due to the degeneracy of the genetic code, there are numerous other nucleotide sequences that can encode such amino acid sequences.

The above nucleic acids, which can be DNA or RNA, and fragments thereof can be synthesized (see, e.g., *Oligonucleotide Synthesis*, Gait, ed., 1984). Such molecules can include non-naturally occurring nucleotides/bases that encode the desired amino acid sequence. For example, the base or sugar can be methylated. In addition, the backbone of the nucleic acid molecule can be modified, e.g., a phosphorothioate backbone, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof.

Alternatively, isolated vRNA can be subjected to reverse transcriptase to produce an RNA/DNA hybrid, from which the RNA is digested away and the residual DNA is treated to produce a dsDNA having a hairpin end, which is treated with a single-strand-specific nuclease to produce a bimolecular double-stranded copy of the vRNA (see, e.g., U.S. Pat. No. 4,357,421). See, e.g., U.S. Pat. App. Pub. No. 2006/0166321 for the use of tandem transcription cassettes for the preparation of influenza in the absence of helper virus.

The nucleic acid is optionally part of a DNA vector comprising at least one promoter, in which case each nucleotide sequence is operably linked to a promoter, which can be the same or different. In addition to promoters, other control sequences, such as terminating signals and the like, can be part of the DNA vector.

For example, the nucleic acid can be introduced into a suitable recombinant expression vector, such as those adapted for bacteria, such as *E. coli* and *Salmonella typhi*, yeast, such as *Saccharomyces cerevisiae* or *Pichia pastoris*, or filamentous fungi, such as *Aspergillus nidulans*. The bacteria, yeast, or fungi can be grown in continuous culture. The polypeptide, which is produced during culture, then can be isolated and purified. Alternatively, the nucleic acid molecule can be introduced into Poxviridae (e.g., fowlpox-based vectors), Herpesviridae (e.g., pseudorabies virus-based vectors, turkey herpes virus-based vectors, feline herpes virus-based vectors, infectious laryngotracheitis virus-based vectors, and bovine herpes virus-based vectors), Adenoviridae (e.g., bovine adenovirus (e.g., serotype 3), human adenovirus (e.g., serotype 4 or 7), and canine adenovirus (e.g., serotype 2; CAV2; see, e.g., U.S. Pat. No. 6,090,393), or an insect virus expression vector, such as recombinant baculovirus (e.g., *Autographa californica* nuclear polyhydrosis virus (AcNPV)), which, in turn, can be used to infect susceptible cultured SF9 cells, which are derived from the insect *Spodoptera frugiperda*. Other viral vectors include vaccinia (see, e.g., U.S. Pat. No. 4,722,848), adenovirus, adeno-like virus, adeno-associated virus, retrovirus, and pox (see, e.g., Hruby, *Vet. Parasitol.* 29: 281-282 (1988); Uiu, “AIDS Research Reviews,” Dekker, Inc., 1991, 1: 403-416), which can be administered by a skin scratch or by injection, optionally as a liposomal formulation. Other vectors include Bacille-Calmette-Guerin (BCG; Stover et al., *Nature* 351: 456-460 (1991)), detoxified anthrax toxin vectors, and the like. Mammalian cells, such as Chinese hamster ovary (CHO) cells, and even plant cells can be used to express the polypeptide from the appropriate construct. One of ordinary skill in the art will appreciate that the choice of host cell will affect the nature of post-translational processing (e.g., glycosylation, folding, and the like), which, in turn, can impact the immunogenicity of the polypeptide, and subsequent purification techniques.

Expression can be achieved in any appropriate host cell transformed/transfected with the expression vector. Examples of suitable host cells include, but are not limited to, those described above. Thus, the present invention also provides a host cell transformed/transfected with an expression vector.

Supernatants from host/vector systems that secrete the protein or fragment thereof into culture media can be applied to a purification matrix, such as an affinity column or an ion exchange column. One or more reverse-phase HPLC steps can be employed to purify further the recombinant protein or fragment thereof.

Production of a protein or fragment thereof as a fusion protein can stabilize production. This can be accomplished by ligating polynucleotide sequences encoding two or more proteins (or fragments thereof) into an appropriate expression vector with or without a peptidic linker. Desirably, the reading frames of the polynucleotide sequences are in phase, so that a single fusion protein that retains the biological activity of each protein (or fragment thereof) is produced. A peptidic linker from 1 to about 50 amino acids can be used to separate the resultant proteins (or fragments thereof) so as to ensure that each protein (or fragment thereof) properly folds into its native secondary, tertiary, and quaternary structures (see, e.g., Maratea et al., *Gene* 49: 39-46 (1985); Murphy et al., *PNAS*

USA 83: 8258-8262 (1986); U.S. Pat. No. 4,935,233; and U.S. Pat. No. 4,751,180). The ability to adopt a flexible extended conformation, the inability to adopt a secondary structure that could interact with functional amino acids on either one or both of the proteins, and the lack of hydrophobic or charged residues that might react with either one or both of the proteins are factors, which are taken into consideration in selecting a peptide linker. Linkers are not required when the ends of the proteins to be joined do not contain essential regions, such that the ends can be used to separate functional domains and prevent steric interference. Preferred peptide linker sequences contain Gly, Asn, and Ser residues. Other near neutral residues, such as Thr and Ala, also can be used.

Other additional amino acid sequence(s) can be selected to enhance the expression and/or immunogenicity of the protein or fragment thereof. For example, the protein or fragment thereof can be fused to the heavy chain of immunoglobulin G (IgG) or an antigen-presenting cell (APC) binding protein or a dendritic cell binding protein, such as IL-D, GM-CSF, IL-1, TNF, IL-4, CD40L, CTLA4, CD28, or FLT-3 ligand. Techniques, such as the use of dehydrating agents, e.g., dicyclohexylcarbodiimide (DCCI), or the creation of linkages between sulfhydryl groups, epsilon amino groups, carboxyl groups, and the like, can be used. If desired, a cleavage site can be introduced into the fusion protein to enable separation of the protein (or fragment thereof) from the non-naturally occurring sequence(s). Examples of cleavage sites include a target sequence for a proteolytic enzyme or, if methionine is not present in the protein (or fragment thereof), methionine, which, in turn, is cleaved by cyanogen bromide. Such methods are known in the art. The protein or fragment thereof can be modified by glycosylation or other derivatization (e.g., acetylation or carboxylation), also in accordance with methods known in the art.

The protein (or fragment thereof) can be expressed in situ from a suitable expression system. Any DNA construct, which is effective in producing the encoded protein or fragment thereof in the desired environment, can be used to express the protein or fragment thereof as described above.

Alternatively, the nucleic acid molecule can behave as an effective expression system in situ when injected into an animal as "naked DNA" (see, e.g., Ulmer et al., *Science* 259: 1745-1749 (1993); and Cohen, *Science* 259: 1691-1692 (1993)). DNA delivery also can be facilitated through the use of bupivacaine, polymers, and peptides; alternatively, cationic lipid complexes, particles, or pressure (see, e.g., U.S. Pat. No. 5,922,687) can be used.

Examples of amino acid sequences that are at least about or greater than 95% identical to, such as at least about or greater than 96%, 97%, 98%, or 99% identical to, SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16 include amino acid sequences that contain one or more substitutions, insertions, additions and/or deletions. Sequence identity can be determined by aligning polypeptide sequences and applying publicly available computer algorithms, such as BLASTP (Pearson et al., *PNAS USA* 85: 2444-2448 (1988); Pearson, *Methods Enzymol.* 183: 63-98 (1990); and Altschul et al., *Nucl. Acids Res.* 25: 3389-3402 (1997)). The software for BLASTP is available on the FTP server of the National Center for Biotechnology Information (NCBI) or NCBI, National Library of Medicine, Building 38A, Room 8N805, Bethesda, Md. 20894. Once the polypeptide sequences are aligned, the number of identical amino acids over the aligned portions is identified, the number of identical amino acids is divided by the total number of amino acids of the polypeptide of interest, and the result is multiplied by 100 to determine the percentage sequence identity.

In this regard, one of ordinary skill in the art will appreciate that a fragment of a given amino acid sequence can be at least about or greater than 95% identical to, such as 96%, 97%, 98% or 99% identical to, the amino acid sequence. Thus, fragments are intended to be encompassed by "an amino acid sequence that is at least about or greater than 95% (or 96%, 97%, 98% or 99%) identical to SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16." Such fragments desirably retain the immunogenicity of the full-length protein. Functional fragments can be generated by mutational analysis of the nucleic acid encoding the protein and subsequent expression of the resulting mutant protein or by chemical/enzymatic digestion of the protein, itself.

Modifications, such as substitutions, insertions, additions and/or deletions, can be introduced into the nucleic acid or the protein (or fragment thereof) in accordance with methods known in the art (see, e.g., Adelman et al., *DNA* 2: 183 (1983), for oligonucleotide-directed site-specific mutagenesis). Desirably, the modification does not substantially diminish the immunogenicity of the protein fragment; rather, it is preferred that the immunogenicity remains substantially the same or increases relative to the unmodified protein.

A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, i.e., similar secondary structure and hydrophobic nature. Amino acid substitutions can be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids, such as aspartic acid and glutamic acid, can be interchanged, whereas positively charged amino acids, such as lysine and arginine, can be interchanged, and amino acids with uncharged polar head groups having similar hydrophilicity values can be interchanged. In this regard, leucine, isoleucine and valine can be interchanged, glycine and alanine can be interchanged, asparagine and glutamine can be interchanged, and serine, threonine, phenylalanine, and tyrosine can be interchanged. Other groups of amino acids that can be interchanged include: (1) ala, pro, gly, glu, asp, gln, asn, ser and thr; (2) cys, ser, tyr and thr; (3) val, ile, leu, met, ala and phe; (4) lys, arg and his; and (5) phe, tyr, trp, and his.

In view of the above, a composition comprising the isolated or purified protein/nucleic acid or fragment of either of the foregoing and a biologically acceptable carrier is also provided. The nucleic acid or fragment thereof can be part of a vector. See, for example, U.S. Pat. No. 4,029,763, which is directed to an influenza vaccine comprising, as an active ingredient, NM, and U.S. Pat. No. 4,140,762, which is directed to an influenza vaccine comprising, as active ingredients, HA and NM. U.S. Pat. No. 4,826,687 describes the addition of muramyl dipeptide to a vaccine comprising HA and NM. If desired, polypeptides corresponding substantially to amino acids 148-162, 163-166, and/or 215-239 of M1 can be added to a composition of a protein/nucleic acid or fragment thereof (see, e.g., U.S. Pat. Nos. 5,136,019; 5,616,327; and 5,741,493). Any suitable biologically acceptable carrier can be used in the composition. For example, the protein(s)/nucleic acid(s)/fragments thereof can be resuspended in a diluent, e.g., 0.9% sodium chloride solution, which is optionally buffered with, for example, a phosphate buffer. Any sucrose that remains from purification of the virus can be reduced by dialysis. Dialysis or gel chromatography can be used to remove any remaining cationic detergent. Preferably, the protein or fragment thereof is present in an amount sufficient to induce an immune response (i.e., cellular or humoral) in an animal. A frequently selected carrier for pharmaceuticals and antigens is poly(D,L-lactide-co-glycolide) (PLGA).

PLGA is a biodegradable polyester, and can be used for the controlled release of antigen (Eldridge et al., *Curr. Topics Micro. Immuno.* 146: 59-66 (1989); see also U.S. Pat. No. 6,090,393). The entrapment of antigens in PLGA microspheres of 1-10  $\mu$  in diameter has been shown to have a remarkable adjuvant effect when administered orally.

If desired, a preserving agent or an inactivating agent, such as formaldehyde, can be added. A conventional amount of preserving/inactivating agent is 1 part per 10,000 parts.

If desired, one or more proteins (or immunogenic fragments thereof), such as the above-described HA, can be combined with proteosomes. See, e.g., U.S. Pat. No. 6,743,900 and U.S. Pat. App. Pub. No. 2004/0156867.

Immunogenicity can be improved by inclusion of conventional immunological adjuvants, such as aluminium hydroxide (e.g., about 0.2%) or aluminium phosphate, aluminum (see, e.g., U.S. Pat. Nos. 6,372,223, 6,635,246, 6,861,244 and 7,052,701 and U.S. Pat. App. Pub. Nos. 2004/0096464 and 2006/0147468), chitosan (see, e.g., U.S. Pat. Nos. 6,136,606 and 6,534,065), alum, such as in the form of aluminum hydroxide, aluminum phosphate or aluminum oxide, mineral oils (e.g., Bayol F® and Marcol 52®), Freund's complete adjuvant, Freund's incomplete adjuvant, muramyl dipeptide, monophosphoryl lipid A, and saponins, including the Quil A component. Immunogenicity also can be improved by adding a cytokine, such as an interleukin, or by conjugating proteins or fragments thereof. Preferably, the protein or fragment thereof is conjugated with a macromolecular carrier, such as a protein (e.g., serum albumin, keyhole limpet hemocyanin, immunoglobulin, throglobulin, and ovalbumin), polysaccharide (e.g., latex-functionalized sepharose, agarose, cellulose beads, and the like), phospholipid, polymeric amino acids (e.g., polyglutamic acid, polylysine, and the like), or amino acid co-polymers (see, e.g., U.S. Pat. Nos. 5,136,019 and 5,612,037). Alternatively, the protein or fragment thereof can be encapsulated with a proteoliposome or lipid vesicle.

The composition, which can induce an immune response, can be prepared in the form of a suspension or can be lyophilized. If lyophilized, it is preferable to add one or more stabilizers. Suitable stabilizers are, for example, sucrose, phosphate, glutamate, and albumin (SPGA; Bovarnick, *J. Bacteriol.* 59: 509 (1950)), carbohydrates (e.g., sorbitol, mannitol, starch, dextran, and glucose), proteins (e.g., albumin and casein) or degradation products thereof, protein-containing agents (e.g., bovine serum or skim milk), and buffers (e.g., alkali metal phosphates).

Alternatively, the composition can be formulated as a controlled-release composition. The attenuated/inactivated virus or recombinant vector can be microencapsulated with polymers, such as polycarbonates, polyesters, polyurethanes, polyorthoesters, and polyamides. The particular polymer selected depends on a number of factors including reproducibility of polymer synthesis and microencapsulation, cost of materials and process, toxicological profile, requirements for variable release kinetics, and the physicochemical compatibility of the polymer and the virus/vector.

The compositions described herein can be used alone or in combination with other active ingredients/compositions. Examples include compositions, which can induce an immune response against canine distemper, infectious canine hepatitis (CAV-1 and CAV-2), rabies, parainfluenza, canine corona virus, measles, leptospirosis, and Bordetella. Polyphenols have been disclosed to inhibit influenza infection in humans (see, e.g., U.S. Pat. No. 5,173,922; the '922 patent). Accordingly, the addition of a polyphenol, such as epigallocatechin gallate, epicatechin gallate, epigallocatechin, epicatechin, free theaflavin, theaflavin monogallate A,

theaflavin monogallate B, and/or theaflavin digallate may be beneficial (see the '922 patent). Inhibitors of NM are disclosed in U.S. Pat. No. 5,453,533. The use of cytokines as immunopotentiators and liposomal encapsulation are described in U.S. Pat. No. 5,919,480.

The amount of nucleic acid in the composition can vary widely. For example, the concentration can range from less than about 0.1% to as much as about 20-50% or more by weight, usually at least about 2%. The concentration of protein in the composition also can vary widely. For example, the concentration can range from less than about 0.1% to as much as about 20-50% or more by weight, usually at least about 2%. Fluid volume and viscosity are taken into consideration when determining the final concentration.

Accordingly, a method of inducing an immune response to canine influenza virus in an animal is also provided. The susceptibility of an animal to infection can be assessed using the plaque reduction neutralization test (U.S. Pat. No. 4,315,073) or the hemagglutination test. The method comprises administering to the animal an above-described composition comprising an isolated or purified protein/nucleic acid or fragment thereof. If the composition comprises a nucleic acid (or fragment thereof) as part of a vector, preferably the protein (or fragment thereof) is expressed in an amount sufficient to induce an immune response in an animal. For example, a single dose of from about 9 to about 43 international units per kg of animal body weight can be administered. For larger mammals, a single dose can comprise from about 600 to about 3,000 international units per kg of body weight. For vaccine compositions prepared by culturing virus in the allantoic cavity of fertile eggs, harvesting the virus, and, if desired, stabilizing the harvested virus with a stabilizer, such as a peptone or sucrose, and then distribution into glass vials for subsequent freeze-drying, an effective vaccine dosage unit can contain at least  $10^7$  EID<sub>50</sub> (50% egg-infective dose) of virus. In the latter situation, the freeze-dried vaccine is reconstituted by addition of water or another pharmaceutically acceptable diluent prior to administration, such as in the form of a nasal spray or nasal drops. If desired, the vaccine can be administered in two successive dosages at a one-week interval.

The composition can be administered to puppies as a single dose at the age of 12 weeks, or repeatedly starting from the age of 6 weeks (e.g., at 6, 9 and 12 weeks), or weekly from 4 weeks on. The effective dosage and route of administration are determined by the nature of the composition, the nature of the expression product, LD<sub>50</sub>, and, if recombinant vector is used, the expression level of the vector, as well as the breed of dog and its age, sex, weight, and condition. Dosages of expressed product can range from a few to a few hundred micrograms, e.g., 5-500  $\mu$ g. Preferred dosages of virus or recombinant vector can range from about  $10^3$  to about  $10^6$  pfu. The dose for the live attenuated strain can be at least about  $10^3$  TCID<sub>50</sub>.

The compositions can be administered parenterally (i.e., by injection (e.g., intradermal, subcutaneous, or intramuscular) or by the route of infection, such as nasally) or enterally (i.e., by oral administration). The use of a gelling agent and a muco- or bio-adhesive to enhance the immune response against an intradermally administered immunogenic composition is described in U.S. Pat. App. Pub. No. 2005/0255121. If desired, the composition for inducing an immune response can be administered through drinking water or syrup in accordance with Chu et al. (U.S. Pat. App. Pub. No. 2006/0171960, which was published on Aug. 3, 2006). Oral administration is advantageous inasmuch as it avoids time-consuming and labor-intensive intramuscular injection, which, in turn, can

create stress for the animal and discomfort. Discomfort, in turn, can affect the performance of race dogs. Alternatively, the composition comprising a recombinant vector expressing at least one immune response-inducing epitope can be applied directly to the skin for localized expression and induction of an immune response.

Efficacy of the composition, which can induce an immune response, can be demonstrated by exposing puppies to a virulent strain of canine influenza virus. Untreated dogs should develop clinical signs characteristic of canine influenza viral infection, whereas treated dogs should not.

The recombinant vectors and the products expressed from them can be used to produce antibodies, such as polyclonal antibodies (pAb) and monoclonal antibodies (mAb), in accordance with methods known in the art (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988); Harlow and Lane, *Using Antibodies: A Laboratory Manual* (1998), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1998); Shepherd and Dean, *Monoclonal Antibodies: A Practical Approach*, Oxford University Press, U.S.A. (2000)); and Harris and Adair, *Antibody Therapeutics*, CRC Press, Inc., Boca Raton, Fla. (1997)). The antibodies, in particular mAbs, can be used in binding assays and diagnostic kits/tests to determine the presence/absence of an antigen of canine influenza virus or whether or not an immune response to the virus has been stimulated. The antibodies also can be used to recover material by immuno-adsorption chromatography.

Antibodies also can provide passive immunization. For example, partially purified immune sera from host animals or from hybridoma cell lines can be injected into an animal. The antibodies provide a therapeutic effect by binding to and neutralizing an infectious influenza virus.

A composition comprising an anti-idiotypic antibody having an internal image of an epitope of an above-described protein, such as a protein consisting of the amino acid sequence SEQ ID NO: 1 or SEQ ID NO: 3, is also provided.

One of ordinary skill in the art will appreciate that an anti-idiotypic antibody, which bears an internal image of an epitope, such as those described herein, can be prepared. See, e.g., Herlyn et al., *Science* 232: 100-102 (1986)). Methods of preparing monoclonal and polyclonal anti-idiotypic antibodies, which bear the internal image of the polypeptide, are described in U.S. Pat. No. 5,053,224, for example. Briefly, polyclonal anti-idiotypic antibodies can be produced by immunizing animals with monoclonal idiotype antibodies raised against the polypeptide and screened for reactivity with the polypeptide and screening for antisera, which react with idiotype antibodies to the polypeptide. Monoclonal antibodies (mAbs) also can be prepared from such animals using standard techniques of immortalizing the antibody-secreting cells of the animal and screening cultures with idiotype antibodies in competition with the polypeptide. While mAbs are preferred, polyclonal antibodies (pAbs), which are prepared in a variety of mammalian systems, also can be used.

Another method for inducing an immune response to CIV in a canine is also provided. This method comprises administering to the canine an effective amount of a composition comprising an anti-idiotypic antibody as described above.

The isolated or purified nucleic acid molecules or vectors comprising them can be used to generate DNA for probes/primers, which can be used to detect the presence or absence of hybridizable DNA or to amplify DNA, such as cDNA.

Labeled proteins or fragments thereof, as well as labeled nucleic acids or fragments thereof, can be used in assays. Assay methods include fluoroimmunoassays (Smith et al., *Ann. Clin. Biochem.* 18: 253-275 (1981)), radioimmunoas-

says (RIA), enzyme-linked immunosorbent assays (ELISA), and enzyme-multiplied immunoassay technique (EMIT; see *Enzyme Immunoassay*, Maggio, ed., CRC Press, Inc., Boca Raton, Fla., 1980. pp. 141-150; 234-235, and 242-243). Such methods can be used to detect the presence of the virus and to diagnose the state of infection.

The virus, itself, can be used as a vector. The use of viruses as vectors is within the skill in the art.

#### EXAMPLE

The following example serves to illustrate the present invention. The example is not intended to limit the scope of the invention in any way. The example describes the identification and partial characterization of a canine influenza virus.

Outbreaks of acute respiratory disease, characterized by cough, fever, rapid respiration, and hemorrhagic nasal discharge, occurred among greyhounds within two race track compounds located in eastern and western Iowa in Apr. 2005. While a large percentage of affected dogs recovered, many succumbed to hemorrhagic pneumonia.

Lungs of affected dogs exhibited extensive red to red-black discoloration with moderate to marked palpable firmness and mild fibrinous pleuritis. Lung sections were characterized by severe hemorrhagic interstitial to bronchointerstitial pneumonia. Patchy interstitial change with alveolar septal thickening, coagulum of debris in alveoli, and associated atelectasis were evident. Focally extensive pyogranulomatous bronchointerstitial pneumonia with dilatation of airways by degenerate cells and debris was observed. Scattered vasculitis and vascular thrombi were apparent.

Microbiological testing for conventional viral and bacterial agents did not reveal any significant pathogens except *Streptococcus equi* subsp. *zooepidemicus*, which was present in lung tissues from all animals examined. Two of four lung samples tested positive for influenza virus using real-time reverse transcriptase-polymerase chain reaction (RT-PCR; Harmon et al., Development of a PCR-based differential test for H1N1 and H3N2 swine influenza viruses. In: Proceedings of the 42nd Annual Meeting of American Association of Veterinary Laboratory Diagnosticians. San Diego, Calif. Oct. 1999. p. 44.). Immunohistochemistry using monoclonal antibody (mAb) specific for the NP of influenza virus (Vincent et al., *J. Vet. Diagn. Invest.* 9: 191-195 (1997)) was also positive within viral pneumonic lesions of both lungs as was antigen-capturing ELISA (Directgen™ Flu A, Becton/Dickinson, Sparks, Md.) testing on the samples. Bronchioalveolar lavage samples from the two positive lungs tested positive for influenza virus by PCR.

Virus isolation was attempted because the detection of influenza virus in canine lungs was an unexpected observation, since only a single report of influenza virus infection in dogs existed (Dubovi et al., Isolation of equine influenza virus from racing greyhounds with fatal hemorrhagic pneumonia. In: Proceedings of the 47th Annual Meeting of American Association of Veterinary Laboratory Diagnosticians. Greensboro, N.C. Oct. 2004. p. 158.). A virus that was able to agglutinate rooster red blood cells was isolated in Madin-Darby canine kidney (MDCK) cells from lung and bronchioalveolar lavage fluid of one of the two animals in which influenza virus was detected by immunohistochemical (IHC) assay and PCR. The isolate was determined by PCR to be influenza virus of H3 subtype. The virus isolate was subtyped as H3N8 using HA-inhibition and NM-inhibition assays. The virus isolate was recognized by antisera raised against various H3 equine influenza viruses, including Miami ((A/Eq/MI/1/



63-H3N8) 640-1280), AK((A/Eq/AK/29759/91-H3N8) 320-640), and Kentucky ((A/Eq/Kentucky/81-H3N8) 160-320).

Sequencing of HA and NA genes of both isolates revealed 100% and 99.8% identity, respectively, between the two isolates. Phylogenetically, the HA gene of the isolates was genetically close (96-98% nucleotide homology) to the HA gene of recent H3N8 equine influenza viruses (Macken et al., The value of a database in surveillance and vaccine selection. In: Options for the Control of Influenza IV. Osterhaus et al., eds. Elsevier Science, Amsterdam. 2001. pp. 103-106.). The NA gene of the isolates also showed 96-98% homology with the NA gene of recent H3N8 equine influenza viruses. Since greyhounds in two different race tracks, which are geographically remote in Iowa, simultaneously succumbed to the disease without the involvement of sick horses indicates that the influenza virus isolate is a canine-adapted strain that can perpetuate in and spread among dogs. *S. zooepidemicus*, which has been implicated in respiratory disease and septicemia-associated problems in many different animal species (Wood et al., *J. Clin. Microbiol.* 43: 120-126 (2005); and Gillespie et al., *The General Staphylococcus and Streptococcus*. In: Hagan and Bruner's *Infectious Diseases of Domestic Animals*. 7th ed. Comstock/Cornell University Press. Ithaca, N.Y. 1981. pp. 164-180)), probably contributed to the severity of the disease.

All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference

to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

The use of the terms "a," "an," "the," and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to illuminate better the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

Preferred embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. It should be understood that the illustrated embodiments are exemplary only, and should not be taken as limiting the scope of the invention.

## SEQUENCE LISTING

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ttg ggg ata tta atc att aat gtc att ctc cat gta gtc agc att ata      98
Leu Gly Ile Leu Ile Ile Asn Val Ile Leu His Val Val Ser Ile Ile
15              20              25              30

gta aca gta ctg gtc ctc aat aac aat aga aca gat ctg aac tgc aaa      146
Val Thr Val Leu Val Leu Asn Asn Asn Arg Thr Asp Leu Asn Cys Lys
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ggg acg atc ata aga gaa tac aat gaa aca gta aga gta gaa aaa ctt      194
Gly Thr Ile Ile Arg Glu Tyr Asn Glu Thr Val Arg Val Glu Lys Leu
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act caa tgg tat aat acc agt aca att aag tac ata gag aga cct tca      242
Thr Gln Trp Tyr Asn Thr Ser Thr Ile Lys Tyr Ile Glu Arg Pro Ser
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aat gaa tac tac atg aat aac act gaa cca ctt tgt gag gcc caa ggc      290
Asn Glu Tyr Tyr Met Asn Asn Thr Glu Pro Leu Cys Glu Ala Gln Gly
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ttt gca cca ttt tcc aaa gat aat gga ata cga att ggg tcg aga ggc      338
Phe Ala Pro Phe Ser Lys Asp Asn Gly Ile Arg Ile Gly Ser Arg Gly
          95              100              105              110

cat gtt ttt gtg ata aga gaa cct ttt gta tca tgt tcg ccc tca gaa      386
His Val Phe Val Ile Arg Glu Pro Phe Val Ser Cys Ser Pro Ser Glu

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-continued

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Ser	Asn	Gly	Thr	Ile	Lys	Asp	Arg	Ser	Pro	Tyr	Arg	Thr	Leu	Met	Ser					
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gtt	gga	gtc	aca	ggg	ccc	gac	aat	caa	gca	att	gca	gta	gtg	aac	tat		626			
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gga	ggt	ggt	ccg	ggt	gat	act	att	aat	tca	tgg	gca	ggg	gat	att	tta		674			
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Lys	Gly	Cys	Leu	Val	Pro	Cys	Phe	Trp	Val	Glu	Met	Ile	Arg	Gly	Lys					
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Ser Ser Asp Leu Ser Tyr Thr Val Gly Tyr Leu Cys Ala Gly Ile Pro			
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 340 345 350

Gln Gly Thr Asp Val Trp Ala Gly Arg Thr Ile Ser Arg Thr Ser Arg  
 355 360 365

Ser Gly Phe Glu Ile Ile Lys Ile Arg Asn Gly Trp Thr Gln Asn Ser  
 370 375 380

Lys Asp Gln Ile Arg Arg Gln Val Ile Ile Asp Asp Pro Asn Trp Ser  
 385 390 395 400

Gly Tyr Ser Gly Ser Phe Thr Leu Pro Val Glu Leu Thr Lys Lys Gly  
 405 410 415

Cys Leu Val Pro Cys Phe Trp Val Glu Met Ile Arg Gly Lys Pro Glu  
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Glu Thr Thr Ile Trp Thr Ser Ser Ser Ser Ile Val Met Cys Gly Val  
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aca gcc aca ctg tgt ctg gga cac cat gca gta gca aat gga aca ttg 149  
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 25 30 35 40

gta aaa aca atg agt gat gat caa att gag gtg aca aat gct aca gaa 197  
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 45 50 55

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 Leu Val Gln Ser Ile Ser Met Gly Lys Ile Cys Asn Lys Ser Tyr Arg  
 60 65 70

att cta gat gga aga aat tgc aca tta ata gat gca atg cta gga gac 293  
 Ile Leu Asp Gly Arg Asn Cys Thr Leu Ile Asp Ala Met Leu Gly Asp  
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ccc cac tgt gac gcc ctt cag tat gag agt tgg gac ctc ttt ata gaa 341  
 Pro His Cys Asp Ala Leu Gln Tyr Glu Ser Trp Asp Leu Phe Ile Glu  
 90 95 100

aga agc agc gct ttc agc aat tgc tac cca tat gac atc cct gac tat 389  
 Arg Ser Ser Ala Phe Ser Asn Cys Tyr Pro Tyr Asp Ile Pro Asp Tyr  
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gca tcg ctc cga tcc att gta gca tcc tca gga aca gtt gaa ttc aca 437  
 Ala Ser Leu Arg Ser Ile Val Ala Ser Ser Gly Thr Val Glu Phe Thr  
 125 130 135

gca gag gga ttc aca tgg aca ggt gta act caa aac gga aga agt gga 485  
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Leu Thr Lys Ser Gly Ser Ser Tyr Pro Thr Leu Asn Val Thr Met Pro	
170 175 180	
aac aat aaa aat ttc gac aag cta tac atc tgg ggg att cat cac ccg	629
Asn Asn Lys Asn Phe Asp Lys Leu Tyr Ile Trp Gly Ile His His Pro	
185 190 195 200	
agc tca aat caa gag cag aca aaa ttg tac atc caa gaa tca gga cga	677
Ser Ser Asn Gln Glu Gln Thr Lys Leu Tyr Ile Gln Glu Ser Gly Arg	
205 210 215	
gta aca gtc tca aca aaa aga agt caa caa aca ata atc cct aac atc	725
Val Thr Val Ser Thr Lys Arg Ser Gln Gln Thr Ile Ile Pro Asn Ile	
220 225 230	
gaa tct aga ccg ttg gtc aga ggt caa tca ggc agg ata agc ata tac	773
Glu Ser Arg Pro Leu Val Arg Gly Gln Ser Gly Arg Ile Ser Ile Tyr	
235 240 245	
tgg acc att gta aaa cct gga gat atc cta atg ata aac agt aat ggc	821
Trp Thr Ile Val Lys Pro Gly Asp Ile Leu Met Ile Asn Ser Asn Gly	
250 255 260	
aac tta gtt gca ccg cgg gga tat ttt aaa ttg aac aca ggg aaa agc	869
Asn Leu Val Ala Pro Arg Gly Tyr Phe Lys Leu Asn Thr Gly Lys Ser	
265 270 275 280	
tct gta atg aga tcc gat gta ccc ata gac att tgt gtg tct gaa tgt	917
Ser Val Met Arg Ser Asp Val Pro Ile Asp Ile Cys Val Ser Glu Cys	
285 290 295	
att aca cca aat gga agc atc tcc aac gac aag cca ttc caa aat gtg	965
Ile Thr Pro Asn Gly Ser Ile Ser Asn Asp Lys Pro Phe Gln Asn Val	
300 305 310	
aac aaa gtt aca tat gga aaa tgc ccc aag tat atc agg caa aac act	1013
Asn Lys Val Thr Tyr Gly Lys Cys Pro Lys Tyr Ile Arg Gln Asn Thr	
315 320 325	
tta aag ctg gcc act ggg atg agg aat gta cca gaa aag caa acc aga	1061
Leu Lys Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg	
330 335 340	
gga atc ttt gga gca ata gcg gga ttc atc gaa aac ggc tgg gaa gga	1109
Gly Ile Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly	
345 350 355 360	
atg gtt gat ggg tgg tat ggg ttc cga tat caa aac tct gaa gga aca	1157
Met Val Asp Gly Trp Tyr Gly Phe Arg Tyr Gln Asn Ser Glu Gly Thr	
365 370 375	
ggg caa gct gca gat cta aag agc act caa gca gcc att gac cag att	1205
Gly Gln Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile	
380 385 390	
aat gga aag tta aac aga gtg att gaa aga acc aat gag aaa ttc cat	1253
Asn Gly Lys Leu Asn Arg Val Ile Glu Arg Thr Asn Glu Lys Phe His	
395 400 405	
caa ata gag aag gaa ttc tca gaa gta gaa gga aga att cag gac ttg	1301
Gln Ile Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu	
410 415 420	
gag aaa tat gta gaa gac acc aaa ata gac cta tgg tcc tac aat gca	1349
Glu Lys Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala	
425 430 435 440	
gaa ttg ctg gtg gct cta gaa aat caa cat aca att gac tta aca gat	1397
Glu Leu Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp	
445 450 455	
gca gaa atg aat aaa tta ttt gag aag act aga cgc cag tta aga gaa	1445
Ala Glu Met Asn Lys Leu Phe Glu Lys Thr Arg Arg Gln Leu Arg Glu	
460 465 470	

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aac gca gaa gac atg gga ggt gga tgt ttc aag att tac cac aaa tgt 1493
Asn Ala Glu Asp Met Gly Gly Gly Cys Phe Lys Ile Tyr His Lys Cys
      475                      480                      485

gat aat gca tgc att gaa tca ata aga act ggg aca tat gac cat tac 1541
Asp Asn Ala Cys Ile Glu Ser Ile Arg Thr Gly Thr Tyr Asp His Tyr
      490                      495                      500

ata tac aga gat gaa gca tta aac aac cga ttt cag atc aaa ggt gta 1589
Ile Tyr Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val
505                      510                      515                      520

gag ttg aaa tca ggc tac aaa gat tgg ata ctg tgg att tca ttc gcc 1637
Glu Leu Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala
      525                      530                      535

ata tca tgc ttc tta att tgc gtt gtt cta ttg ggt ttc att atg tgg 1685
Ile Ser Cys Phe Leu Ile Cys Val Val Leu Leu Gly Phe Ile Met Trp
      540                      545                      550

gct tgc caa aaa ggc aac atc aga tgc aac att tgc att tgagtaaact 1734
Ala Cys Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
      555                      560                      565

gatagttaaa aacacccttg tttctact 1762

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<210> SEQ ID NO 4
<211> LENGTH: 565
<212> TYPE: PRT
<213> ORGANISM: Influenza A Virus

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<400> SEQUENCE: 4

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Met Lys Thr Thr Ile Ile Leu Ile Leu Leu Thr His Trp Ala Tyr Ser
1                      5                      10                      15

Gln Asn Pro Ile Ser Gly Asn Asn Thr Ala Thr Leu Cys Leu Gly His
20                      25                      30

His Ala Val Ala Asn Gly Thr Leu Val Lys Thr Met Ser Asp Asp Gln
35                      40                      45

Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ile Ser Met Gly
50                      55                      60

Lys Ile Cys Asn Lys Ser Tyr Arg Ile Leu Asp Gly Arg Asn Cys Thr
65                      70                      75                      80

Leu Ile Asp Ala Met Leu Gly Asp Pro His Cys Asp Ala Leu Gln Tyr
85                      90                      95

Glu Ser Trp Asp Leu Phe Ile Glu Arg Ser Ser Ala Phe Ser Asn Cys
100                      105                      110

Tyr Pro Tyr Asp Ile Pro Asp Tyr Ala Ser Leu Arg Ser Ile Val Ala
115                      120                      125

Ser Ser Gly Thr Val Glu Phe Thr Ala Glu Gly Phe Thr Trp Thr Gly
130                      135                      140

Val Thr Gln Asn Gly Arg Ser Gly Ala Cys Lys Arg Gly Ser Ala Asp
145                      150                      155                      160

Ser Phe Phe Ser Arg Leu Asn Trp Leu Thr Lys Ser Gly Ser Ser Tyr
165                      170                      175

Pro Thr Leu Asn Val Thr Met Pro Asn Asn Lys Asn Phe Asp Lys Leu
180                      185                      190

Tyr Ile Trp Gly Ile His His Pro Ser Ser Asn Gln Glu Gln Thr Lys
195                      200                      205

Leu Tyr Ile Gln Glu Ser Gly Arg Val Thr Val Ser Thr Lys Arg Ser
210                      215                      220

Gln Gln Thr Ile Ile Pro Asn Ile Glu Ser Arg Pro Leu Val Arg Gly
225                      230                      235                      240

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Gln Ser Gly Arg Ile Ser Ile Tyr Trp Thr Ile Val Lys Pro Gly Asp  
 245 250 255  
 Ile Leu Met Ile Asn Ser Asn Gly Asn Leu Val Ala Pro Arg Gly Tyr  
 260 265 270  
 Phe Lys Leu Asn Thr Gly Lys Ser Ser Val Met Arg Ser Asp Val Pro  
 275 280 285  
 Ile Asp Ile Cys Val Ser Glu Cys Ile Thr Pro Asn Gly Ser Ile Ser  
 290 295 300  
 Asn Asp Lys Pro Phe Gln Asn Val Asn Lys Val Thr Tyr Gly Lys Cys  
 305 310 315 320  
 Pro Lys Tyr Ile Arg Gln Asn Thr Leu Lys Leu Ala Thr Gly Met Arg  
 325 330 335  
 Asn Val Pro Glu Lys Gln Thr Arg Gly Ile Phe Gly Ala Ile Ala Gly  
 340 345 350  
 Phe Ile Glu Asn Gly Trp Glu Gly Met Val Asp Gly Trp Tyr Gly Phe  
 355 360 365  
 Arg Tyr Gln Asn Ser Glu Gly Thr Gly Gln Ala Ala Asp Leu Lys Ser  
 370 375 380  
 Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu Asn Arg Val Ile  
 385 390 395 400  
 Glu Arg Thr Asn Glu Lys Phe His Gln Ile Glu Lys Glu Phe Ser Glu  
 405 410 415  
 Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu Asp Thr Lys  
 420 425 430  
 Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Leu Glu Asn  
 435 440 445  
 Gln His Thr Ile Asp Leu Thr Asp Ala Glu Met Asn Lys Leu Phe Glu  
 450 455 460  
 Lys Thr Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp Met Gly Gly Gly  
 465 470 475 480  
 Cys Phe Lys Ile Tyr His Lys Cys Asp Asn Ala Cys Ile Glu Ser Ile  
 485 490 495  
 Arg Thr Gly Thr Tyr Asp His Tyr Ile Tyr Arg Asp Glu Ala Leu Asn  
 500 505 510  
 Asn Arg Phe Gln Ile Lys Gly Val Glu Leu Lys Ser Gly Tyr Lys Asp  
 515 520 525  
 Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser Cys Phe Leu Ile Cys Val  
 530 535 540  
 Val Leu Leu Gly Phe Ile Met Trp Ala Cys Gln Lys Gly Asn Ile Arg  
 545 550 555 560  
 Cys Asn Ile Cys Ile  
 565

<210> SEQ ID NO 5  
 <211> LENGTH: 1585  
 <212> TYPE: DNA  
 <213> ORGANISM: Influenza A Virus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (51)..(1544)

<400> SEQUENCE: 5

cagggagcaa aagcaggta gataatcact cactgagtga catcaaagtc atg gcg 56  
 Met Ala  
 1

tct caa ggc acc aaa cga tcc tat gaa cag atg gaa act gat ggg gaa 104  
 Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu

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5	10	15	
cgc cag aat gca act gaa atc aga gca tct gtc gga agg atg gtg gga Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Arg Met Val Gly 20 25 30			152
gga atc gga cgg ttt tat gtc cag atg tgt act gag ctt aaa cta aac Gly Ile Gly Arg Phe Tyr Val Gln Met Cys Thr Glu Leu Lys Leu Asn 35 40 45 50			200
gac cat gaa ggg cgg ctg att cag aac agc ata aca ata gaa agg atg Asp His Glu Gly Arg Leu Ile Gln Asn Ser Ile Thr Ile Glu Arg Met 55 60 65			248
gta ctt tca gca ttc gac gaa aga aga aac aag tat ctc gag gag cat Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu Glu His 70 75 80			296
ccc agt gct ggg aaa gac cct aag aaa acg gga ggc ccg ata tac aga Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile Tyr Arg 85 90 95			344
aga aaa gat ggg aaa tgg atg agg gaa ctc atc ctc cat gat aaa gaa Arg Lys Asp Gly Lys Trp Met Arg Glu Leu Ile Leu His Asp Lys Glu 100 105 110			392
gaa atc atg aga atc tgg cgt cag gcc aac aat ggt gaa gac gct act Glu Ile Met Arg Ile Trp Arg Gln Ala Asn Asn Gly Glu Asp Ala Thr 115 120 125 130			440
gct ggt ctt act cat atg atg atc tgg cac tcc aat ctc aat gac acc Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn Asp Thr 135 140 145			488
aca tac caa aga aca agg gct ctt gtt cgg act ggg atg gat ccc aga Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp Pro Arg 150 155 160			536
atg tgc tct ctg atg caa ggc tca acc ctc cca cgg aga tct gga gcc Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser Gly Ala 165 170 175			584
gct ggt gct gca gta aaa ggt gtt gga aca atg gta atg gaa ctc atc Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu Leu Ile 180 185 190			632
agg atg atc aaa cgc gga ata aat gat cgg aat ttc tgg aga ggt gaa Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg Gly Glu 195 200 205 210			680
aat ggt cga aga acc aga att gct tat gaa aga atg tgc aat atc ctc Asn Gly Arg Arg Thr Arg Ile Ala Tyr Glu Arg Met Cys Asn Ile Leu 215 220 225			728
aaa ggg aaa ttt cag aca gca gca caa cgg gct atg atg gac cag gtg Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp Gln Val 230 235 240			776
agg gaa ggc cgc aat cct gga aac gct gag att gag gat ctc att ttc Arg Glu Gly Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu Ile Phe 245 250 255			824
ttg gca cga tca gca ctt att ttg aga gga tca gta gcc cat aaa tca Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His Lys Ser 260 265 270			872
tgc cta cct gcc tgt gtt tat ggc ctt gca gta acc agt ggg tat gac Cys Leu Pro Ala Cys Val Tyr Gly Leu Ala Val Thr Ser Gly Tyr Asp 275 280 285 290			920
ttt gag aag gaa gga tac tct ctg gtt gga att gat cct ttc aaa cta Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe Lys Leu 295 300 305			968
ctc cag aac agt caa att ttc agt cta atc aga cca aaa gaa aac cca Leu Gln Asn Ser Gln Ile Phe Ser Leu Ile Arg Pro Lys Glu Asn Pro 310 315 320			1016
gca cac aaa agc cag ttg gtg tgg atg gca tgc cat tct gca gca ttt Ala His Lys Ser Gln Leu Val Trp Met Ala Cys His Ser Ala Ala Phe			1064



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325	330	335	
gag gat ctg aga gtt tta aat ttc att aga gga acc aaa gta atc cca			1112
Glu Asp Leu Arg Val Leu Asn Phe Ile Arg Gly Thr Lys Val Ile Pro			
340	345	350	
aga gga cag tta aca acc aga gga gtt caa att gct tca aat gaa aac			1160
Arg Gly Gln Leu Thr Thr Arg Gly Val Gln Ile Ala Ser Asn Glu Asn			
355	360	365	370
atg gag aca ata aat tct agc aca ctt gaa ctg aga agc aaa tat tgg			1208
Met Glu Thr Ile Asn Ser Ser Thr Leu Glu Leu Arg Ser Lys Tyr Trp			
375	380	385	
gca ata agg acc aga agc gga gga aac acc agt caa cag aga gca ttt			1256
Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Ser Gln Gln Arg Ala Phe			
390	395	400	
gca gga cag ata agt gtg caa cct act ttc tca gta cag aga aat ctt			1304
Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg Asn Leu			
405	410	415	
ccc ttt gag aga gca acc att atg gct gca ttc act ggt aac act gaa			1352
Pro Phe Glu Arg Ala Thr Ile Met Ala Ala Phe Thr Gly Asn Thr Glu			
420	425	430	
ggg agg act tcc gac atg aga acg gaa atc ata agg atg atg gaa aat			1400
Gly Arg Thr Ser Asp Met Arg Thr Glu Ile Ile Arg Met Met Glu Asn			
435	440	445	450
gcc aaa tca gaa gat gtg tct ttc cag ggg cgg gga gtc ttc gag ctc			1448
Ala Lys Ser Glu Asp Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu			
455	460	465	
tcg gac gaa aag gca acg aac ccg atc gtg cct tcc ttt gac atg agc			1496
Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser			
470	475	480	
aat gaa ggg tct tat ttc ttc gga gac aat gct gag gag ttt gac agt			1544
Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Phe Asp Ser			
485	490	495	
taaagaaaaa tacccttggt tctactaata cgagacgata t			1585

&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 498

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Influenza A Virus

&lt;400&gt; SEQUENCE: 6

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp			
1	5	10	15
Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Arg Met			
	20	25	30
Val Gly Gly Ile Gly Arg Phe Tyr Val Gln Met Cys Thr Glu Leu Lys			
	35	40	45
Leu Asn Asp His Glu Gly Arg Leu Ile Gln Asn Ser Ile Thr Ile Glu			
	50	55	60
Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu			
	65	70	75
Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile			
	85	90	95
Tyr Arg Arg Lys Asp Gly Lys Trp Met Arg Glu Leu Ile Leu His Asp			
	100	105	110
Lys Glu Glu Ile Met Arg Ile Trp Arg Gln Ala Asn Asn Gly Glu Asp			
	115	120	125
Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn			
	130	135	140
Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp			

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145		150		155		160
Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser						
		165		170		175
Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu		180		185		190
Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg		195		200		205
Gly Glu Asn Gly Arg Arg Thr Arg Ile Ala Tyr Glu Arg Met Cys Asn		210		215		220
Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp		225		230		235
		235		240		245
Gln Val Arg Glu Gly Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu		245		250		255
Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His		260		265		270
Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Leu Ala Val Thr Ser Gly		275		280		285
Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe		290		295		300
Lys Leu Leu Gln Asn Ser Gln Ile Phe Ser Leu Ile Arg Pro Lys Glu		305		310		315
Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys His Ser Ala		325		330		335
Ala Phe Glu Asp Leu Arg Val Leu Asn Phe Ile Arg Gly Thr Lys Val		340		345		350
Ile Pro Arg Gly Gln Leu Thr Thr Arg Gly Val Gln Ile Ala Ser Asn		355		360		365
Glu Asn Met Glu Thr Ile Asn Ser Ser Thr Leu Glu Leu Arg Ser Lys		370		375		380
Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Ser Gln Gln Arg		385		390		395
Ala Phe Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg		405		410		415
Asn Leu Pro Phe Glu Arg Ala Thr Ile Met Ala Ala Phe Thr Gly Asn		420		425		430
Thr Glu Gly Arg Thr Ser Asp Met Arg Thr Glu Ile Ile Arg Met Met		435		440		445
Glu Asn Ala Lys Ser Glu Asp Val Ser Phe Gln Gly Arg Gly Val Phe		450		455		460
Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp		465		470		475
		475		480		485
Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Phe		485		490		495

Asp Ser

<210> SEQ ID NO 7  
 <211> LENGTH: 1056  
 <212> TYPE: DNA  
 <213> ORGANISM: Influenza A virus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (40)..(795)

&lt;400&gt; SEQUENCE: 7

tattcgtctc agggagcaaa agcaggtaga tatttaaag atg agt ctt cta acc  
 Met Ser Leu Leu Thr

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													1	5			
gag gtc gaa acg tac gtt ctc tct atc gta cca tca ggc ccc ctc aaa																	102
Glu Val Glu Thr Tyr Val Leu Ser Ile Val Pro Ser Gly Pro Leu Lys																	
				10					15							20	
gcc gag atc gcg cag aga ctt gaa gat gtc ttt gcg gga aag aac acc																	150
Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe Ala Gly Lys Asn Thr																	
				25					30							35	
gat ctt gag gca ctc atg gaa tgg cta aag aca aga cca atc ctg tca																	198
Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr Arg Pro Ile Leu Ser																	
				40					45							50	
cct ctg act aaa ggg att tta gga ttt gta ttc acg ctc acc gtg ccc																	246
Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe Thr Leu Thr Val Pro																	
				55					60							65	
agt gag cga gga ctg cag cgt aga cgc ttt gtc caa aat gcc ctt agt																	294
Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val Gln Asn Ala Leu Ser																	
				70					75							80	85
gga aac gga gat cca aac aac atg gac aga gca gta aaa ctg tac agg																	342
Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala Val Lys Leu Tyr Arg																	
				90					95							100	
aag ctt aaa aga gaa ata aca ttc cat gag gca aaa gag gtg gca ctc																	390
Lys Leu Lys Arg Glu Ile Thr Phe His Glu Ala Lys Glu Val Ala Leu																	
				105					110							115	
agc tat tcc act ggt gca cta gcc agc tgc atg gga ctc ata tac aac																	438
Ser Tyr Ser Thr Gly Ala Leu Ala Ser Cys Met Gly Leu Ile Tyr Asn																	
				120					125							130	
aga atg gga act gtt aca acc gaa gtg gca ttt ggc ctg gta tgc gcc																	486
Arg Met Gly Thr Val Thr Thr Glu Val Ala Phe Gly Leu Val Cys Ala																	
				135					140							145	
aca tgt gaa cag att gct gat tcc cag cat cga tct cac agg cag atg																	534
Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg Ser His Arg Gln Met																	
				150					155							160	165
gtg aca aca acc aac cca tta atc aga cat gaa aac aga atg gta tta																	582
Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu Asn Arg Met Val Leu																	
				170					175							180	
gcc agt acc acg gct aaa gcc atg gaa cag atg gca gga tcg agt gag																	630
Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met Ala Gly Ser Ser Glu																	
				185					190							195	
cag gca gca gag gcc atg gag gtt gct agt agg gct agg cag atg gta																	678
Gln Ala Ala Glu Ala Met Glu Val Ala Ser Arg Ala Arg Gln Met Val																	
				200					205							210	
cag gca atg aga acc att ggg acc cac cct agc tcc agt gcc ggt ttg																	726
Gln Ala Met Arg Thr Ile Gly Thr His Pro Ser Ser Ser Ala Gly Leu																	
				215					220							225	
aaa gat gat ctc ctt gaa aat tta cag gcc tac cag aaa cgg atg gga																	774
Lys Asp Asp Leu Leu Glu Asn Leu Gln Ala Tyr Gln Lys Arg Met Gly																	
				230					235							240	245
gtg caa atg cag cga ttc aag tgatcctctc gttattgcag caagtatcat																	825
Val Gln Met Gln Arg Phe Lys																	
				250													
tggaatcttg cacttgatat tgtggattct tgatcgctctt ttcttcaaat tcatttatcg																	885
tcgccttaaa tacgggttga aaagagggcc ttctacggaa ggagtacctg agtctatgag																	945
ggaagaatat cggcaggaac agcagaatgc tgtggatggt gacgatggtc atttgtcaa																	1005
catagagctg gagtaaaaaa ctaccttggt tctactaata cgagacgata t																	1056

&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 252

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Influenza A virus

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&lt;400&gt; SEQUENCE: 8

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Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Val Pro
1           5           10           15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
          20           25           30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
          35           40           45

Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
          50           55           60

Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65           70           75           80

Gln Asn Ala Leu Ser Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
          85           90           95

Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Glu Ala
          100          105          110

Lys Glu Val Ala Leu Ser Tyr Ser Thr Gly Ala Leu Ala Ser Cys Met
          115          120          125

Gly Leu Ile Tyr Asn Arg Met Gly Thr Val Thr Thr Glu Val Ala Phe
130          135          140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145          150          155          160

Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
          165          170          175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
          180          185          190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Arg
          195          200          205

Ala Arg Gln Met Val Gln Ala Met Arg Thr Ile Gly Thr His Pro Ser
210          215          220

Ser Ser Ala Gly Leu Lys Asp Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225          230          235          240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
          245          250

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&lt;210&gt; SEQ ID NO 9

&lt;211&gt; LENGTH: 870

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Influenza A virus

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (29)..(718)

&lt;400&gt; SEQUENCE: 9

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ggagcaaaag cagggtgaca aaaacata atg gat tcc aac act gtg tca agc      52
          Met Asp Ser Asn Thr Val Ser Ser
          1           5

ttt cag gta gac tgt ttt ctt tgg cat gtc cgc aaa cga ttc gca gac      100
Phe Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Arg Phe Ala Asp
          10           15           20

caa gaa ctg ggt gat gcc cca ttc ctt gac cgg ctt cgc cga gac cag      148
Gln Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln
          25           30           35           40

aag tcc cta agg gga aga ggt agc act ctt ggt ctg gac atc gaa aca      196
Lys Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr
          45           50           55

gcc act cat gca gga aag cag ata gtg gag cag att ctg gaa aag gaa      244
Ala Thr His Ala Gly Lys Gln Ile Val Glu Gln Ile Leu Glu Lys Glu
          60           65           70

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tca gat gag gca ctt aaa atg acc att gcc tct gtt cct gct tca cgc	292
Ser Asp Glu Ala Leu Lys Met Thr Ile Ala Ser Val Pro Ala Ser Arg	
75 80 85	
tac tta act gac atg act ctt gat gag atg tca aga gac tgg ttc atg	340
Tyr Leu Thr Asp Met Thr Leu Asp Glu Met Ser Arg Asp Trp Phe Met	
90 95 100	
ctc atg ccc aag caa aaa gta aca ggc tcc cta tgt ata aga atg gac	388
Leu Met Pro Lys Gln Lys Val Thr Gly Ser Leu Cys Ile Arg Met Asp	
105 110 115 120	
caa gca atc atg gat aag aac atc ata ctt aaa gca aac ttt agt gtg	436
Gln Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val	
125 130 135	
att ttc gaa agg ctg gaa aca cta ata cta ctt aga gcc ttc acc gaa	484
Ile Phe Glu Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu	
140 145 150	
gaa gga gca gtc gtt ggc gaa att tca cca tta cct tct ctt cca gga	532
Glu Gly Ala Val Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly	
155 160 165	
cat act aat gag gat gtc aaa aat gca att ggg gtc ctc atc gga gga	580
His Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly	
170 175 180	
ctt aaa tgg aat gat aat acg gtt aga atc tct gaa act cta cag aga	628
Leu Lys Trp Asn Asp Asn Thr Val Arg Ile Ser Glu Thr Leu Gln Arg	
185 190 195 200	
ttc gct tgg aga agc agt cat gaa aat ggg aga cct tca ttc cct tca	676
Phe Ala Trp Arg Ser Ser His Glu Asn Gly Arg Pro Ser Phe Pro Ser	
205 210 215	
aag cag aaa cga aaa atg gag aga aca att aag cca gaa att	718
Lys Gln Lys Arg Lys Met Glu Arg Thr Ile Lys Pro Glu Ile	
220 225 230	
tgaagaaata agatggttga ttgaagaagt gcgacataga ttgaaaaata cagaaaatag	778
ttttgaacaa ataacattta tgcaagcctt acaactattg cttgaagtag aacaagagat	838
aagaactttc tcgtttcagc ttatttaatg at	870

&lt;210&gt; SEQ ID NO 10

&lt;211&gt; LENGTH: 230

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Influenza A virus

&lt;400&gt; SEQUENCE: 10

Met Asp Ser Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp	
1 5 10 15	
His Val Arg Lys Arg Phe Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe	
20 25 30	
Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser	
35 40 45	
Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr His Ala Gly Lys Gln Ile	
50 55 60	
Val Glu Gln Ile Leu Glu Lys Glu Ser Asp Glu Ala Leu Lys Met Thr	
65 70 75 80	
Ile Ala Ser Val Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Leu Asp	
85 90 95	
Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Thr	
100 105 110	
Gly Ser Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile	
115 120 125	
Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Glu Arg Leu Glu Thr Leu	

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130	135	140
Ile Leu Leu Arg Ala Phe Thr Glu Glu Gly Ala Val Val Gly Glu Ile		
145	150	155 160
Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn		
	165	170 175
Ala Ile Gly Val Leu Ile Gly Gly Leu Lys Trp Asn Asp Asn Thr Val		
	180	185 190
Arg Ile Ser Glu Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser His Glu		
	195	200 205
Asn Gly Arg Pro Ser Phe Pro Ser Lys Gln Lys Arg Lys Met Glu Arg		
	210	215 220
Thr Ile Lys Pro Glu Ile		
225	230	

<210> SEQ ID NO 11  
 <211> LENGTH: 2191  
 <212> TYPE: DNA  
 <213> ORGANISM: Influenza A virus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (4)..(2151)

<400> SEQUENCE: 11

taa atg gaa gac ttt gtg cga cag tgc ttc aat cca atg atc gtc gag	48
Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu	
1 5 10 15	
ctt gcg gaa aag gca atg aaa gaa tat gga gag aac ccg aaa atc gaa	96
Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asn Pro Lys Ile Glu	
20 25 30	
aca aac aaa ttt gca gca ata tgc act cac ttg gaa gtc tgc ttc atg	144
Thr Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met	
35 40 45	
tac tcg gat ttc cac ttt ata aat gaa ctg ggt gag tca gtg gtc ata	192
Tyr Ser Asp Phe His Phe Ile Asn Glu Leu Gly Glu Ser Val Val Ile	
50 55 60	
gag tct ggt gac cca aat gct ctt ttg aaa cac aga ttt gaa atc att	240
Glu Ser Gly Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile	
65 70 75	
gag ggg aga gat cga aca atg gca tgg aca gta gta aac agc atc tgc	288
Glu Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys	
80 85 90 95	
aac acc aca aga gct gaa aaa cct aaa ttt ctt cca gat tta tac gac	336
Asn Thr Thr Arg Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp	
100 105 110	
tat aag gag aac aga ttt gtt gaa att ggt gtg aca agg aga gaa gtt	384
Tyr Lys Glu Asn Arg Phe Val Glu Ile Gly Val Thr Arg Arg Glu Val	
115 120 125	
cac ata tac tac ctg gag aaa gcc aac aaa ata aag tct gag aaa aca	432
His Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr	
130 135 140	
cat atc cac att ttc tca ttt aca gga gaa gaa atg gct aca aaa gcg	480
His Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala	
145 150 155	
gac tat act ctt gat gaa gag agt aga gcc agg atc aag acc aga cta	528
Asp Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu	
160 165 170 175	
ttc act ata aga caa gaa atg gcc agt aga ggc ctc tgg gat tcc ttt	576
Phe Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe	
180 185 190	
cgt cag tcc gag aga ggc gaa gag aca att gaa gaa aga ttt gaa atc	624

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Arg	Gln	Ser	Glu	Arg	Gly	Glu	Glu	Thr	Ile	Glu	Glu	Arg	Phe	Glu	Ile		
			195					200					205				
aca	gga	acg	atg	cgc	aag	ctt	gcc	aat	tac	agt	ctc	cca	ccg	aac	ttc	672	
Thr	Gly	Thr	Met	Arg	Lys	Leu	Ala	Asn	Tyr	Ser	Leu	Pro	Pro	Asn	Phe		
		210					215					220					
tcc	agc	ctt	gaa	aat	ttt	aga	gtc	tat	ata	gat	gga	ttc	gaa	ccg	aac	720	
Ser	Ser	Leu	Glu	Asn	Phe	Arg	Val	Tyr	Ile	Asp	Gly	Phe	Glu	Pro	Asn		
		225				230					235						
ggc	tgc	att	gag	agt	aag	ctt	tct	caa	atg	tcc	aaa	gaa	gta	aat	gcc	768	
Gly	Cys	Ile	Glu	Ser	Lys	Leu	Ser	Gln	Met	Ser	Lys	Glu	Val	Asn	Ala		
240					245					250					255		
aaa	atc	gaa	cca	ttt	tca	aag	aca	aca	ccc	cga	cca	ctc	aaa	atg	cca	816	
Lys	Ile	Glu	Pro	Phe	Ser	Lys	Thr	Thr	Pro	Arg	Pro	Leu	Lys	Met	Pro		
				260						265					270		
ggt	ggt	cca	ccc	tgc	cat	cag	cga	tcc	aaa	ttc	ttg	cta	atg	gat	gct	864	
Gly	Gly	Pro	Pro	Cys	His	Gln	Arg	Ser	Lys	Phe	Leu	Leu	Met	Asp	Ala		
			275					280							285		
ctg	aaa	ctg	agc	att	gag	gac	cca	agt	cac	gag	gga	gag	ggg	ata	cca	912	
Leu	Lys	Leu	Ser	Ile	Glu	Asp	Pro	Ser	His	Glu	Gly	Glu	Gly	Ile	Pro		
		290						295							300		
cta	tat	gat	gca	atc	aaa	tgc	atg	aaa	act	ttc	ttt	gga	tgg	aaa	gag	960	
Leu	Tyr	Asp	Ala	Ile	Lys	Cys	Met	Lys	Thr	Phe	Phe	Gly	Trp	Lys	Glu		
	305					310						315					
ccc	agt	att	ggt	aaa	cca	cat	aaa	aag	ggt	ata	aac	ccg	aac	tat	ctc	1008	
Pro	Ser	Ile	Val	Lys	Pro	His	Lys	Lys	Gly	Ile	Asn	Pro	Asn	Tyr	Leu		
320						325					330				335		
caa	act	tgg	aag	caa	gta	tta	gaa	gaa	ata	caa	gac	ctt	gag	aac	gaa	1056	
Gln	Thr	Trp	Lys	Gln	Val	Leu	Glu	Glu	Ile	Gln	Asp	Leu	Glu	Asn	Glu		
				340						345					350		
gaa	agg	acc	ccc	aag	acc	aag	aat	atg	aaa	aaa	aca	agc	caa	ttg	aaa	1104	
Glu	Arg	Thr	Pro	Lys	Thr	Lys	Asn	Met	Lys	Lys	Thr	Ser	Gln	Leu	Lys		
			355					360							365		
tgg	gca	cta	ggt	gaa	aat	atg	gca	cca	gag	aaa	gtg	gat	ttt	gag	gat	1152	
Trp	Ala	Leu	Gly	Glu	Asn	Met	Ala	Pro	Glu	Lys	Val	Asp	Phe	Glu	Asp		
		370						375							380		
tgt	aaa	gac	atc	aat	gat	tta	aaa	caa	tat	gac	agt	gat	gag	cca	gaa	1200	
Cys	Lys	Asp	Ile	Asn	Asp	Leu	Lys	Gln	Tyr	Asp	Ser	Asp	Glu	Pro	Glu		
	385					390									395		
gca	agg	tct	ctt	gca	agt	tgg	att	caa	agt	gag	ttc	aac	aag	gct	tgt	1248	
Ala	Arg	Ser	Leu	Ala	Ser	Trp	Ile	Gln	Ser	Glu	Phe	Asn	Lys	Ala	Cys		
400						405					410				415		
gag	ctg	aca	gat	tca	agc	tgg	ata	gag	ctc	gat	gaa	att	ggg	gag	gat	1296	
Glu	Leu	Thr	Asp	Ser	Ser	Trp	Ile	Glu	Leu	Asp	Glu	Ile	Gly	Glu	Asp		
				420						425					430		
gtc	gcc	cca	ata	gaa	tac	att	gcg	agc	atg	agg	aga	aat	tat	ttt	act	1344	
Val	Ala	Pro	Ile	Glu	Tyr	Ile	Ala	Ser	Met	Arg	Arg	Asn	Tyr	Phe	Thr		
			435							440					445		
gct	gag	att	tcc	cat	tgt	aga	gca	aca	gaa	tat	ata	atg	aaa	gga	gta	1392	
Ala	Glu	Ile	Ser	His	Cys	Arg	Ala	Thr	Glu	Tyr	Ile	Met	Lys	Gly	Val		
		450						455							460		
tac	atc	aac	act	gct	cta	ctc	aat	gca	tcc	tgt	gct	gcg	atg	gat	gaa	1440	
Tyr	Ile	Asn	Thr	Ala	Leu	Leu	Asn	Ala	Ser	Cys	Ala	Ala	Met	Asp	Glu		
		465					470					475					
ttt	caa	tta	att	ccg	atg	ata	agt	aaa	tgc	agg	acc	aaa	gaa	ggg	aga	1488	
Phe	Gln	Leu	Ile	Pro	Met	Ile	Ser	Lys	Cys	Arg	Thr	Lys	Glu	Gly	Arg		
480						485				490					495		
agg	aaa	aca	aat	tta	tat	gga	ttc	ata	ata	aag	gga	agg	tcc	cat	tta	1536	
Arg	Lys	Thr	Asn	Leu	Tyr	Gly	Phe	Ile	Ile	Lys	Gly	Arg	Ser	His	Leu		
				500						505					510		
aga	aat	gat	act	gac	gtg	gtg	aac	ttt	gta	agt	atg	gaa	ttt	tct	ctc	1584	

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Arg	Asn	Asp	Thr	Asp	Val	Val	Asn	Phe	Val	Ser	Met	Glu	Phe	Ser	Leu	
			515					520					525			
act	gat	cca	aga	ttt	gag	cca	cac	aaa	tgg	gaa	aaa	tac	tgc	ggt	cta	1632
Thr	Asp	Pro	Arg	Phe	Glu	Pro	His	Lys	Trp	Glu	Lys	Tyr	Cys	Val	Leu	
		530					535					540				
gaa	att	gga	gac	atg	ctt	cta	aga	act	gct	gta	ggg	caa	gtg	tca	aga	1680
Glu	Ile	Gly	Asp	Met	Leu	Leu	Arg	Thr	Ala	Val	Gly	Gln	Val	Ser	Arg	
	545					550					555					
ccc	ata	ttt	ttg	tat	gta	agg	aca	aat	gga	acc	tct	aaa	att	aaa	atg	1728
Pro	Ile	Phe	Leu	Tyr	Val	Arg	Thr	Asn	Gly	Thr	Ser	Lys	Ile	Lys	Met	
560					565				570						575	
aaa	tgg	gga	atg	gaa	atg	aga	cgc	tgc	ctc	ctt	cag	tct	ctg	caa	cag	1776
Lys	Trp	Gly	Met	Glu	Met	Arg	Arg	Cys	Leu	Leu	Gln	Ser	Leu	Gln	Gln	
				580					585						590	
att	gaa	agc	atg	atc	gaa	gct	gag	tcc	tca	gtc	aaa	gaa	aag	gac	atg	1824
Ile	Glu	Ser	Met	Ile	Glu	Ala	Glu	Ser	Ser	Val	Lys	Glu	Lys	Asp	Met	
			595					600						605		
acc	aaa	gaa	ttt	ttt	gag	aac	aaa	tca	gag	aca	tgg	cct	ata	gga	gag	1872
Thr	Lys	Glu	Phe	Phe	Glu	Asn	Lys	Ser	Glu	Thr	Trp	Pro	Ile	Gly	Glu	
		610					615					620				
tcc	ccc	aaa	gga	gtg	gaa	gag	ggc	tca	atc	ggg	aag	ggt	tgc	agg	acc	1920
Ser	Pro	Lys	Gly	Val	Glu	Glu	Gly	Ser	Ile	Gly	Lys	Val	Cys	Arg	Thr	
	625					630					635					
tta	tta	gca	aaa	tct	gtg	ttt	aac	agt	tta	tat	gca	tct	cca	caa	ctg	1968
Leu	Leu	Ala	Lys	Ser	Val	Phe	Asn	Ser	Leu	Tyr	Ala	Ser	Pro	Gln	Leu	
640					645					650					655	
gaa	gga	ttt	tca	gct	gaa	tct	agg	aaa	tta	ctt	ctc	att	ggt	cag	gct	2016
Glu	Gly	Phe	Ser	Ala	Glu	Ser	Arg	Lys	Leu	Leu	Leu	Ile	Val	Gln	Ala	
				660					665						670	
ctt	aga	gat	gac	ctg	gaa	cct	gga	acc	ttt	gat	att	ggg	ggg	tta	tat	2064
Leu	Arg	Asp	Asp	Leu	Glu	Pro	Gly	Thr	Phe	Asp	Ile	Gly	Gly	Leu	Tyr	
			675					680						685		
gaa	tca	att	gag	gag	tgc	ctg	att	aat	gat	ccc	tgg	ggt	ttg	ctt	aat	2112
Glu	Ser	Ile	Glu	Glu	Cys	Leu	Ile	Asn	Asp	Pro	Trp	Val	Leu	Leu	Asn	
		690						695				700				
gca	tct	tgg	ttc	aac	tcc	ttc	ctc	aca	cat	gca	ctg	aag	tagttgtggc			2161
Ala	Ser	Trp	Phe	Asn	Ser	Phe	Leu	Thr	His	Ala	Leu	Lys				
	705					710					715					
aatgctacta	tttgttatcc	atactgtcca														2191

<210> SEQ ID NO 12  
<211> LENGTH: 716  
<212> TYPE: PRT  
<213> ORGANISM: Influenza A virus

<400> SEQUENCE: 12

Met	Glu	Asp	Phe	Val	Arg	Gln	Cys	Phe	Asn	Pro	Met	Ile	Val	Glu	Leu	
1				5					10					15		
Ala	Glu	Lys	Ala	Met	Lys	Glu	Tyr	Gly	Glu	Asn	Pro	Lys	Ile	Glu	Thr	
			20					25					30			
Asn	Lys	Phe	Ala	Ala	Ile	Cys	Thr	His	Leu	Glu	Val	Cys	Phe	Met	Tyr	
		35					40					45				
Ser	Asp	Phe	His	Phe	Ile	Asn	Glu	Leu	Gly	Glu	Ser	Val	Val	Ile	Glu	
	50					55					60					
Ser	Gly	Asp	Pro	Asn	Ala	Leu	Leu	Lys	His	Arg	Phe	Glu	Ile	Ile	Glu	
	65				70					75					80	
Gly	Arg	Asp	Arg	Thr	Met	Ala	Trp	Thr	Val	Val	Asn	Ser	Ile	Cys	Asn	
				85					90					95		
Thr	Thr	Arg	Ala	Glu	Lys	Pro	Lys	Phe	Leu	Pro	Asp	Leu	Tyr	Asp	Tyr	



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100					105					110					
Lys	Glu	Asn	Arg	Phe	Val	Glu	Ile	Gly	Val	Thr	Arg	Arg	Glu	Val	His
		115					120					125			
Ile	Tyr	Tyr	Leu	Glu	Lys	Ala	Asn	Lys	Ile	Lys	Ser	Glu	Lys	Thr	His
	130					135					140				
Ile	His	Ile	Phe	Ser	Phe	Thr	Gly	Glu	Glu	Met	Ala	Thr	Lys	Ala	Asp
145					150					155					160
Tyr	Thr	Leu	Asp	Glu	Glu	Ser	Arg	Ala	Arg	Ile	Lys	Thr	Arg	Leu	Phe
				165					170					175	
Thr	Ile	Arg	Gln	Glu	Met	Ala	Ser	Arg	Gly	Leu	Trp	Asp	Ser	Phe	Arg
			180						185				190		
Gln	Ser	Glu	Arg	Gly	Glu	Glu	Thr	Ile	Glu	Glu	Arg	Phe	Glu	Ile	Thr
		195					200					205			
Gly	Thr	Met	Arg	Lys	Leu	Ala	Asn	Tyr	Ser	Leu	Pro	Pro	Asn	Phe	Ser
	210					215					220				
Ser	Leu	Glu	Asn	Phe	Arg	Val	Tyr	Ile	Asp	Gly	Phe	Glu	Pro	Asn	Gly
225					230					235					240
Cys	Ile	Glu	Ser	Lys	Leu	Ser	Gln	Met	Ser	Lys	Glu	Val	Asn	Ala	Lys
				245					250					255	
Ile	Glu	Pro	Phe	Ser	Lys	Thr	Thr	Pro	Arg	Pro	Leu	Lys	Met	Pro	Gly
			260					265						270	
Gly	Pro	Pro	Cys	His	Gln	Arg	Ser	Lys	Phe	Leu	Leu	Met	Asp	Ala	Leu
		275					280					285			
Lys	Leu	Ser	Ile	Glu	Asp	Pro	Ser	His	Glu	Gly	Glu	Gly	Ile	Pro	Leu
	290					295					300				
Tyr	Asp	Ala	Ile	Lys	Cys	Met	Lys	Thr	Phe	Phe	Gly	Trp	Lys	Glu	Pro
305					310					315					320
Ser	Ile	Val	Lys	Pro	His	Lys	Lys	Gly	Ile	Asn	Pro	Asn	Tyr	Leu	Gln
				325					330					335	
Thr	Trp	Lys	Gln	Val	Leu	Glu	Glu	Ile	Gln	Asp	Leu	Glu	Asn	Glu	Glu
			340					345						350	
Arg	Thr	Pro	Lys	Thr	Lys	Asn	Met	Lys	Lys	Thr	Ser	Gln	Leu	Lys	Trp
		355					360					365			
Ala	Leu	Gly	Glu	Asn	Met	Ala	Pro	Glu	Lys	Val	Asp	Phe	Glu	Asp	Cys
	370					375					380				
Lys	Asp	Ile	Asn	Asp	Leu	Lys	Gln	Tyr	Asp	Ser	Asp	Glu	Pro	Glu	Ala
385					390					395					400
Arg	Ser	Leu	Ala	Ser	Trp	Ile	Gln	Ser	Glu	Phe	Asn	Lys	Ala	Cys	Glu
				405					410					415	
Leu	Thr	Asp	Ser	Ser	Trp	Ile	Glu	Leu	Asp	Glu	Ile	Gly	Glu	Asp	Val
			420					425					430		
Ala	Pro	Ile	Glu	Tyr	Ile	Ala	Ser	Met	Arg	Arg	Asn	Tyr	Phe	Thr	Ala
		435					440					445			
Glu	Ile	Ser	His	Cys	Arg	Ala	Thr	Glu	Tyr	Ile	Met	Lys	Gly	Val	Tyr
	450					455					460				
Ile	Asn	Thr	Ala	Leu	Leu	Asn	Ala	Ser	Cys	Ala	Ala	Met	Asp	Glu	Phe
465					470					475					480
Gln	Leu	Ile	Pro	Met	Ile	Ser	Lys	Cys	Arg	Thr	Lys	Glu	Gly	Arg	Arg
				485					490					495	
Lys	Thr	Asn	Leu	Tyr	Gly	Phe	Ile	Ile	Lys	Gly	Arg	Ser	His	Leu	Arg
			500					505					510		
Asn	Asp	Thr	Asp	Val	Val	Asn	Phe	Val	Ser	Met	Glu	Phe	Ser	Leu	Thr
		515					520					525			

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Asp Pro Arg Phe Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu  
 530 535 540  
 Ile Gly Asp Met Leu Leu Arg Thr Ala Val Gly Gln Val Ser Arg Pro  
 545 550 555 560  
 Ile Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys  
 565 570 575  
 Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile  
 580 585 590  
 Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr  
 595 600 605  
 Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser  
 610 615 620  
 Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu  
 625 630 635 640  
 Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu  
 645 650 655  
 Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Ile Val Gln Ala Leu  
 660 665 670  
 Arg Asp Asp Leu Glu Pro Gly Thr Phe Asp Ile Gly Gly Leu Tyr Glu  
 675 680 685  
 Ser Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala  
 690 695 700  
 Ser Trp Phe Asn Ser Phe Leu Thr His Ala Leu Lys  
 705 710 715

<210> SEQ ID NO 13  
 <211> LENGTH: 2299  
 <212> TYPE: DNA  
 <213> ORGANISM: Influenza A virus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (22)..(2292)  
 <220> FEATURE:  
 <221> NAME/KEY: misc\_feature  
 <222> LOCATION: (547)..(547)  
 <223> OTHER INFORMATION: Xaa stands for Ala or Val

<400> SEQUENCE: 13

gaaagcaggc aaaccatttg a atg gat gtc aat ccg act cta ctt ttc tta 51  
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu  
 1 5 10  
 aag gtg cca gcg caa aat gct ata agc aca aca ttc cct tat act gga 99  
 Lys Val Pro Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly  
 15 20 25  
 gat cct ccc tac agt cat gga aca ggg aca gga tac acc atg gat act 147  
 Asp Pro Pro Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr  
 30 35 40  
 gtc aac aga aca cac caa tat tca gaa aaa ggg aaa tgg aca aca aac 195  
 Val Asn Arg Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn  
 45 50 55  
 act gag att gga gca cca caa ctt aat cca atc gat gga cca ctt cct 243  
 Thr Glu Ile Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro  
 60 65 70  
 gaa gac aat gaa cca agt ggg tac gcc caa aca gat tgt gta ttg gaa 291  
 Glu Asp Asn Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu  
 75 80 85 90  
 gca atg gct ttc ctt gaa gaa tcc cat ccc gga atc ttt gaa aat tcg 339  
 Ala Met Ala Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn Ser  
 95 100 105  
 tgt ctt gaa acg atg gag gtg att cag cag aca aga gtg gac aaa cta 387

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Cys	Leu	Glu	Thr	Met	Glu	Val	Ile	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	
			110					115					120			
aca	caa	ggc	cga	caa	act	tat	gat	tgg	acc	ttg	aat	agg	aat	caa	cct	435
Thr	Gln	Gly	Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	
		125					130					135				
gcc	gca	aca	gca	ctt	gct	aat	acg	att	gaa	gta	ttc	aga	tca	aat	ggt	483
Ala	Ala	Thr	Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	
		140					145				150					
ctg	act	tcc	aat	gaa	tcg	ggg	aga	ttg	atg	gac	ttc	ctc	aaa	gat	gtc	531
Leu	Thr	Ser	Asn	Glu	Ser	Gly	Arg	Leu	Met	Asp	Phe	Leu	Lys	Asp	Val	
					160					165					170	
atg	gag	tcc	atg	aac	aag	gag	gaa	atg	gaa	ata	aca	aca	cac	ttc	caa	579
Met	Glu	Ser	Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	
				175						180					185	
cgg	aag	aga	aga	gta	aga	gac	aac	atg	aca	aag	aga	atg	ata	aca	cag	627
Arg	Lys	Arg	Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Arg	Met	Ile	Thr	Gln	
				190				195					200			
aga	acc	ata	ggg	aag	aaa	aaa	caa	cga	tta	agc	aga	aag	agc	tat	cta	675
Arg	Thr	Ile	Gly	Lys	Lys	Lys	Gln	Arg	Leu	Ser	Arg	Lys	Ser	Tyr	Leu	
		205					210					215				
atc	aga	aca	tta	acc	cta	aac	aca	atg	acc	aag	gac	gct	gaa	aga	ggg	723
Ile	Arg	Thr	Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	
		220				225					230					
aaa	ttg	aaa	cga	cga	gca	atc	gct	acc	cca	ggg	atg	cag	ata	aga	gga	771
Lys	Leu	Lys	Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	
					240					245					250	
ttt	gta	tat	ttt	gtt	gaa	aca	cta	gct	cga	aga	ata	tgt	gaa	aag	ctt	819
Phe	Val	Tyr	Phe	Val	Glu	Thr	Leu	Ala	Arg	Arg	Ile	Cys	Glu	Lys	Leu	
				255					260						265	
gaa	caa	tca	gga	ttg	cca	ggt	ggc	ggt	aat	gag	aaa	aag	gcc	aaa	ctg	867
Glu	Gln	Ser	Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	
			270					275					280			
gct	aat	gtc	gtc	aga	aaa	atg	atg	act	aat	tcc	caa	gac	act	gaa	ctc	915
Ala	Asn	Val	Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	
		285					290					295				
tcc	ttc	acc	atc	act	ggg	gac	aat	acc	aaa	tgg	aat	gaa	aat	cag	aac	963
Ser	Phe	Thr	Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	
		300				305					310					
cca	cgc	ata	ttc	ctg	gca	atg	atc	aca	tac	ata	act	aga	aat	cag	cca	1011
Pro	Arg	Ile	Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	
					320					325					330	
gaa	tgg	ttc	aga	aat	gtt	cta	agc	att	gca	ccg	att	atg	ttc	tca	aat	1059
Glu	Trp	Phe	Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	
				335					340						345	
aaa	atg	gca	aga	ctg	ggg	aaa	gga	tat	atg	ttt	gaa	agc	aaa	agt	atg	1107
Lys	Met	Ala	Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	
				350				355						360		
aaa	ttg	aga	act	caa	ata	cca	gca	gaa	atg	cta	gca	agc	att	gac	cta	1155
Lys	Leu	Arg	Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	
			365				370					375				
aaa	tat	ttc	aat	gat	tca	aca	aaa	aag	aaa	att	gaa	aag	ata	cga	cca	1203
Lys	Tyr	Phe	Asn	Asp	Ser	Thr	Lys	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	
		380				385					390					
ctc	ctg	ggt	gac	ggg	act	gct	tca	ctg	agt	cct	ggc	atg	atg	atg	gga	1251
Leu	Leu	Val	Asp	Gly	Thr	Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	
				400						405					410	
atg	ttc	aac	atg	ttg	agc	act	gtg	ctg	ggt	gta	tcc	ata	tta	aac	ctg	1299
Met	Phe	Asn	Met	Leu	Ser	Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	
				415					420						425	
ggc	cag	agg	aaa	tat	aca	aag	acc	aca	tac	tgg	tgg	gat	ggt	ctg	caa	1347

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Gly	Gln	Arg	Lys	Tyr	Thr	Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	
			430					435					440			
tca	tcc	gat	gac	ttt	gct	ttg	ata	gtg	aat	gcg	cct	aat	cat	gaa	gga	1395
Ser	Ser	Asp	Asp	Phe	Ala	Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	
		445				450			455							
ata	caa	gct	gga	gta	gac	aga	ttc	tat	aga	act	tgc	aaa	ctg	gtc	ggg	1443
Ile	Gln	Ala	Gly	Val	Asp	Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Val	Gly	
	460					465					470					
atc	aac	atg	agc	aaa	aag	aag	tcc	tac	ata	aat	aga	act	gga	aca	ttc	1491
Ile	Asn	Met	Ser	Lys	Lys	Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	Phe	
475					480					485					490	
gaa	ttc	aca	agc	ttt	ttc	tac	cgg	tat	ggt	ttt	gta	gcc	aat	ttc	agc	1539
Glu	Phe	Thr	Ser	Phe	Phe	Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	
				495					500					505		
atg	gaa	cta	ccc	agt	ttt	ggg	ggt	tcc	gga	ata	aat	gaa	tct	gca	gac	1587
Met	Glu	Leu	Pro	Ser	Phe	Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	
			510					515					520			
atg	agc	att	gga	gtg	aca	gtc	atc	aaa	aac	aac	atg	ata	aat	aat	gat	1635
Met	Ser	Ile	Gly	Val	Thr	Val	Ile	Lys	Asn	Asn	Met	Ile	Asn	Asn	Asp	
			525					530					535			
ctc	ggt	cct	gcc	acg	gca	caa	atg	gaa	ctc	caa	ctc	ttc	att	aag	gat	1683
Leu	Gly	Pro	Ala	Thr	Ala	Gln	Met	Xaa	Leu	Gln	Leu	Phe	Ile	Lys	Asp	
	540					545						550				
tat	cgg	tac	aca	tac	cgg	tgc	cat	aga	ggt	gat	acc	cag	ata	caa	acc	1731
Tyr	Arg	Tyr	Thr	Tyr	Arg	Cys	His	Arg	Gly	Asp	Thr	Gln	Ile	Gln	Thr	
555					560					565					570	
aga	aga	tct	ttt	gag	ttg	aag	aaa	ctg	tgg	gaa	cag	act	cga	tca	aag	1779
Arg	Arg	Ser	Phe	Glu	Leu	Lys	Lys	Leu	Trp	Glu	Gln	Thr	Arg	Ser	Lys	
				575					580					585		
act	ggt	cta	ctg	gta	tca	gat	ggg	ggt	cca	aac	cta	tat	aac	atc	aga	1827
Thr	Gly	Leu	Leu	Val	Ser	Asp	Gly	Gly	Pro	Asn	Leu	Tyr	Asn	Ile	Arg	
			590					595					600			
aac	cta	cac	atc	ccg	gaa	gtc	tgt	tta	aaa	tgg	gag	cta	atg	gat	gaa	1875
Asn	Leu	His	Ile	Pro	Glu	Val	Cys	Leu	Lys	Trp	Glu	Leu	Met	Asp	Glu	
		605						610					615			
gat	tat	aag	ggg	agg	cta	tgc	aat	cca	ttg	aat	cct	ttc	ggt	agt	cac	1923
Asp	Tyr	Lys	Gly	Arg	Leu	Cys	Asn	Pro	Leu	Asn	Pro	Phe	Val	Ser	His	
	620					625						630				
aaa	gaa	att	gaa	tca	gtc	aac	agt	gca	gta	gta	atg	cct	gcg	cat	ggc	1971
Lys	Glu	Ile	Glu	Ser	Val	Asn	Ser	Ala	Val	Val	Met	Pro	Ala	His	Gly	
	635					640					645				650	
cct	gcc	aaa	agc	atg	gag	tat	gat	gct	ggt	gca	aca	aca	cat	tct	tgg	2019
Pro	Ala	Lys	Ser	Met	Glu	Tyr	Asp	Ala	Val	Ala	Thr	Thr	His	Ser	Trp	
				655					660					665		
atc	ccc	aag	agg	aac	cgg	tcc	ata	ttg	aac	aca	agc	caa	agg	gga	ata	2067
Ile	Pro	Lys	Arg	Asn	Arg	Ser	Ile	Leu	Asn	Thr	Ser	Gln	Arg	Gly	Ile	
				670					675					680		
cta	gaa	gat	gag	cag	atg	tat	cag	aaa	tgc	tgc	aac	ctg	ttt	gaa	aaa	2115
Leu	Glu	Asp	Glu	Gln	Met	Tyr	Gln	Lys	Cys	Cys	Asn	Leu	Phe	Glu	Lys	
			685					690					695			
ttc	ttc	ccc	agc	agc	tca	tac	aga	aga	cca	gtc	gga	att	tct	agt	atg	2163
Phe	Phe	Pro	Ser	Ser	Ser	Tyr	Arg	Arg	Pro	Val	Gly	Ile	Ser	Ser	Met	
		700						705								
ggt	gag	gcc	atg	gta	tcc	agg	gcc	cgc	att	gat	gca	cga	att	gac	ttc	2211
Val	Glu	Ala	Met	Val	Ser	Arg	Ala	Arg	Ile	Asp	Ala	Arg	Ile	Asp	Phe	
					715				720			725			730	
gaa	tct	gga	cgg	ata	aag	aag	gat	gag	ttc	gct	gag	atc	atg	aag	atc	2259
Glu	Ser	Gly	Arg	Ile	Lys	Lys	Asp	Glu	Phe	Ala	Glu	Ile	Met	Lys	Ile	
				735						740					745	
tgt	tcc	acc	att	gaa	gag	ctc	aga	cgg	caa	aaa	tagtgaa					2299

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Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys  
750 755

<210> SEQ ID NO 14  
<211> LENGTH: 757  
<212> TYPE: PRT  
<213> ORGANISM: Influenza A virus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (547)..(547)  
<223> OTHER INFORMATION: The 'Xaa' at location 547 stands for Ala, or Val.

<400> SEQUENCE: 14

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn  
1 5 10 15  
Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His  
20 25 30  
Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln  
35 40 45  
Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Ile Gly Ala Pro  
50 55 60  
Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser  
65 70 75 80  
Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu  
85 90 95  
Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu  
100 105 110  
Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr  
115 120 125  
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala  
130 135 140  
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ser Asn Glu Ser  
145 150 155 160  
Gly Arg Leu Met Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys  
165 170 175  
Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg  
180 185 190  
Asp Asn Met Thr Lys Arg Met Ile Thr Gln Arg Thr Ile Gly Lys Lys  
195 200 205  
Lys Gln Arg Leu Ser Arg Lys Ser Tyr Leu Ile Arg Thr Leu Thr Leu  
210 215 220  
Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala  
225 230 235 240  
Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu  
245 250 255  
Thr Leu Ala Arg Arg Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro  
260 265 270  
Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys  
275 280 285  
Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly  
290 295 300  
Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Ile Phe Leu Ala  
305 310 315 320  
Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val  
325 330 335  
Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly



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<210> SEQ ID NO 15
<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Influenza A virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (42)..(2318)

<400> SEQUENCE: 15

tattggtctc agggagcgaa agcagggtcaa atatattcaa t atg gag aga ata aaa      56
                                     Met Glu Arg Ile Lys
                                     1           5

gaa ctg aga gat ctg atg tta caa tcc cgc acc cgc gag ata cta aca      104
Glu Leu Arg Asp Leu Met Leu Gln Ser Arg Thr Arg Glu Ile Leu Thr
                10           15           20

aaa act act gtg gac cac atg gcc ata atc aag aaa tac aca tca gga      152
Lys Thr Thr Val Asp His Met Ala Ile Ile Lys Lys Tyr Thr Ser Gly
                25           30           35

aga caa gag aag aac cct gca ctt agg atg aaa tgg atg atg gca atg      200
Arg Gln Glu Lys Asn Pro Ala Leu Arg Met Lys Trp Met Met Ala Met
                40           45           50

aaa tac cca att aca gca gat aag agg ata atg gag atg att cct gag      248
Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Met Glu Met Ile Pro Glu
                55           60           65

aga aat gaa cag gga caa acc ctt tgg agc aaa acg aac gat gct ggc      296
Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys Thr Asn Asp Ala Gly
                70           75           80           85

tca gac cgc gta atg gta tca cct ctg gca gtg aca tgg tgg aat agg      344
Ser Asp Arg Val Met Val Ser Pro Leu Ala Val Thr Trp Trp Asn Arg
                90           95           100

aat gga cca aca acg aac aca att cat tat ccg aaa gtc tac aaa act      392
Asn Gly Pro Thr Thr Asn Thr Ile His Tyr Pro Lys Val Tyr Lys Thr
                105           110           115

tat ttt gaa aag gtt gaa aga ttg aaa cac gga acc ttt ggc ccc gtt      440
Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly Thr Phe Gly Pro Val
                120           125           130

cat ttt agg aat caa gtc aag ata aga cga aga gtt gat gta aac cct      488
His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg Val Asp Val Asn Pro
                135           140           145

ggt cac gcg gac ctc agt gct aaa gaa gca caa gat gtg atc atg gaa      536
Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln Asp Val Ile Met Glu
                150           155           160           165

gtt gtt ttc cca aat gaa gtg gga gcc aga att cta aca tca gaa tca      584
Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile Leu Thr Ser Glu Ser
                170           175           180

caa cta aca ata acc aaa gag aaa aag gaa gaa ctt cag gac tgc aaa      632
Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu Leu Gln Asp Cys Lys
                185           190           195

att gct ccc ttg atg gta gca tac atg cta gaa aga gag ttg gtc cga      680
Ile Ala Pro Leu Met Val Ala Tyr Met Leu Glu Arg Glu Leu Val Arg
                200           205           210

aaa aca agg ttc ctc cca gta gta ggc gga aca agc agt gta tac att      728
Lys Thr Arg Phe Leu Pro Val Val Gly Gly Thr Ser Ser Val Tyr Ile
                215           220           225

gaa gtg ttg cat ctg act cag gga aca tgc tgg gag caa atg tac acc      776
Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp Glu Gln Met Tyr Thr
                230           235           240           245

cca gga gga gaa gtt aga aac gat gat att gat caa agt tta att att      824
Pro Gly Gly Glu Val Arg Asn Asp Asp Ile Asp Gln Ser Leu Ile Ile
                250           255           260

gca gcc cgg aac ata gtg aga aga gca aca gta tca gca gat cca cta      872

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Ala	Ala	Arg	Asn	Ile	Val	Arg	Arg	Ala	Thr	Val	Ser	Ala	Asp	Pro	Leu	
			265					270					275			
gca	tcc	cta	ctg	gaa	atg	tgc	cac	agt	aca	cag	att	ggt	gga	aca	agg	920
Ala	Ser	Leu	Leu	Glu	Met	Cys	His	Ser	Thr	Gln	Ile	Gly	Gly	Thr	Arg	
		280					285					290				
atg	gta	gac	atc	ctt	aag	cag	aac	cca	aca	gag	gaa	caa	gct	gtg	gat	968
Met	Val	Asp	Ile	Leu	Lys	Gln	Asn	Pro	Thr	Glu	Glu	Gln	Ala	Val	Asp	
	295					300						305				
ata	tgc	aaa	gca	gca	atg	gga	ttg	aga	att	agc	tca	tca	ttc	agc	ttt	1016
Ile	Cys	Lys	Ala	Ala	Met	Gly	Leu	Arg	Ile	Ser	Ser	Ser	Phe	Ser	Phe	
	310				315					320					325	
ggt	gga	ttc	acc	ttc	aaa	agg	aca	agt	gga	tca	tca	gtc	aag	aga	gaa	1064
Gly	Gly	Phe	Thr	Phe	Lys	Arg	Thr	Ser	Gly	Ser	Ser	Val	Lys	Arg	Glu	
				330						335					340	
gaa	gaa	atg	ctt	acg	ggc	aac	ctt	caa	aca	ttg	aaa	ata	aga	gtg	cat	1112
Glu	Glu	Met	Leu	Thr	Gly	Asn	Leu	Gln	Thr	Leu	Lys	Ile	Arg	Val	His	
			345					350					355			
gag	ggc	tat	gaa	gaa	ttc	aca	atg	gtc	gga	aga	aga	gca	aca	gcc	att	1160
Glu	Gly	Tyr	Glu	Glu	Phe	Thr	Met	Val	Gly	Arg	Arg	Ala	Thr	Ala	Ile	
		360					365					370				
atc	aga	aag	gca	acc	aga	aga	ttg	att	caa	ttg	ata	gta	agt	ggg	aga	1208
Ile	Arg	Lys	Ala	Thr	Arg	Arg	Leu	Ile	Gln	Leu	Ile	Val	Ser	Gly	Arg	
		375					380					385				
gat	gaa	caa	tca	att	gct	gaa	gca	ata	att	gta	gcc	atg	gtg	ttt	tcg	1256
Asp	Glu	Gln	Ser	Ile	Ala	Glu	Ala	Ile	Ile	Val	Ala	Met	Val	Phe	Ser	
					395					400					405	
caa	gaa	gat	tgc	atg	ata	aaa	gca	ggt	cga	ggc	gat	ttg	aac	ttt	gtt	1304
Gln	Glu	Asp	Cys	Met	Ile	Lys	Ala	Val	Arg	Gly	Asp	Leu	Asn	Phe	Val	
				410					415					420		
aat	aga	gca	aat	cag	cgt	ttg	aac	ccc	atg	cat	caa	ctc	ttg	agg	cat	1352
Asn	Arg	Ala	Asn	Gln	Arg	Leu	Asn	Pro	Met	His	Gln	Leu	Leu	Arg	His	
			425					430					435			
ttc	caa	aaa	gat	gca	aaa	gtg	ctt	ttc	caa	aat	tgg	gga	att	gaa	ccc	1400
Phe	Gln	Lys	Asp	Ala	Lys	Val	Leu	Phe	Gln	Asn	Trp	Gly	Ile	Glu	Pro	
		440					445					450				
atc	gac	aat	gta	atg	ggg	atg	att	gga	ata	ttg	cct	gac	atg	acc	cca	1448
Ile	Asp	Asn	Val	Met	Gly	Met	Ile	Gly	Ile	Leu	Pro	Asp	Met	Thr	Pro	
		455				460					465					
agc	acc	gag	atg	tca	ttg	aga	gga	gtg	aga	gtc	agc	aaa	atg	gga	gtg	1496
Ser	Thr	Glu	Met	Ser	Leu	Arg	Gly	Val	Arg	Val	Ser	Lys	Met	Gly	Val	
					475					480					485	
gat	gag	tac	tcc	agc	act	gag	aga	gtg	gtg	gtg	agc	att	gac	cgt	ttt	1544
Asp	Glu	Tyr	Ser	Ser	Thr	Glu	Arg	Val	Val	Val	Ser	Ile	Asp	Arg	Phe	
				490						495					500	
tta	aga	ggt	cgg	gat	caa	agg	gga	aac	ata	cta	ctg	tcc	cct	gaa	gaa	1592
Leu	Arg	Val	Arg	Asp	Gln	Arg	Gly	Asn	Ile	Leu	Leu	Ser	Pro	Glu	Glu	
			505					510								
gtc	agt	gaa	aca	caa	gga	acg	gaa	aag	ctg	aca	ata	att	tat	tcg	tca	1640
Val	Ser	Glu	Thr	Gln	Gly	Thr	Glu	Lys	Leu	Thr	Ile	Ile	Tyr	Ser	Ser	
			520				525					530				
tca	atg	atg	tgg	gag	att	aat	ggt	ccc	gaa	tca	gtg	ttg	gtc	aat	act	1688
Ser	Met	Met	Trp	Glu	Ile	Asn	Gly	Pro	Glu	Ser	Val	Leu	Val	Asn	Thr	
			535			540						545				
tat	caa	tgg	atc	atc	aga	aac	tgg	gaa	att	gta	aaa	att	cag	tgg	tca	1736
Tyr	Gln	Trp	Ile	Ile	Arg	Asn	Trp	Glu	Ile	Val	Lys	Ile	Gln	Trp	Ser	
					555					560					565	
cag	gac	ccc	aca	atg	tta	tac	aat	aag	ata	gaa	ttt	gaa	cca	ttc	caa	1784
Gln	Asp	Pro	Thr	Met	Leu	Tyr	Asn	Lys	Ile	Glu	Phe	Glu	Pro	Phe	Gln	
				570					575						580	
tcc	ctg	gtc	cct	agg	gcc	acc	aga	agc	caa	tac	agc	ggt	ttc	gta	aga	1832



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Ser Leu Val Pro Arg Ala Thr Arg Ser Gln Tyr Ser Gly Phe Val Arg  
585 590 595

acc ctg ttt cag caa atg cga gat gta ctt gga aca ttt gat act gct 1880  
Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly Thr Phe Asp Thr Ala  
600 605 610

caa ata ata aaa ctc ctc cct ttt gcc gct gct cct ccg gaa cag agt 1928  
Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala Pro Pro Glu Gln Ser  
615 620 625

agg atg cag ttc tct tct ttg act gtt aat gta aga ggt tcg gga atg 1976  
Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val Arg Gly Ser Gly Met  
630 635 640 645

agg ata ctt gta aga ggc aat tcc ccg gtg ttc aac tac aat aaa gtc 2024  
Arg Ile Leu Val Arg Gly Asn Ser Pro Val Phe Asn Tyr Asn Lys Val  
650 655 660

act aaa agg ctc aca gtc ctc gga aag gat gca ggt gcg ctt act gag 2072  
Thr Lys Arg Leu Thr Val Leu Gly Lys Asp Ala Gly Ala Leu Thr Glu  
665 670 675

gac cca gat gaa ggt acg gct gga gta gaa tct gct gtt cta aga ggg 2120  
Asp Pro Asp Glu Gly Thr Ala Gly Val Glu Ser Ala Val Leu Arg Gly  
680 685 690

ttt ctc att tta ggt aaa gaa aac aag aga tat ggc cca gca cta agc 2168  
Phe Leu Ile Leu Gly Lys Glu Asn Lys Arg Tyr Gly Pro Ala Leu Ser  
695 700 705

atc aat gaa ctt agc aaa ctt gca aaa ggg gag aaa gcc aat gta cta 2216  
Ile Asn Glu Leu Ser Lys Leu Ala Lys Gly Glu Lys Ala Asn Val Leu  
710 715 720 725

att ggg caa ggg gac gta gtg ttg gta atg aaa cgg aaa cgt gac tct 2264  
Ile Gly Gln Gly Asp Val Val Leu Val Met Lys Arg Lys Arg Asp Ser  
730 735 740

agc ata ctt act gac agc cag aca gcg acc aaa agg att cgg atg gcc 2312  
Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys Arg Ile Arg Met Ala  
745 750 755

atc aat tagtggtgaa ttgtttaaaa acgaccttgt ttctactaat acgagaccat at 2370  
Ile Asn

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 759

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Influenza A virus

&lt;400&gt; SEQUENCE: 16

Met Glu Arg Ile Lys Glu Leu Arg Asp Leu Met Leu Gln Ser Arg Thr  
1 5 10 15

Arg Glu Ile Leu Thr Lys Thr Thr Val Asp His Met Ala Ile Ile Lys  
20 25 30

Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ala Leu Arg Met Lys  
35 40 45

Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Met  
50 55 60

Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys  
65 70 75 80

Thr Asn Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val  
85 90 95

Thr Trp Trp Asn Arg Asn Gly Pro Thr Thr Asn Thr Ile His Tyr Pro  
100 105 110

Lys Val Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly  
115 120 125

Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg  
130 135 140

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Val	Asp	Val	Asn	Pro	Gly	His	Ala	Asp	Leu	Ser	Ala	Lys	Glu	Ala	Gln
145					150					155					160
Asp	Val	Ile	Met	Glu	Val	Val	Phe	Pro	Asn	Glu	Val	Gly	Ala	Arg	Ile
				165					170					175	
Leu	Thr	Ser	Glu	Ser	Gln	Leu	Thr	Ile	Thr	Lys	Glu	Lys	Lys	Glu	Glu
			180					185						190	
Leu	Gln	Asp	Cys	Lys	Ile	Ala	Pro	Leu	Met	Val	Ala	Tyr	Met	Leu	Glu
		195					200					205			
Arg	Glu	Leu	Val	Arg	Lys	Thr	Arg	Phe	Leu	Pro	Val	Val	Gly	Gly	Thr
	210					215					220				
Ser	Ser	Val	Tyr	Ile	Glu	Val	Leu	His	Leu	Thr	Gln	Gly	Thr	Cys	Trp
225					230					235					240
Glu	Gln	Met	Tyr	Thr	Pro	Gly	Gly	Glu	Val	Arg	Asn	Asp	Asp	Ile	Asp
				245					250					255	
Gln	Ser	Leu	Ile	Ile	Ala	Ala	Arg	Asn	Ile	Val	Arg	Arg	Ala	Thr	Val
			260					265					270		
Ser	Ala	Asp	Pro	Leu	Ala	Ser	Leu	Leu	Glu	Met	Cys	His	Ser	Thr	Gln
		275					280					285			
Ile	Gly	Gly	Thr	Arg	Met	Val	Asp	Ile	Leu	Lys	Gln	Asn	Pro	Thr	Glu
	290					295					300				
Glu	Gln	Ala	Val	Asp	Ile	Cys	Lys	Ala	Ala	Met	Gly	Leu	Arg	Ile	Ser
305					310					315					320
Ser	Ser	Phe	Ser	Phe	Gly	Gly	Phe	Thr	Phe	Lys	Arg	Thr	Ser	Gly	Ser
				325					330					335	
Ser	Val	Lys	Arg	Glu	Glu	Glu	Met	Leu	Thr	Gly	Asn	Leu	Gln	Thr	Leu
			340					345					350		
Lys	Ile	Arg	Val	His	Glu	Gly	Tyr	Glu	Glu	Phe	Thr	Met	Val	Gly	Arg
		355					360					365			
Arg	Ala	Thr	Ala	Ile	Ile	Arg	Lys	Ala	Thr	Arg	Arg	Leu	Ile	Gln	Leu
		370				375					380				
Ile	Val	Ser	Gly	Arg	Asp	Glu	Gln	Ser	Ile	Ala	Glu	Ala	Ile	Ile	Val
385					390					395					400
Ala	Met	Val	Phe	Ser	Gln	Glu	Asp	Cys	Met	Ile	Lys	Ala	Val	Arg	Gly
				405					410					415	
Asp	Leu	Asn	Phe	Val	Asn	Arg	Ala	Asn	Gln	Arg	Leu	Asn	Pro	Met	His
			420					425					430		
Gln	Leu	Leu	Arg	His	Phe	Gln	Lys	Asp	Ala	Lys	Val	Leu	Phe	Gln	Asn
		435					440					445			
Trp	Gly	Ile	Glu	Pro	Ile	Asp	Asn	Val	Met	Gly	Met	Ile	Gly	Ile	Leu
	450					455					460				
Pro	Asp	Met	Thr	Pro	Ser	Thr	Glu	Met	Ser	Leu	Arg	Gly	Val	Arg	Val
465					470					475					480
Ser	Lys	Met	Gly	Val	Asp	Glu	Tyr	Ser	Ser	Thr	Glu	Arg	Val	Val	Val
				485					490					495	
Ser	Ile	Asp	Arg	Phe	Leu	Arg	Val	Arg	Asp	Gln	Arg	Gly	Asn	Ile	Leu
		500						505					510		
Leu	Ser	Pro	Glu	Glu	Val	Ser	Glu	Thr	Gln	Gly	Thr	Glu	Lys	Leu	Thr
		515					520					525			
Ile	Ile	Tyr	Ser	Ser	Ser	Met	Met	Trp	Glu	Ile	Asn	Gly	Pro	Glu	Ser
	530					535					540				
Val	Leu	Val	Asn	Thr	Tyr	Gln	Trp	Ile	Ile	Arg	Asn	Trp	Glu	Ile	Val
545					550					555					560
Lys	Ile	Gln	Trp	Ser	Gln	Asp	Pro	Thr	Met	Leu	Tyr	Asn	Lys	Ile	Glu

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565	570	575
Phe Glu Pro Phe Gln Ser Leu Val Pro Arg Ala Thr Arg Ser Gln Tyr 580 585 590		
Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly 595 600 605		
Thr Phe Asp Thr Ala Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala 610 615 620		
Pro Pro Glu Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val 625 630 635 640		
Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Val Phe 645 650 655		
Asn Tyr Asn Lys Val Thr Lys Arg Leu Thr Val Leu Gly Lys Asp Ala 660 665 670		
Gly Ala Leu Thr Glu Asp Pro Asp Glu Gly Thr Ala Gly Val Glu Ser 675 680 685		
Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asn Lys Arg Tyr 690 695 700		
Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Lys Leu Ala Lys Gly Glu 705 710 715 720		
Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys 725 730 735		
Arg Lys Arg Asp Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys 740 745 750		
Arg Ile Arg Met Ala Ile Asn 755		

What is claimed is:

1. An isolated or purified *Hemagglutinin* HA, which (i) has the amino acid sequence of SEQ ID NO: 4 or (ii) is derived from an influenza virus and which has an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4, [with the proviso that the amino acid sequence is identical to that of SEQ ID NO: 4 at amino acid positions 94 and 233] and the isolated or purified HA has a leucine at position 94 and a glutamic acid at position 233, according to the numbering of SEQ ID NO: 4.

2. A composition comprising the isolated or purified HA of claim 1 in an amount sufficient to induce an immune response in an animal and a biologically acceptable carrier.

3. A method of inducing an immune response to a canine influenza H3 virus in an animal, which method comprises administering to the animal the composition of claim 2, [whereupon] where upon an immune response to canine influenza H3 virus is induced in the animal.

4. [An] A vector comprising the isolated or purified nucleic acid encoding the HA of claim 1, optionally as part of a vector].

5. [The isolated or purified nucleic acid] The vector of claim 4, wherein the nucleic acid encoding the HA comprises the nucleotide sequence of SEQ ID NO: 3.

6. A composition comprising the [isolated or purified nucleic acid] vector of claim 4, which expresses HA in an amount sufficient to induce an immune response in an animal, and a biologically acceptable carrier.

7. An isolated or purified HA peptide fragment comprising a contiguous nine amino acid fragment of [SEQ ID NO: 4, or a contiguous nine amino acid fragment of] an amino acid sequence that is greater than 99% identical to SEQ ID NO: 4,

35 that either includes the Leu at position 94 of SEQ ID NO: 4 or the Glu at position 233 of SEQ ID NO: 4, according to the numbering of SEQ ID NO: 4.

8. A composition comprising the isolated or purified HA peptide fragment of claim 7 in an amount sufficient to induce an immune response in an animal and a biologically acceptable carrier.

9. A method of inducing an immune response to a canine influenza H3 virus in an animal, which method comprises administering to the animal the composition of claim 8, [whereupon] where upon an immune response to canine influenza H3 virus is induced in the animal.

10. [An] A vector comprising an isolated or purified nucleic acid encoding the HA peptide fragment of claim 7, optionally as part of a vector].

50 11. A composition comprising the [isolated or purified nucleic acid] vector of claim 10, which expresses the HA peptide in an amount sufficient to induce an immune response in an animal, and a biologically acceptable carrier.

12. An isolated polypeptide that is 97% or greater identical to SEQ ID NO: 4 and has a leucine at position 94 and a glutamic acid at position 233, according to the numbering of SEQ ID NO: 4 and a biologically acceptable carrier.

13. An isolated DNA which encodes a polypeptide that is 97% or greater identical to SEQ ID NO: 4 and has a leucine at position 94 and a glutamic acid at position 233 according to the numbering of SEQ ID NO: 4.

14. An isolated polypeptide comprising a contiguous nine amino acid sequence that is greater than 97% identical to a sequence fragment of SEQ ID NO: 4, wherein said sequence fragment comprises either the Leu at position 94 or the Glu at position 233 of SEQ ID NO: 4, according to the numbering of SEQ ID NO: 4.

15. A method of inducing an immune response to a canine influenza H3 virus in an animal, which method comprises administering to the animal the composition of claim 4 or claim 12, where upon an immune response to a canine influenza H3 virus is induced in the animal.

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