SEQUENCE LISTING

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<120> Influenza Virus Vaccine Composition and Methods of Use

<130> 1530.0640002/EJH/J-H

<160> 112

<170> PatentIn version 3.3

<210> 1
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<212> DNA
<213> Influenza A virus

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<210> 2
<211> 498
<212> PRT
<213> Influenza A virus

<400> 2

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Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
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Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
35 40 45

Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu 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 80

Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile
85 90 95

Tyr Arg Arg Val Asn Gly Lys Trp Met Arg Glu Leu Ile Leu Tyr Asp
100 105 110

Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
115 120 125

Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
130 135 140

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Asp Ala Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
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 Val Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
        195                 200                 205

Gly Glu Asn Gly Arg Lys Thr Arg Ile Ala Tyr Glu Arg Met Cys Asn
    210                 215                 220

Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Lys Ala Met Met Asp
225                 230                 235                 240

Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Phe Glu Asp Leu
                245                 250                 255

Thr 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 Pro Ala Val Ala Ser Gly
        275                 280                 285

Tyr Asp Phe Glu Arg Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
    290                 295                 300

Arg Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305                 310                 315                 320

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 Ser Phe Ile Lys Gly Thr Lys Val
            340                 345                 350

Leu Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
        355                 360                 365

Glu Asn Met Glu Thr Met Glu Ser Ser Thr Leu Glu Leu Arg Ser Arg
    370                 375                 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
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385 390 395 400

Ala Ser Ala Gly Gln Ile Ser Ile Gln Pro Thr Phe Ser Val Gln Arg
405 410 415

Asn Leu Pro Phe Asp Arg Thr Thr Val Met Ala Ala Phe Ser 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 Ser Ala Arg Pro Glu Asp Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460

Glu Leu Ser Asp Glu Lys Ala Ala Ser Pro Ile Val Pro Ser Phe Asp
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Asp Asn

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<212> DNA
<213> Influenza A virus

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tgcagggaag aacactgatc ttgaggttct catggaatgg ctaaagacaa gaccaatcct 180

gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg 240

aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa 300

catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc 360

caaagaaatc tcactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420

caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga 480

acagattgct gactcccagc atcggtctca taggcaaatg gtgacaacaa ccaatccact 540

aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat 600

ggctggatcg agtgagcaag cagcagaggc catggaggtt gctagtcagg ctagacaaat 660

ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgctggtc tgaaaaatga 720

tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa 780

gtgatcctct cgctattgcc gcaaatatca ttgggatctt gcacttgaca ttgtggattc 840

ttgatcgtct ttttttcaaa tgcatttacc gtcgctttaa atacggactg aaaggagggc 900

cttctacgga aggagtgcca aagtctatga gggaagaata tcgaaaggaa cagcagagtg 960

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<210> 4
<211> 252
<212> PRT
<213> Influenza A virus

<400> 4

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20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Val 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 Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Lys Ala
85 90 95

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

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

Gly Leu Ile Tyr Asn Arg Met Gly Ala 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

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                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 Gln
        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 Asn 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


<210>  5
<211>  97
<212>  PRT
<213>  Influenza A virus

<400>  5

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1               5                   10                  15

Cys Arg Cys Asn Gly Ser Ser Asp Pro Leu Ala Ile Ala Ala Asn Ile
            20                  25                  30

Ile Gly Ile Leu His Leu Thr Leu Trp Ile Leu Asp Arg Leu Phe Phe
        35                  40                  45

Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
    50                  55                  60

Thr Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65                  70                  75                  80

Gln Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
                85                  90                  95

Glu


<210>  6
<211>  1566
<212>  DNA
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<213> Artificial sequence

<220>
<223> eM2NP fusion

<400> 6
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ggagaacgcc agaatgccac tgaaatcaga gcatccgtcg gaaaaatgat tggtggaatt 180

ggacgattct acatccaaat gtgcaccgaa ctcaaactca gtgattatga gggacggttg 240

atccaaaaca gcttaacaat agagagaatg gtgctctctg cttttgacga aaggagaaat 300

aaataccttg aagaacatcc cagtgcgggg aaagatccta agaaaactgg aggacctata 360

tacaggagag taaacggaaa gtggatgaga gaactcatcc tttatgacaa agaagaaata 420

aggcgaatct ggcgccaagc taataatggt gacgatgcaa cggctggtct gactcacatg 480

atgatctggc attccaattt gaatgatgca acttatcaga ggacaagagc tcttgttcgc 540

accggaatgg atcccaggat gtgctctctg atgcaaggtt caactctccc taggaggtct 600

ggagccgcag gtgctgcagt caaaggagtt ggaacaatgg tgatggaatt ggtcagaatg 660

atcaaacgtg ggatcaatga tcggaacttc tggaggggtg agaatggacg aaaaacaaga 720

attgcttatg aaagaatgtg caacattctc aaagggaaat ttcaaactgc tgcacaaaaa 780

gcaatgatgg atcaagtgag agagagccgg aacccaggga atgctgagtt cgaagatctc 840

acttttctag cacggtctgc actcatattg agagggtcgg ttgctcacaa gtcctgcctg 900

cctgcctgtg tgtatggacc tgccgtagcc agtgggtacg actttgaaag ggagggatac 960

tctctagtcg gaatagaccc tttcagactg cttcaaaaca gccaagtgta cagcctaatc 1020

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gcatttgaag atctaagagt attaagcttc atcaaaggga cgaaggtgct cccaagaggg 1140

aagctttcca ctagaggagt tcaaattgct tccaatgaaa atatggagac tatggaatca 1200

agtacacttg aactgagaag caggtactgg gccataagga ccagaagtgg aggaaacacc 1260

aatcaacaga gggcatctgc gggccaaatc agcatacaac ctacgttctc agtacagaga 1320

aatctccctt ttgacagaac aaccgttatg gcagcattca gtgggaatac agaggggaga 1380

acatctgaca tgaggaccga aatcataagg atgatggaaa gtgcaagacc agaagatgtg 1440

tctttccagg ggcggggagt cttcgagctc tcggacgaaa aggcagcgag cccgatcgtg 1500

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<210> 7
<211> 522
<212> PRT
<213> Artificial sequence

<220>
<223> eM2NP fusion

<400> 7

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            20                  25                  30

Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg Gln Asn Ala Thr Glu
        35                  40                  45

Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly Ile Gly Arg Phe Tyr
    50                  55                  60

Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp Tyr Glu Gly Arg Leu
65                  70                  75                  80

Ile Gln Asn Ser Leu Thr Ile Glu Arg Met Val Leu Ser Ala Phe Asp
                85                  90                  95

Glu Arg Arg Asn Lys Tyr Leu Glu Glu His Pro Ser Ala Gly Lys Asp
            100                 105                 110

Pro Lys Lys Thr Gly Gly Pro Ile Tyr Arg Arg Val Asn Gly Lys Trp
        115                 120                 125

Met Arg Glu Leu Ile Leu Tyr Asp Lys Glu Glu Ile Arg Arg Ile Trp
    130                 135                 140

Arg Gln Ala Asn Asn Gly Asp Asp Ala Thr Ala Gly Leu Thr His Met
145                 150                 155                 160

Met Ile Trp His Ser Asn Leu Asn Asp Ala Thr Tyr Gln Arg Thr Arg
                165                 170                 175

Ala Leu Val Arg Thr Gly Met Asp Pro Arg Met Cys Ser Leu Met Gln
            180                 185                 190

Gly Ser Thr Leu Pro Arg Arg Ser Gly Ala Ala Gly Ala Ala Val Lys
        195                 200                 205
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Gly Val Gly Thr Met Val Met Glu Leu Val Arg Met Ile Lys Arg Gly
    210                 215                 220

Ile Asn Asp Arg Asn Phe Trp Arg Gly Glu Asn Gly Arg Lys Thr Arg
225                 230                 235                 240

Ile Ala Tyr Glu Arg Met Cys Asn Ile Leu Lys Gly Lys Phe Gln Thr
                245                 250                 255

Ala Ala Gln Lys Ala Met Met Asp Gln Val Arg Glu Ser Arg Asn Pro
            260                 265                 270

Gly Asn Ala Glu Phe Glu Asp Leu Thr Phe Leu Ala Arg Ser Ala Leu
        275                 280                 285

Ile Leu Arg Gly Ser Val Ala His Lys Ser Cys Leu Pro Ala Cys Val
    290                 295                 300

Tyr Gly Pro Ala Val Ala Ser Gly Tyr Asp Phe Glu Arg Glu Gly Tyr
305                 310                 315                 320

Ser Leu Val Gly Ile Asp Pro Phe Arg Leu Leu Gln Asn Ser Gln Val
                325                 330                 335

Tyr Ser Leu Ile Arg Pro Asn Glu Asn Pro Ala His Lys Ser Gln Leu
            340                 345                 350

Val Trp Met Ala Cys His Ser Ala Ala Phe Glu Asp Leu Arg Val Leu
        355                 360                 365

Ser Phe Ile Lys Gly Thr Lys Val Leu Pro Arg Gly Lys Leu Ser Thr
    370                 375                 380

Arg Gly Val Gln Ile Ala Ser Asn Glu Asn Met Glu Thr Met Glu Ser
385                 390                 395                 400

Ser Thr Leu Glu Leu Arg Ser Arg Tyr Trp Ala Ile Arg Thr Arg Ser
                405                 410                 415

Gly Gly Asn Thr Asn Gln Gln Arg Ala Ser Ala Gly Gln Ile Ser Ile
            420                 425                 430

Gln Pro Thr Phe Ser Val Gln Arg Asn Leu Pro Phe Asp Arg Thr Thr
        435                 440                 445
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Val Met Ala Ala Phe Ser Gly Asn Thr Glu Gly Arg Thr Ser Asp Met
    450                 455                 460

Arg Thr Glu Ile Ile Arg Met Met Glu Ser Ala Arg Pro Glu Asp Val
465                 470                 475                 480

Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser Asp Glu Lys Ala Ala
                485                 490                 495

Ser Pro Ile Val Pro Ser Phe Asp Met Ser Asn Glu Gly Ser Tyr Phe
            500                 505                 510

Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn
        515                 520
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<210> 8
<211> 1566
<212> DNA
<213> Artificial sequence

<220>
<223> NPeM2 Fusion Construct

<400> 8

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atccaaatgt gcaccgaact caaactcagt gattatgagg gacggttgat ccaaaacagc    180

ttaacaatag agagaatggt gctctctgct tttgacgaaa ggagaaataa ataccttgaa    240

gaacatccca gtgcggggaa agatcctaag aaaactggag gacctatata caggagagta    300

aacggaaagt ggatgagaga actcatcctt tatgacaaag aagaaataag gcgaatctgg    360

cgccaagcta ataatggtga cgatgcaacg gctggtctga ctcacatgat gatctggcat    420

tccaatttga atgatgcaac ttatcagagg acaagagctc ttgttcgcac cggaatggat    480

cccaggatgt gctctctgat gcaaggttca actctcccta ggaggtctgg agccgcaggt    540

gctgcagtca aaggagttgg aacaatggtg atggaattgg tcagaatgat caaacgtggg    600

atcaatgatc ggaacttctg gaggggtgag aatggacgaa aaacaagaat tgcttatgaa    660

agaatgtgca acattctcaa agggaaattt caaactgctg cacaaaaagc aatgatggat    720

caagtgagag agagccggaa cccagggaat gctgagttcg aagatctcac ttttctagca    780

cggtctgcac tcatattgag agggtcggtt gctcacaagt cctgcctgcc tgcctgtgtg    840

tatggacctg ccgtagccag tgggtacgac tttgaaaggg agggatactc tctagtcgga    900

atagaccctt tcagactgct tcaaaacagc caagtgtaca gcctaatcag accaaatgag    960
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aatccagcac acaagagtca actggtgtgg atggcatgcc attctgccgc atttgaagat   1020

ctaagagtat taagcttcat caaagggacg aaggtgctcc caagagggaa gctttccact   1080

agaggagttc aaattgcttc caatgaaaat atggagacta tggaatcaag tacacttgaa   1140

ctgagaagca ggtactgggc cataaggacc agaagtggag gaaacaccaa tcaacagagg   1200

gcatctgcgg gccaaatcag catacaacct acgttctcag tacagagaaa tctccctttt   1260

gacagaacaa ccgttatggc agcattcagt gggaatacag aggggagaac atctgacatg   1320

aggaccgaaa tcataaggat gatggaaagt gcaagaccag aagatgtgtc tttccagggg   1380

cggggagtct tcgagctctc ggacgaaaag gcagcgagcc cgatcgtgcc ttcctttgac   1440

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<210> 9
<211> 522
<212> PRT
<213> Artificial sequence

<220>
<223> NPeM2 Fusion Construct

<400> 9

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Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp
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Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
            20                  25                  30

Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
        35                  40                  45

Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu 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                  80

Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile
                85                  90                  95

Tyr Arg Arg Val Asn Gly Lys Trp Met Arg Glu Leu Ile Leu Tyr Asp
            100                 105                 110
```

```
Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
        115                 120                 125

Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
    130                 135                 140

Asp Ala Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
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 Val Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
        195                 200                 205

Gly Glu Asn Gly Arg Lys Thr Arg Ile Ala Tyr Glu Arg Met Cys Asn
    210                 215                 220

Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Lys Ala Met Met Asp
225                 230                 235                 240

Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Phe Glu Asp Leu
                245                 250                 255

Thr 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 Pro Ala Val Ala Ser Gly
        275                 280                 285

Tyr Asp Phe Glu Arg Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
    290                 295                 300

Arg Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305                 310                 315                 320

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 Ser Phe Ile Lys Gly Thr Lys Val
            340                 345                 350

Leu Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
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```
        355                 360                 365

Glu Asn Met Glu Thr Met Glu Ser Ser Thr Leu Glu Leu Arg Ser Arg
    370                 375                 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385                 390                 395                 400

Ala Ser Ala Gly Gln Ile Ser Ile Gln Pro Thr Phe Ser Val Gln Arg
                405                 410                 415

Asn Leu Pro Phe Asp Arg Thr Thr Val Met Ala Ala Phe Ser 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 Ser Ala Arg Pro Glu Asp Val Ser Phe Gln Gly Arg Gly Val Phe
    450                 455                 460

Glu Leu Ser Asp Glu Lys Ala Ala Ser Pro Ile Val Pro Ser Phe Asp
465                 470                 475                 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
                485                 490                 495

Asp Asn Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu
            500                 505                 510

Trp Gly Cys Arg Cys Asn Gly Ser Ser Asp
        515                 520


<210>  10
<211>  6
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Linker Peptide

<400>  10

Gly Tyr Ala Thr Arg Ala
1               5


<210>  11
<211>  6
<212>  PRT
<213>  Artificial sequence
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<220>
<223> Linker Peptide

<400> 11

Phe Gln Met Gly Glu Thr
1 5

<210> 12
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Linker Peptide

<400> 12

Phe Asp Arg Val Lys His Leu Lys
1 5

<210> 13
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Linker Peptide

<400> 13

Gly Arg Asn Thr Asn Gly Val Ile Thr
1 5

<210> 14
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Linker Peptide

<400> 14

Val Asn Glu Lys Thr Ile Pro Asp His Asp
1 5 10

<210> 15
<211> 1683
<212> DNA
<213> Influenza B virus

<400> 15
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ccaagcaaca aacgaacccg aaatccatct ccagaaagga caaccacaag cagtgaaacc 180

gatatcggaa ggaaaatcca aaagaaacaa accccaacag agataaagaa gagcgtctac 240

aaaatggtgg taaaactggg tgaattctac aaccagatga tggtcaaagc tggacttaat 300

gatgacatgg aaaggaatct aattcaaaat gcacaagctg tggagagaat cctattggct 360

gcaactgatg acaagaaaac tgaataccaa aagaaaagga atgccagaga tgtcaaagaa 420

gggaaggaag aaatagacca caacaagaca ggaggcacct tttataagat ggtaagagat 480

gataaaacca tctacttcag ccctataaaa attacctttt taaaagaaga ggtgaaaaca 540

atgtacaaga ccaccatggg gagtgatggt ttcagtggac taaatcacat tatgattgga 600

cattcacaga tgaacgatgt ctgtttccaa agatcaaagg gactgaaaag ggttggactt 660

gacccttcat taatcagtac ttttgccgga agcacactac ccagaagatc aggtacaact 720

ggtgttgcaa tcaaaggagg tggaacttta gtggatgaag ccatccgatt tataggaaga 780

gcaatggcag acagagggct actgagagac atcaaggcca agacggccta tgaaaagatt 840

cttctgaatc tgaaaaacaa gtgctctgcg ccgcaacaaa aggctctagt tgatcaagtg 900

atcggaagta ggaacccagg gattgcagac atagaagacc taactctgct tgccagaagc 960

atggtagttg tcagaccctc tgtagcgagc aaagtggtgc ttcccataag catttatgct 1020

aaaatacctc aactaggatt caataccgaa gaatactcta tggttgggta tgaagccatg 1080

gctctttata atatggcaac acctgtttcc atattaagaa tgggagatga cgcaaaagat 1140

aaatctcaac tattcttcat gtcgtgcttc ggagctgcct atgaagatct aagagtgtta 1200

tctgcactaa cgggcaccga atttaagcct agatcagcac taaaatgcaa gggtttccat 1260

gtcccggcta aggagcaagt agaaggaatg ggggcagctc tgatgtccat caagcttcag 1320

ttctgggccc caatgaccag atctggaggg aatgaagtaa gtggagaagg agggtctggt 1380

caaataagtt gcagccctgt gtttgcagta gaaagaccta ttgctctaag caagcaagct 1440

gtaagaagaa tgctgtcaat gaacgttgaa ggacgtgatg cagatgtcaa aggaaatcta 1500

ctcaaaatga tgaatgattc aatggcaaag aaaaccagtg gaaatgcttt cattgggaag 1560

aaaatgtttc aaatatcaga caaaaacaaa gtcaatccca ttgagattcc aattaagcag 1620

accatcccca atttcttctt tgggagggac acagcagagg attatgatga cctcgattat 1680

taa 1683

<210> 16
<211> 560
<212> PRT
<213> Artificial sequence

<220>
<223> Influenza B Virus

<400> 16

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Met Ser Asn Met Asp Ile Asp Ser Ile Asn Thr Gly Thr Ile Asp Lys
1               5                  10                  15

Thr Pro Glu Glu Leu Thr Pro Gly Thr Ser Gly Ala Thr Arg Pro Ile
            20                  25                  30

Ile Lys Pro Ala Thr Leu Ala Pro Pro Ser Asn Lys Arg Thr Arg Asn
        35                  40                  45

Pro Ser Pro Glu Arg Thr Thr Thr Ser Ser Glu Thr Asp Ile Gly Arg
    50                  55                  60

Lys Ile Gln Lys Lys Gln Thr Pro Thr Glu Ile Lys Lys Ser Val Tyr
65                  70                  75                  80

Lys Met Val Val Lys Leu Gly Glu Phe Tyr Asn Gln Met Met Val Lys
                85                  90                  95

Ala Gly Leu Asn Asp Asp Met Glu Arg Asn Leu Ile Gln Asn Ala Gln
            100                 105                 110

Ala Val Glu Arg Ile Leu Leu Ala Ala Thr Asp Asp Lys Lys Thr Glu
        115                 120                 125

Tyr Gln Lys Lys Arg Asn Ala Arg Asp Val Lys Glu Gly Lys Glu Glu
    130                 135                 140

Ile Asp His Asn Lys Thr Gly Gly Thr Phe Tyr Lys Met Val Arg Asp
145                 150                 155                 160

Asp Lys Thr Ile Tyr Phe Ser Pro Ile Lys Ile Thr Phe Leu Lys Glu
                165                 170                 175

Glu Val Lys Thr Met Tyr Lys Thr Thr Met Gly Ser Asp Gly Phe Ser
            180                 185                 190

Gly Leu Asn His Ile Met Ile Gly His Ser Gln Met Asn Asp Val Cys
        195                 200                 205

Phe Gln Arg Ser Lys Gly Leu Lys Arg Val Gly Leu Asp Pro Ser Leu
    210                 215                 220
```

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Ile Ser Thr Phe Ala Gly Ser Thr Leu Pro Arg Arg Ser Gly Thr Thr
225                 230                 235                 240

Gly Val Ala Ile Lys Gly Gly Gly Thr Leu Val Asp Glu Ala Ile Arg
                245                 250                 255

Phe Ile Gly Arg Ala Met Ala Asp Arg Gly Leu Leu Arg Asp Ile Lys
            260                 265                 270

Ala Lys Thr Ala Tyr Glu Lys Ile Leu Leu Asn Leu Lys Asn Lys Cys
        275                 280                 285

Ser Ala Pro Gln Gln Lys Ala Leu Val Asp Gln Val Ile Gly Ser Arg
    290                 295                 300

Asn Pro Gly Ile Ala Asp Ile Glu Asp Leu Thr Leu Leu Ala Arg Ser
305                 310                 315                 320

Met Val Val Val Arg Pro Ser Val Ala Ser Lys Val Val Leu Pro Ile
                325                 330                 335

Ser Ile Tyr Ala Lys Ile Pro Gln Leu Gly Phe Asn Thr Glu Glu Tyr
            340                 345                 350

Ser Met Val Gly Tyr Glu Ala Met Ala Leu Tyr Asn Met Ala Thr Pro
        355                 360                 365

Val Ser Ile Leu Arg Met Gly Asp Asp Ala Lys Asp Lys Ser Gln Leu
    370                 375                 380

Phe Phe Met Ser Cys Phe Gly Ala Ala Tyr Glu Asp Leu Arg Val Leu
385                 390                 395                 400

Ser Ala Leu Thr Gly Thr Glu Phe Lys Pro Arg Ser Ala Leu Lys Cys
                405                 410                 415

Lys Gly Phe His Val Pro Ala Lys Glu Gln Val Glu Gly Met Gly Ala
            420                 425                 430

Ala Leu Met Ser Ile Lys Leu Gln Phe Trp Ala Pro Met Thr Arg Ser
        435                 440                 445

Gly Gly Asn Glu Val Ser Gly Glu Gly Gly Ser Gly Gln Ile Ser Cys
    450                 455                 460

Ser Pro Val Phe Ala Val Glu Arg Pro Ile Ala Leu Ser Lys Gln Ala
```

```
465                 470                 475                 480

Val Arg Arg Met Leu Ser Met Asn Val Glu Gly Arg Asp Ala Asp Val
                485                 490                 495

Lys Gly Asn Leu Leu Lys Met Met Asn Asp Ser Met Ala Lys Lys Thr
            500                 505                 510

Ser Gly Asn Ala Phe Ile Gly Lys Lys Met Phe Gln Ile Ser Asp Lys
        515                 520                 525

Asn Lys Val Asn Pro Ile Glu Ile Pro Ile Lys Gln Thr Ile Pro Asn
    530                 535                 540

Phe Phe Phe Gly Arg Asp Thr Ala Glu Asp Tyr Asp Asp Leu Asp Tyr
545                 550                 555                 560
```

<210> 17
<211> 1220
<212> DNA
<213> Influenza A virus

<400> 17

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atggaggcaa gactactggt cttgttatgt gcatttgcag ctacaaatgc agacacaata     60

tgtataggct accatgcgaa taactcaacc gacactgttg acacagtact cgaaaagaat    120

gtgaccgtga cacactctgt taacctgctc gaagacagcc acaacggaaa actatgtaaa    180

ttaaaaggaa tagccccatt acaattgggg aaatgtaata tcgccggatg gctcttggga    240

aacccggaat gcgatttact gctcacagcg agctcatggt cctatattgt agaaacatcg    300

aactcagaga atggaacatg ttacccagga gatttcatcg actatgaaga actgagggag    360

caattgagct cagtgtcatc gtttgaaaaa ttcgaaatat ttcccaagac aagctcgtgg    420

cccaatcatg aaacaaccaa aggtgtaacg gcagcatgct cctatgcggg agcaagcagt    480

ttttacagaa atttgctgtg gctgacaaag aagggaagct catacccaaa gcttagcaag    540

tcctatgtga acaataaagg gaaagaagtc cttgtactat ggggtgttca tcatccgcct    600

accggtactg atcaacagag tctctatcag aatgcagatg cttatgtctc tgtagggtca    660

tcaaaatata acaggagatt caccccggaa atagcagcga gacccaaagt aagaggtcaa    720

gctgggagga tgaactatta ctggacatta ctagaacccg gagacacaat aacatttgag    780

gcaactggaa atctaatagc accatggtat gctttcgcac tgaatagagg ttctggatcc    840

ggtatcatca cttcagacgc accagtgcat gattgtaaca cgaagtgtca aacaccccat    900

ggtgctataa acagcagtct ccctttccag aatatacatc cagtcacaat aggagagtgc    960
```

ccaaaatacg tcaggagtac caaattgagg atggctacag gactaagaaa cattccatct 1020

attcaatcca ggggtctatt tggagccatt gccggtttta ttgaggggg atggactgga 1080

atgatagatg gatggtatgg ttatcatcat cagaatgaac agggatcagg ctatgcagcg 1140

gatcaaaaaa gcacacaaaa tgccattgac gggattacaa acaaggtgaa ttctgttatc 1200

gagaaaatga acacccaatt 1220

<210> 18
<211> 406
<212> PRT
<213> Influenza A virus

<400> 18

Met Glu Ala Arg Leu Leu Val Leu Leu Cys Ala Phe Ala Ala Thr Asn
1 5 10 15

Ala Asp Thr Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Asp Thr
20 25 30

Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His Ser Val Asn
35 40 45

Leu Leu Glu Asp Ser His Asn Gly Lys Leu Cys Lys Leu Lys Gly Ile
50 55 60

Ala Pro Leu Gln Leu Gly Lys Cys Asn Ile Ala Gly Trp Leu Leu Gly
65 70 75 80

Asn Pro Glu Cys Asp Leu Leu Leu Thr Ala Ser Ser Trp Ser Tyr Ile
85 90 95

Val Glu Thr Ser Asn Ser Glu Asn Gly Thr Cys Tyr Pro Gly Asp Phe
100 105 110

Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val Ser Ser Phe
115 120 125

Glu Lys Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro Asn His Glu
130 135 140

Thr Thr Lys Gly Val Thr Ala Ala Cys Ser Tyr Ala Gly Ala Ser Ser
145 150 155 160

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

```
Lys Leu Ser Lys Ser Tyr Val Asn Asn Lys Gly Lys Glu Val Leu Val
            180                 185                 190

Leu Trp Gly Val His His Pro Pro Thr Gly Thr Asp Gln Gln Ser Leu
        195                 200                 205

Tyr Gln Asn Ala Asp Ala Tyr Val Ser Val Gly Ser Ser Lys Tyr Asn
    210                 215                 220

Arg Arg Phe Thr Pro Glu Ile Ala Ala Arg Pro Lys Val Arg Gly Gln
225                 230                 235                 240

Ala Gly Arg Met Asn Tyr Tyr Trp Thr Leu Leu Glu Pro Gly Asp Thr
                245                 250                 255

Ile Thr Phe Glu Ala Thr Gly Asn Leu Ile Ala Pro Trp Tyr Ala Phe
            260                 265                 270

Ala Leu Asn Arg Gly Ser Gly Ser Gly Ile Ile Thr Ser Asp Ala Pro
        275                 280                 285

Val His Asp Cys Asn Thr Lys Cys Gln Thr Pro His Gly Ala Ile Asn
    290                 295                 300

Ser Ser Leu Pro Phe Gln Asn Ile His Pro Val Thr Ile Gly Glu Cys
305                 310                 315                 320

Pro Lys Tyr Val Arg Ser Thr Lys Leu Arg Met Ala Thr Gly Leu Arg
                325                 330                 335

Asn Ile Pro Ser Ile Gln Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly
            340                 345                 350

Phe Ile Glu Gly Gly Trp Thr Gly Met Ile Asp Gly Trp Tyr Gly Tyr
        355                 360                 365

His His Gln Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Gln Lys Ser
    370                 375                 380

Thr Gln Asn Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile
385                 390                 395                 400

Glu Lys Met Asn Thr Gln
                405
```

<210> 19
<211> 1741
<212> DNA
<213> Influenza A virus

<400> 19
ctgtcaaaat ggagaaaata gtgcttcttc ttgcaacagt cagtcttgtt aaaagtgatc 60

agatttgcat tggttaccat gcaaacaact cgacagagca ggttgacaca ataatggaaa 120

agaatgttac tgttacacat gcccaagaca tactggaaag gacacacaac gggaagctct 180

gcgatctaaa tggagtgaaa cctctcattt tgagggattg tagtgtagct ggatggctcc 240

tcggaaaccc tatgtgtgac gaattcatca atgtgccgga atggtcttac atagtggaga 300

aggccagtcc agccaatgac ctctgttatc cagggaattt caacgactat gaagaactga 360

aacacctatt gagcagaata aaccattttg agaaaattca gatcatcccc aaaagttctt 420

ggtccaatca tgatgcctca tcaggggtga gctcagcatg tccatacctt gggaggtcct 480

ccttttcag aaatgtggta tggcttatca aaaagaacag tgcataccca acaataaaga 540

ggagctacaa taataccaac caagaagatc ttttggtact gtgggggatt caccatccta 600

atgatgcggc agagcagaca aagctctatc aaaatccaac cacctacatt tccgttggaa 660

catcaacact gaaccagaga ttggttccag aaatagctac tagacccaaa gtaaacgggc 720

aaagtggaag aatggagttc ttctggacaa ttttaaagcc gaatgatgcc atcaatttcg 780

agagtaatgg aaatttcatt gccccagaat atgcatacaa aattgtcaag aaaggggact 840

caacaattat gaaaagtgaa ttggaatatg gtaactgcaa caccaagtgt caaactccaa 900

tgggggcgat aaactctagt atgccattcc acaacataca ccccctcacc atcggggaat 960

gccccaaata tgtgaaatca aacagattag ttcttgcgac tggactcaga aataccctc 1020

aaagggagag aagaagaaaa aagagaggac tatttggagc tatagcaggt tttatagagg 1080

gaggatggca gggcatggta gatggttggt atgggtacca ccatagcaat gagcagggga 1140

gtggatacgc tgcagacaaa gaatccactc aaaaggcaat agatggagtc accaataagg 1200

tcaactcgat cattaacaaa atgaacactc agtttgaggc cgttggaagg gaatttaata 1260

acttagaaag gagaatagag aatttaaaca agaaaatgga agacggattc ctagatgtct 1320

ggacttacaa tgctgaactt ctggttctca tggaaaatga gagaactctc gactttcatg 1380

actcaaatgt caagaacctt tacgacaagg tccgactaca gcttagggat aatgcaaagg 1440

aactgggtaa tggttgtttc gaattctatc acaaatgtga taatgaatgt atggaaagtg 1500

taaaaaacgg aacgtatgac tacccgcagt attcagaaga agcaagacta aacagagagg 1560

aaataagtgg agtaaaattg gaatcaatgg gaacttacca aatactgtca atttattcaa 1620

cagtggcgag ttccctagca ctggcaatca tggtagctgg tctatcttta tggatgtgct 1680

ccaatggatc gttacaatgc agaatttgca tttaaatttg tgagttcaga ttgtagttaa 1740

a 1741

<210> 20
<211> 568
<212> PRT
<213> Influenza A virus

<400> 20

Met Glu Lys Ile Val Leu Leu Leu Ala Thr Val Ser Leu Val Lys Ser
1 5 10 15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
20 25 30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
35 40 45

Leu Glu Arg Thr His Asn Gly Lys Leu Cys Asp Leu Asn Gly Val Lys
50 55 60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65 70 75 80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
85 90 95

Glu Lys Ala Ser Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asn His Asp Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Arg Ser Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Ala Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
180 185 190

```
Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
    210                 215                 220

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

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Thr
                325                 330                 335

Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
    370                 375                 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

Ile Ile Asn Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
```

```
        435                 440                 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Met Gly
        515                 520                 525

Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545                 550                 555                 560

Ser Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 21
<211> 1714
<212> DNA
<213> Influenza A virus

<400> 21

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gcaaaagcag gggaattact taactagcaa aatggaaaca atatcactaa taactatact     60

actagtagta acagcaagca atgcagataa aatctgcatc ggccaccagt caacaaactc    120

cacagaaact gtggacacgc taacagaaac caatgttcct gtgacacatg ccaaagaatt    180

gctccacaca gagcataatg gaatgctgtg tgcaacaagc ctgggacatc ccctcattct    240

agacacatgc actattgaag gactagtcta tggcaaccct tcttgtgacc tgctgttggg    300

aggaagagaa tggtcctaca tcgtcgaaag atcatcagct gtaaatggaa cgtgttaccc    360

tgggaatgta gaaaacctag aggaactcag gacacttttt agttccgcta gttcctacca    420

aagaatccaa atcttcccag acacaacctg gaatgtgact tacactggaa caagcagagc    480

atgttcaggt tcattctaca ggagtatgag atggctgact caaaagagcg gtttttaccc    540

tgttcaagac gcccaataca caaataacag gggaaagagc attcttttcg tgtggggcat    600
```

```
acatcaccca cccacctata ccgagcaaac aaatttgtac ataagaaacg acacaacaac    660

aagcgtgaca acagaagatt tgaataggac cttcaaacca gtgatagggc caaggcccct    720

tgtcaatggt ctgcagggaa gaattgatta ttattggtcg gtactaaaac caggccaaac    780

attgcgagta cgatccaatg ggaatctaat tgctccatgg tatggacacg ttctttcagg    840

agggagccat ggaagaatcc tgaagactga tttaaaaggt ggtaattgtg tagtgcaatg    900

tcagactgaa aaaggtggct taaacagtac attgccattc cacaatatca gtaaatatgc    960

atttggaacc tgccccaaat atgtaagagt taatagtctc aaactggcag tcggtctgag   1020

gaacgtgcct gctagatcaa gtagaggact atttggagcc atagctggat tcatagaagg   1080

aggttggcca ggactagtcg ctggctggta tggtttccag cattcaaatg atcaaggggt   1140

tggtatggct gcagataggg attcaactca aaaggcaatt gataaaataa catccaaggt   1200

gaataatata gtcgacaaga tgaacaagca atatgaaata attgatcatg aattcagtga   1260

ggttgaaact agactcaata tgatcaataa taagattgat gaccaaatac aagacgtatg   1320

ggcatataat gcagaattgc tagtactact tgaaaatcaa aaaacactcg atgagcatga   1380

tgcgaacgtg aacaatctat ataacaaggt gaagagggca ctgggctcca atgctatgga   1440

agatgggaaa ggctgtttcg agctatacca taaatgtgat gatcagtgca tggaaacaat   1500

tcggaacggg acctataata ggagaaagta tagagaggaa tcaagactag aaaggcagaa   1560

aatagagggg gttaagctgg aatctgaggg aacttacaaa atcctcacca tttattcgac   1620

tgtcgcctca tctcttgtgc ttgcaatggg gtttgctgcc ttcctgttct gggccatgtc   1680

caatggatct tgcagatgca acatttgtat ataa                               1714
```

<210> 22
<211> 560
<212> PRT
<213> Influenza A virus

<400> 22

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Met Glu Thr Ile Ser Leu Ile Thr Ile Leu Leu Val Val Thr Ala Ser
1               5                  10                  15

Asn Ala Asp Lys Ile Cys Ile Gly His Gln Ser Thr Asn Ser Thr Glu
            20                  25                  30

Thr Val Asp Thr Leu Thr Glu Thr Asn Val Pro Val Thr His Ala Lys
        35                  40                  45

Glu Leu Leu His Thr Glu His Asn Gly Met Leu Cys Ala Thr Ser Leu
    50                  55                  60
```

```
Gly His Pro Leu Ile Leu Asp Thr Cys Thr Ile Glu Gly Leu Val Tyr
65                  70                  75                  80

Gly Asn Pro Ser Cys Asp Leu Leu Leu Gly Gly Arg Glu Trp Ser Tyr
                85                  90                  95

Ile Val Glu Arg Ser Ser Ala Val Asn Gly Thr Cys Tyr Pro Gly Asn
            100                 105                 110

Val Glu Asn Leu Glu Glu Leu Arg Thr Leu Phe Ser Ser Ala Ser Ser
        115                 120                 125

Tyr Gln Arg Ile Gln Ile Phe Pro Asp Thr Thr Trp Asn Val Thr Tyr
    130                 135                 140

Thr Gly Thr Ser Arg Ala Cys Ser Gly Ser Phe Tyr Arg Ser Met Arg
145                 150                 155                 160

Trp Leu Thr Gln Lys Ser Gly Phe Tyr Pro Val Gln Asp Ala Gln Tyr
                165                 170                 175

Thr Asn Asn Arg Gly Lys Ser Ile Leu Phe Val Trp Gly Ile His His
            180                 185                 190

Pro Pro Thr Tyr Thr Glu Gln Thr Asn Leu Tyr Ile Arg Asn Asp Thr
        195                 200                 205

Thr Thr Ser Val Thr Thr Glu Asp Leu Asn Arg Thr Phe Lys Pro Val
    210                 215                 220

Ile Gly Pro Arg Pro Leu Val Asn Gly Leu Gln Gly Arg Ile Asp Tyr
225                 230                 235                 240

Tyr Trp Ser Val Leu Lys Pro Gly Gln Thr Leu Arg Val Arg Ser Asn
                245                 250                 255

Gly Asn Leu Ile Ala Pro Trp Tyr Gly His Val Leu Ser Gly Gly Ser
            260                 265                 270

His Gly Arg Ile Leu Lys Thr Asp Leu Lys Gly Gly Asn Cys Val Val
        275                 280                 285

Gln Cys Gln Thr Glu Lys Gly Gly Leu Asn Ser Thr Leu Pro Phe His
    290                 295                 300
```

```
Asn Ile Ser Lys Tyr Ala Phe Gly Thr Cys Pro Lys Tyr Val Arg Val
305                 310                 315                 320

Asn Ser Leu Lys Leu Ala Val Gly Leu Arg Asn Val Pro Ala Arg Ser
                325                 330                 335

Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp
            340                 345                 350

Pro Gly Leu Val Ala Gly Trp Tyr Gly Phe Gln His Ser Asn Asp Gln
        355                 360                 365

Gly Val Gly Met Ala Ala Asp Arg Asp Ser Thr Gln Lys Ala Ile Asp
    370                 375                 380

Lys Ile Thr Ser Lys Val Asn Asn Ile Val Asp Lys Met Asn Lys Gln
385                 390                 395                 400

Tyr Glu Ile Ile Asp His Glu Phe Ser Glu Val Glu Thr Arg Leu Asn
                405                 410                 415

Met Ile Asn Asn Lys Ile Asp Asp Gln Ile Gln Asp Val Trp Ala Tyr
            420                 425                 430

Asn Ala Glu Leu Leu Val Leu Leu Glu Asn Gln Lys Thr Leu Asp Glu
        435                 440                 445

His Asp Ala Asn Val Asn Asn Leu Tyr Asn Lys Val Lys Arg Ala Leu
    450                 455                 460

Gly Ser Asn Ala Met Glu Asp Gly Lys Gly Cys Phe Glu Leu Tyr His
465                 470                 475                 480

Lys Cys Asp Asp Gln Cys Met Glu Thr Ile Arg Asn Gly Thr Tyr Asn
                485                 490                 495

Arg Arg Lys Tyr Arg Glu Glu Ser Arg Leu Glu Arg Gln Lys Ile Glu
            500                 505                 510

Gly Val Lys Leu Glu Ser Glu Gly Thr Tyr Lys Ile Leu Thr Ile Tyr
        515                 520                 525

Ser Thr Val Ala Ser Ser Leu Val Leu Ala Met Gly Phe Ala Ala Phe
    530                 535                 540

Leu Phe Trp Ala Met Ser Asn Gly Ser Cys Arg Cys Asn Ile Cys Ile
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545 550 555 560

<210> 23
<211> 1494
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus H1N1 Nucleoprotein

<400> 23
atggcctctc aggggacaaa gcggtcctac gagcagatgg agaccgatgg agaaaggcag 60

aatgctaccg agatacgagc ctcggtggga aagatgatag gcgggatcgg taggttttac 120

attcagatgt gcactgagct taagctgagt gattatgaag gtagactgat acagaattca 180

ctcaccatcg aaagaatggt gctgagtgca ttcgacgagc gccgaaacaa atacctggag 240

gaacatcctt cagccggcaa ggatcccaag aaaactggcg gacccatcta ccggagggtg 300

aacgggaaat ggatgcgcga gctgattctg tatgataaag aagaaatccg gcgtatctgg 360

aggcaagcta acaacggaga tgatgccaca gccggactga cgcatatgat gatttggcac 420

tctaacctta acgacgcgac ctaccagagg acccgggccc tcgtgagaac aggcatggat 480

ccacgaatgt gctcacttat gcaggggtcc accctgccaa ggaggagcgg ggcagctggt 540

gccgcagtca aaggggtggg aactatggtg atggagctag tgcgtatgat taagcgcggc 600

ataaatgacc gcaatttctg gcgggggggaa aacggacgaa agacacgcat tgcatatgaa 660

cgcatgtgca atattctcaa ggggaaattc cagacggctg ctcaaaaggc catgatggac 720

caggtgaggg agtcaagaaa cccaggcaac gccgagtttg aagacctgac cttcctggca 780

cggtctgctc taatcctcag aggtagtgta gcacacaaga gttgtcttcc ggcttgtgtg 840

tatggaccag ctgttgcatc agggtatgat ttcgaaaggg aaggctacag cctagttggt 900

atcgacccgt ttagactctt acagaattcc caagtctatt ccctgatcag acccaacgag 960

aatcctgctc acaaaagcca gttggtctgg atggcctgtc actccgccgc cttcgaggac 1020

ctccgggtct tgtcctttat caaaggcact aaggttctgc cccgcggcaa gttaagcact 1080

aggggagttc agatcgcaag taacgagaac atggagacaa tggagtctag caccttggaa 1140

ttgcgctccc gttattgggc gatccggaca agaagcggag gtaacacgaa tcagcaacgg 1200

gccagcgcgg gccaaatttc gatacagcct actttcagcg tgcagcggaa tctccccttc 1260

gatcgcacca ccgtaatggc cgcgtttagt ggtaatacag agggcagaac ttctgacatg 1320

cgaacagaga ttatccgtat gatggagagc gctcgacctg aagatgtgtc atttcagggc 1380

agaggcgtat ttgagctgtc cgacgagaaa gcagcctctc ctattgtccc ctctttcgac 1440

atgtccaacg aggggagcta cttctttggc gacaatgccg aagaatacga caat 1494

<210> 24
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> Human Codon Optimized Influenza A Virus H1N1 Nucleoprotein

<400> 24
atggccagcc agggcaccaa gcggagctac gagcagatgg agaccgacgg cgagcggcag 60

aacgccaccg agatccgggc cagcgtgggc aagatgatcg gcggcatcgg ccggttctac 120

atccagatgt gcaccgagct gaagctgagc gactacgagg gccggctgat ccagaacagc 180

ctgaccatcg agcggatggt gctgagcgcc ttcgacgagc ggcggaacaa gtacctggag 240

gagcacccca gcgccggcaa ggaccccaag aagaccggcg gccccatcta ccggcgggtg 300

aacggcaagt ggatgcggga gctgatcctg tacgacaagg aggagatccg gcggatctgg 360

cggcaggcca acaacggcga cgacgccacc gccggcctga cccacatgat gatctggcac 420

agcaacctga acgacgccac ctaccagcgg acccgggccc tggtgcggac cggcatggac 480

ccccggatgt gcagcctgat gcagggcagc accctgcccc ggcggagcgg cgccgccggc 540

gccgccgtga agggcgtggg caccatggtg atggagctgg tgcggatgat caagcggggc 600

atcaacgacc ggaacttctg gcggggcgag aacggccgga agacccggat cgcctacgag 660

cggatgtgca acatcctgaa gggcaagttc cagaccgccg cccagaaggc catgatggac 720

caggtgcggg agagccggaa ccccggcaac gccgagttcg aggacctgac cttcctggcc 780

cggagcgccc tgatcctgcg gggcagcgtg gcccacaaga gctgcctgcc cgcctgcgtg 840

tacggccccg ccgtggccag cggctacgac ttcgagcggg agggctacag cctggtgggc 900

atcgaccccc tccggctgct gcagaacagc caggtgtaca gcctgatccg gcccaacgag 960

aaccccgccc acaagagcca gctggtgtgg atggcctgcc acagcgccgc cttcgaggac 1020

ctgcgggtgc tgagcttcat caagggcacc aaggtgctgc cccggggcaa gctgagcacc 1080

cggggcgtgc agatcgccag caacgagaac atggagacca tggagagcag caccctggag 1140

ctgcggagcc ggtactgggc catccggacc cggagcggcg gcaacaccaa ccagcagcgg 1200

gccagcgccg gccagatcag catccagccc accttcagcg tgcagcggaa cctgcccttc 1260

gaccggacca ccgtgatggc cgccttcagc ggcaacaccg agggccggac cagcgacatg 1320

cggaccgaga tcatccggat gatggagagc gcccggcccg aggacgtgag cttccagggc 1380

cggggcgtgt tcgagctgag cgacgagaag gccgccagcc ccatcgtgcc cagcttcgac 1440

atgagcaacg agggcagcta cttcttcggc gacaacgccg aggagtacga caactga 1497

<210> 25
<211> 1497
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus H1N1 Nucleoprotein

<400> 25
atggcctcac agggcaccaa gcggagttat gagcagatgg agaccgatgg cgagagacag 60

aacgccacag agatcagagc ctcagttggc aagatgatcg gcggcatcgg ccggttctat 120

atccagatgt gcacggagct gaagctgagc gactacgagg gcagactgat tcagaactct 180

ctgaccatcg agagaatggt cctgagtgcc ttcgatgaga gacgaaacaa gtatctggag 240

gagcatccct ccgccggcaa ggaccccaag aagacgggcg gccccatata tagaagagtt 300

aacggcaagt ggatgagaga gctgatcctg tacgataagg aggagatccg cagaatatgg 360

aggcaggcca acaacggcga cgatgccact gccggcctga cacatatgat gatatggcac 420

agtaacctga acgacgccac ctaccagaga acaagggccc tggttcgcac gggcatggat 480

cccagaatgt gttcactgat gcagggctct acactgccca gaaggtctgg cgccgccggc 540

gccgccgtca agggcgttgg cacaatggtg atggagctgg tgcggatgat caagagaggc 600

attaacgatc ggaacttttg gaggggcgag aacggcagaa agaccaggat agcctacgag 660

cgaatgtgca acattctgaa gggcaagttc cagactgccg cccagaaggc catgatggat 720

caggtgcggg agagcagaaa ccccggcaac gccgagttcg aggacctgac tttcctggcc 780

agatctgccc tgatactgag gggctctgta gcccacaagt cctgcctgcc cgcctgcgtg 840

tacggccccg ccgtggcctc cggctatgac ttcgagcgag agggctactc cctggtaggc 900

atcgatccct ttagactgct gcagaactct caggtctaca gtctgattag acccaacgag 960

aaccccgccc ataagagcca gctggtgtgg atggcctgcc acagtgccgc cttcgaggac 1020

ctgagggtgc tgtcttttat aaagggcaca aaggtgctgc cccgcggcaa gctgtctact 1080

aggggcgtcc agatagcctc caacgagaac atggagacaa tggagtctag tactctggag 1140

ctgaggtcta ggtactgggc catcaggact aggagcggcg gcaacaccaa ccagcagagg 1200

gccagcgccg gccagatcag cattcagccc accttcagtg tacagagaaa cctgcccttt 1260

gatagaacta ctgttatggc cgccttctct ggcaacactg agggcagaac tagtgacatg 1320

cgaacagaga tcataagaat gatggagtcg gcccgtcccg aggatgtgtc ctttcagggc 1380

aggggcgtct tcgagctgag cgacgagaag gccgccagcc ccatcgtacc ctctttcgat 1440

atgagtaacg agggctcgta ctttttggc gacaacgccg aggagtatga taactga 1497

<210> 26
<211> 756
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus M1 Protein

<400> 26
atgagcttgc taacagaagt ggaaacctat gtcctcagta tcattcctag cggcccctta 60

aaagccgaaa tcgctcagcg gctcgaggat gtttttgccg gcaagaacac cgacctggag 120

gtattgatgg agtggctgaa aacgcgacct attctgagcc ccctgactaa gggaatactc 180

ggcttcgttt ttacattgac cgtgccctca gagaggggtc tccaaaggag gcgcttcgtg 240

cagaacgcct taaacgggaa cggggaccca aataatatgg ataaggcagt gaaactgtat 300

cgcaaattaa agcgggagat aaccttccat ggagccaagg agatctccct gtcttactct 360

gcaggtgctc tcgcgtcgtg tatgggactt atctacaacc gaatgggcgc cgtcacaaca 420

gaagtggctt tcgggctggt gtgcgcaact tgcgaacaga ttgctgacag tcagcaccgg 480

tcccaccgtc aaatggtcac caccaccaat ccgctgatta gacatgaaaa tcgcatggtt 540

ctagcatcaa ctacagccaa agcaatggaa caaatggccg gaagctccga gcaggctgcc 600

gaggcgatgg aggtggcgtc ccaggccaga cagatggtac aggctatgag aactatcggt 660

acgcacccaa gttcttcagc tgggctgaag aatgatcttc ttgagaacct gcaggcctac 720

caaaagcgga tgggcgtcca gatgcagaga tttaaa 756

<210> 27
<211> 756
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus M1 Protein

<400> 27
atgagcctgc tgaccgaggt ggagacctac gtgctgagca tcatccccag cggcccctg 60

aaggccgaga tcgcccagag gctggaggac gtgttcgccg gcaagaacac cgacctggag 120

gtgctgatgg agtggctgaa gaccaggccc atcctgagcc ccctgaccaa gggcatcctg 180

ggcttcgtgt tcaccctgac cgtgcccagc gagaggggcc tgcagaggag gaggttcgtg 240

cagaacgccc tgaacggcaa cggcgacccc aacaacatgg acaaggccgt gaagctgtac 300

aggaagctga agagggagat caccttccac ggcgccaagg agatcagcct gagctacagc 360

gccggcgccc tggccagctg catgggcctg atctacaaca ggatgggcgc cgtgaccacc 420

gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag ccagcacagg 480

agccacaggc agatggtgac caccaccaac cccctgatca ggcacgagaa caggatggtg 540

ctggccagca ccaccgccaa ggccatggag cagatggccg gcagcagcga gcaggccgcc 600

gaggccatgg aggtggccag ccaggccagg cagatggtgc aggccatgag gaccatcggc 660

acccacccca gcagcagcgc cggcctgaag aacgacctgc tggagaacct gcaggcctac 720

cagaagagga tgggcgtgca gatgcagagg ttcaag 756

<210> 28
<211> 756
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus M1 Protein

<400> 28
atgagtctgc tgacagaggt tgagacgtac gtgctgtcca tcattccctc aggcccctg 60

aaggccgaga ttgcccagag actggaggac gtcttcgccg gcaagaacac cgatctggag 120

gtgctgatgg agtggctgaa gactcgcccc atcctgtctc ccctgacaaa gggcatcctg 180

ggcttcgtat ttacactgac cgtcccctcc gagagaggcc tgcagcggag gaggttcgtt 240

cagaacgccc tgaacggcaa cggcgatccc aacaacatgg ataaggccgt gaagctgtat 300

agaaagctga agcgagagat cacatttcat ggcgccaagg agatatcgct gagctacagt 360

gccggcgccc tggcctcttg catgggcctg atatacaaca gaatgggcgc cgttactaca 420

gaggtagcct ttggcctggt ctgcgccact tgcgagcaga tcgccgactc tcagcataga 480

tctcacagac agatggtgac gactacaaac cccctgatac ggcacgagaa caggatggtg 540

ctggcctcta ctaccgccaa ggccatggag cagatggccg gcagcagtga gcaggccgcc 600

gaggccatgg aggtagcctc acaggccagg cagatggtgc aggccatgcg aaccatcggc 660

actcaccct ccagctctgc cggcctgaag aacgacctgc tggagaacct gcaggcctat 720

cagaagagaa tgggcgtaca gatgcagagg ttcaag 756

<210> 29
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus M2 Protein

<400> 29
atgagtcttc taaccgaggt cgaaacgcct atcagaaacg aatgggggtg cagatgcaac 60

ggttcaagtg atcctctcgc tattgccgca aatatcattg ggatcttgca cttgacattg 120

tggattcttg atcgtctttt tttcaaatgc atttaccgtc gctttaaata cggactgaaa 180

ggagggcctt ctacggaagg agtgccaaag tctatgaggg aagaatatcg aaaggaacag 240

cagagtgctg tggatgctga cgatggtcat tttgtcagca tagagctgga gtaa 294

<210> 30
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Influenza A Virus M2 Protein

<400> 30
atgagcctgc tgaccgaggt ggagaccccc atccggaacg agtggggctg ccggtgcaac 60

ggcagcagcg acccccctggc catcgccgcc aacatcatcg gcatcctgca cctgaccctg 120

tggatcctgg accggctgtt cttcaagtgc atctaccggc ggttcaagta cggcctgaag 180

ggcggcccca gcaccgaggg cgtgcccaag agcatgcggg aggagtaccg gaaggagcag 240

cagagcgccg tggacgccga cgacggccac ttcgtgagca tcgagctgga gtga 294

<210> 31
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon-Optimized Influenza A Virus M2 Protein

<400> 31
atgtctctgc tgacagaggt ggagacaccc ataaggaacg agtggggctg caggtgcaac 60

ggctctagtg atcccctggc catcgccgcc aacatcattg gcatactgca tctgaccctg 120

tggatcctgg atagactgtt ctttaagtgc atttacagac gatttaagta tggcctgaag 180

ggcggccccct caactgaggg cgtgcccaag agtatgagag aggagtaccg gaaggagcag 240

cagagcgccg ttgacgccga tgacggccac ttcgtctcca tcgagctgga gtga 294

<210> 32
<211> 1566
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Coding Region Encoding eM2NP

<400> 32
atgagccttc tcacagaagt ggaaacacct atcagaaatg aatggggatg cagatgcaat 60

gggtcgagtg atatggcctc tcaaggtacg aaaagaagct acgagcaaat ggaaacggat 120

ggagaaagac aaaacgcgac cgaaatcaga gcatccgtcg ggaagatgat tggaggaatc 180

ggacgattct acatccagat gtgcacagag ctaaagctat cggattatga agggagacta 240

atacaaaata gcctaactat cgagagaatg gtgctgtctg catttgacga aaggagaaac 300

aaatacctgg aagaacaccc ctctgcaggg aaagacccaa aaaaaactgg aggtccgata 360

taccggagag tcaacggtaa atggatgaga gagctgatct tgtatgataa ggaagaaata 420

agacgcatct ggcggcaagc taataatgga gacgacgcta ctgcagggct cacgcatatg 480

atgatctggc actctaattt gaatgatgca acgtaccaaa gaacccgcgc acttgtgcgg 540

accggaatgg accctcgtat gtgcagcctt atgcaggggt ccacactgcc cagaaggtcc 600

ggagcagctg gagcagcagt aaaggggttt ggaaccatgg tgatggagct ggtgagaatg 660

attaagaggg ggatcaatga caggaacttc tggcgaggag aaaacgggag aaaaactagg 720

atagcatatg agaggatgtg taacatcctc aaaggaaaat tccaaaccgc tgctcagaaa 780

gcaatgatgg atcaagtacg cgaaagtaga aatcctggaa atgcagagtt tgaagatctc 840

actttcctcg cgcgaagcgc tctcatcctc agagggagtg tcgctcataa aagttgcctg 900

cctgcctgcg tatatggtcc tgccgtggca agtggatacg actttgagag agaggggtac 960

tctcttgttg gaatagatcc attcagatta cttcagaatt cccaggtgta cagtttaata 1020

aggccaaacg aaaatcctgc acacaaatca caacttgttt ggatggcatg ccatagtgcc 1080

gcattcgaag atctaagagt tctctctttc atcaaaggta caaaggtcct tccaagggga 1140

aaactctcta ccagaggggt acaaatagct tcaaatgaga acatggagac aatggaatct 1200

agcacattgg aattgagaag taggtattgg gccattagaa ccaggagtgg aggcaatact 1260

aatcaacagc gggcttctgc cggtcaaatt agcatacaac ctacttttc agtgcaacgg 1320

aatctccctt ttgataggac aactgtcatg gcggcattct ctggaaatac cgaaggaagg 1380

acttccgata tgaggactga gatcattagg atgatggaaa gtgcccgacc tgaagacgtc 1440

agttttcaag gaagaggtgt gttcgaactc tctgacgaaa aggcagctag cccaatcgtt 1500

ccttcttttg atatgtcaaa tgaaggatcc tacttcttcg gcgataatgc ggaggaatat 1560

gacaac 1566

<210> 33
<211> 1566
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Coding Region Encoding eM2NP

<400> 33
atgagcctgc tgaccgaggt ggagaccccc atcaggaacg agtggggctg caggtgcaac 60

ggcagcagcg acatggccag ccagggcacc aagaggagct acgagcagat ggagaccgac 120

ggcgagaggc agaacgccac cgagatcagg gccagcgtgg gcaagatgat cggcggcatc 180

ggcaggttct acatccagat gtgcaccgag ctgaagctga gcgactacga gggcaggctg 240

atccagaaca gcctgaccat cgagaggatg gtgctgagcg ccttcgacga gaggaggaac 300

aagtacctgg aggagcaccc cagcgccggc aaggacccca agaagaccgg cggccccatc 360

tacaggaggg tgaacggcaa gtggatgagg gagctgatcc tgtacgacaa ggaggagatc 420

aggaggatct ggaggcaggc caacaacggc gacgacgcca ccgccggcct gacccacatg 480

atgatctggc acagcaacct gaacgacgcc acctaccaga ggaccagggc cctggtgagg 540

accggcatgg accccaggat gtgcagcctg atgcagggca gcaccctgcc caggaggagc 600

ggcgccgccg gcgccgccgt gaagggcgtg ggcaccatgg tgatggagct ggtgaggatg 660

atcaagaggg gcatcaacga caggaacttc tggaggggcg agaacggcag gaagaccagg 720

atcgcctacg agaggatgtg caacatcctg aagggcaagt tccagaccgc cgcccagaag 780

gccatgatgg accaggtgag ggagagcagg aaccccggca acgccgagtt cgaggacctg 840

accttcctgg ccaggagcgc cctgatcctg aggggcagcg tggcccacaa gagctgcctg 900

cccgcctgcg tgtacggccc cgccgtggcc agcggctacg acttcgagag ggagggctac 960

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aacctgccct tcgacaggac caccgtgatg gccgccttca gcggcaacac cgagggcagg 1380

accagcgaca tgaggaccga gatcatcagg atgatggaga gcgccaggcc cgaggacgtg 1440

agcttccagg gcaggggcgt gttcgagctg agcgacgaga aggccgccag ccccatcgtg 1500

cccagcttcg acatgagcaa cgagggcagc tacttcttcg gcgacaacgc cgaggagtac 1560

gacaac 1566

<210> 34
<211> 1566
<212> DNA
<213> Artificial seequence

<220>
<223> Human Codon Optimized Coding Region Encoding NPeM2

<400> 34

atggcaagcc agggcacaaa acgcagttac gagcagatgg agactgatgg tgagaggcag 60

aacgccaccg aaatccgggc ctccgtcggc aagatgattg gtggcatcgg aagattctat 120

atccagatgt gcacggagct taagctgtcc gattacgagg ggcgcttaat acagaactct 180

ctgactatcg agcgaatggt cttgagcgcc tttgatgagc ggcgtaataa gtatctcgaa 240

gagcaccctt ctgctggaaa agaccccaaa aagaccgggg gacctatcta ccgacgtgtg 300

aacggaaaat ggatgcgcga actgatactg tacgacaagg aggagatccg taggatctgg 360

agacaggcta ataacggaga tgatgccaca gctgggctga cccatatgat gatatggcat 420

agcaacctga acgacgcaac ctatcaacgc actagagcac tcgtgaggac cggtatggac 480

ccacgcatgt gctcattgat gcaaggtagc acattgcctc ggaggtcagg cgccgccggt 540

gccgccgtaa agggggtggg cacaatggtg atggaactgg tccgaatgat caaaagaggc 600

atcaatgaca ggaacttttg gcgcggagaa aacgggcgca agacccgcat tgcctacgag 660

cgcatgtgta acattttaaa aggcaaattc cagactgcag cccagaaagc aatgatggac 720

caagttagag aaagtagaaa tcccgggaat gccgagtttg aagacctgac tttcctggct 780

agaagcgcct tgatcctgcg gggctctgtc gcccacaaga gctgcctccc cgcttgcgtt 840

tacggccccg cggtcgcaag tggctacgat ttcgagaggg aggggtattc cctagttggg 900

atcgatccct tccggctcct acagaattct caggtgtata gtctgattag acccaacgaa 960

aacccggctc acaagagtca gcttgtttgg atggcatgtc actcagcagc tttcgaagac 1020

ctgcgggtac tcagctttat taaaggcacc aaggtcctgc caagaggaaa gctctccacg 1080

aggggagtac agatcgcctc aaacgagaac atggagacaa tggaaagctc cacccttgag 1140

cttaggtcgc ggtattgggc tattagaaca cgatctgggg ggaataccaa tcagcaacga 1200

gcgagtgctg gtcagatttc cattcagcct actttctctg tgcaacggaa tctaccattt 1260

gacaggacaa ctgtgatggc agcgttctcc ggcaatacag aaggacgaac atcagacatg 1320

aggaccgaaa ttatccggat gatggagagc gctcggccag aagatgtgtc gttccagggc 1380

cggggcgtgt ttgagctcag cgacgagaag gccgcgtctc caattgtgcc ttcctttgat 1440

atgagcaatg aggggtcata ctttttcgga gacaatgccg aagagtatga taatatgtct 1500

ctgcttaccg aggtggaaac gccgatacgc aacgaatggg gttgtcgttg taacggctcc 1560

agtgat 1566

<210> 35
<211> 1566
<212> DNA
<213> Artificial sequence

<220>

<223> Human Codon Optimized Coding Region Encoding NPeM2

<400> 35

atggccagcc agggcaccaa gaggagctac gagcagatgg agaccgacgg cgagaggcag 60

aacgccaccg agatcagggc cagcgtgggc aagatgatcg gcggcatcgg caggttctac 120

atccagatgt gcaccgagct gaagctgagc gactacgagg gcaggctgat ccagaacagc 180

ctgaccatcg agaggatggt gctgagcgcc ttcgacgaga ggaggaacaa gtacctggag 240

gagcacccca gcgccggcaa ggaccccaag aagaccggcg gccccatcta caggagggtg 300

aacggcaagt ggatgaggga gctgatcctg tacgacaagg aggagatcag gaggatctgg 360

aggcaggcca acaacggcga cgacgccacc gccggcctga cccacatgat gatctggcac 420

agcaacctga acgacgccac ctaccagagg accagggccc tggtgaggac cggcatggac 480

cccaggatgt gcagcctgat gcagggcagc accctgccca ggaggagcgg cgccgccggc 540

gccgccgtga agggcgtggg caccatggtg atggagctgg tgaggatgat caagaggggc 600

atcaacgaca ggaacttctg gaggggcgag aacggcagga agaccaggat cgcctacgag 660

aggatgtgca acatcctgaa gggcaagttc cagaccgccg cccagaaggc catgatggac 720

caggtgaggg agagcaggaa ccccggcaac gccgagttcg aggacctgac cttcctggcc 780

aggagcgccc tgatcctgag gggcagcgtg gcccacaaga gctgcctgcc cgcctgcgtg 840

tacggccccg ccgtggccag cggctacgac ttcgagaggg agggctacag cctggtgggc 900

atcgacccct tcaggctgct gcagaacagc caggtgtaca gcctgatcag gcccaacgag 960

aaccccgccc acaagagcca gctggtgtgg atggcctgcc acagcgccgc cttcgaggac 1020

ctgagggtgc tgagcttcat caagggcacc aaggtgctgc ccaggggcaa gctgagcacc 1080

aggggcgtgc agatcgccag caacgagaac atggagacca tggagagcag caccctggag 1140

ctgaggagca ggtactgggc catcaggacc aggagcggcg gcaacaccaa ccagcagagg 1200

gccagcgccg gccagatcag catccagccc accttcagcg tgcagaggaa cctgcccttc 1260

gacaggacca ccgtgatggc cgccttcagc ggcaacaccg agggcaggac cagcgacatg 1320

aggaccgaga tcatcaggat gatggagagc gccaggcccg aggacgtgag cttccagggc 1380

aggggcgtgt tcgagctgag cgacgagaag gccgccagcc ccatcgtgcc cagcttcgac 1440

atgagcaacg agggcagcta cttcttcggc gacaacgccg aggagtacga caacatgagc 1500

ctgctgaccg aggtggagac ccccatcagg aacgagtggg gctgcaggtg caacggcagc 1560

agcgac 1566

<210> 36
<211> 1683
<212> DNA

<213> Artificial sequence

<220>
<223> Human Codon Optimized Coding Region Encoding IBV NP Protein

<400> 36
atgtcgaaca tggacatcga cagcattaac acaggtacta ttgacaaaac ccccgaagaa 60

ctaacccctg gaacctcagg agcaacacgc ccaataatca aaccggccac cctcgcgccc 120

cctagcaata agaggacccg caatccaagt cctgagagaa ccactacttc atctgaaacg 180

gatatcggtc ggaaaattca aaaaaagcag acgcccacag agataaagaa gtctgtttac 240

aaaatggtgg taaagctcgg tgagttttat aaccagatga tggtcaaggc ggggcttaac 300

gacgatatgg aacgaaatct tatacagaat gcacaggcag tagagagaat actgctggcc 360

gctactgatg acaagaaaac ggagtaccaa aaaaaacgga atgctcgaga tgtgaaagaa 420

ggaaaagaag aaattgacca taacaaaact ggggggacat tctataagat ggtgcgggac 480

gataagacaa tctattttag cccgataaag attaccttcc tgaaggagga ggttaaaaca 540

atgtacaaga cgacgatggg cagcgatggg ttttccggac ttaatcatat aatgattggt 600

cactcgcaga tgaacgatgt atgtttccag cgctccaagg gcttaaagag ggtaggtctt 660

gacccgtctc taatatcaac tttcgcagga tccactttgc cgaggcgttc tggcacgaca 720

ggcgtggcta tcaagggcgg ggggacgctg gtcgatgagg ccattcgctt tattggtagg 780

gccatggccg atagagggct tctacgagac atcaaagcaa aaacagcata tgagaagata 840

ttattaaact taaagaacaa atgctccgct cctcagcaaa aagcgctcgt tgaccaagta 900

atcggttcga gaaatccagg cattgccgat atcgaagatc ttacactctt ggcgcgaagc 960

atggtcgttg tccgtcccag tgtcgctagt aaggtggtac taccaatctc gatttacgca 1020

aaaattccac aactcggctt taatacagag gaatattcta tggtaggtta tgaagccatg 1080

gcgttgtata atatggctac accagtctcc atattgcgta tgggagatga cgcaaaagat 1140

aagagtcaac tctttttcat gtcatgtttc ggcgcagcgt acgaagatct gagagtacta 1200

tccgccttga ctggaacgga atttaaacca cggtcagcct taaagtgtaa gggttttcac 1260

gtccctgcta aggagcaagt tgagggaatg ggcgcggcac tgatgagtat aaaattacaa 1320

ttttgggctc caatgacgcg ttcgggaggg aatgaagttt ctggtgaggg agggagtgga 1380

cagatatcat gctcgcccgt gttcgcggtt gaacgtccga ttgctttgag taagcaggcg 1440

gttaggcgga tgttaagtat gaatgtggag ggccgcgatg ccgacgtcaa aggcaactta 1500

ttaaaaatga tgaacgacag catggcaaag aagactagtg ggaatgcttt atagggaaa 1560

aaaatgttcc aaataagtga caaaaacaaa gtgaacccca tcgaaatacc tatcaagcaa 1620

accatcccga atttcttttt cggtcgagac accgcggagg actacgatga cctagattac 1680

taa 1683

<210> 37
<211> 1683
<212> DNA
<213> Artificial sequence

<220>
<223> Human Codon Optimized Coding Region Encoding IBV NP Protein

<400> 37
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cccagcaaca agcggacccg gaaccccagc cccgagcgga ccaccaccag cagcgagacc 180

gacatcggcc ggaagatcca gaagaagcag acccccaccg agatcaagaa gagcgtgtac 240

aagatggtgg tgaagctggg cgagttctac aaccagatga tggtgaaggc cggcctgaac 300

gacgacatgg agcggaacct gatccagaac gcccaggccg tggagcggat cctgctggcc 360

gccaccgacg acaagaagac cgagtaccag aagaagcgga acgcccggga cgtgaaggag 420

ggcaaggagg agatcgacca caacaagacc ggcggcacct tctacaagat ggtgcgggac 480

gacaagacca tctacttcag ccccatcaag atcaccttcc tgaaggagga ggtgaagacc 540

atgtacaaga ccaccatggg cagcgacggc ttcagcggcc tgaaccacat catgatcggc 600

cacagccaga tgaacgacgt gtgcttccag cggagcaagg gcctgaagcg ggtgggcctg 660

gaccccagcc tgatcagcac cttcgccggc agcaccctgc cccggcggag cggcaccacc 720

ggcgtggcca tcaagggcgg cggcaccctg gtggacgagg ccatccggtt catcggccgg 780

gccatggccg accggggcct gctgcgggac atcaaggcca agaccgccta cgagaagatc 840

ctgctgaacc tgaagaacaa gtgcagcgcc ccccagcaga aggccctggt ggaccaggtg 900

atcggcagcc ggaaccccgg catcgccgac atcgaggacc tgaccctgct ggcccggagc 960

atggtggtgg tgcggcccag cgtggccagc aaggtggtgc tgcccatcag catctacgcc 1020

aagatccccc agctgggctt caacaccgag gagtacagca tggtgggcta cgaggccatg 1080

gccctgtaca acatggccac ccccgtgagc atcctgcgga tgggcgacga cgccaaggac 1140

aagagccagc tgttcttcat gagctgcttc ggcgccgcct acgaggacct gcgggtgctg 1200

agcgccctga ccggcaccga gttcaagccc cggagcgccc tgaagtgcaa gggcttccac 1260

gtgcccgcca aggagcaggt ggagggcatg ggcgccgccc tgatgagcat caagctgcag 1320

ttctgggccc ccatgacccg gagcggcggc aacgaggtga gcggcgaggg cggcagcggc 1380

cagatcagct gcagccccgt gttcgccgtg gagcggccca tcgccctgag caagcaggcc 1440

gtgcggcgga tgctgagcat gaacgtggag ggccgggacg ccgacgtgaa gggcaacctg 1500

ctgaagatga tgaacgacag catggccaag aagaccagcg gcaacgcctt catcggcaag 1560

aagatgttcc agatcagcga caagaacaag gtgaacccca tcgagatccc catcaagcag 1620

accatcccca acttcttctt cggccgggac accgccgagg actacgacga cctggactac 1680

tga 1683

<210> 38
<211> 1683
<212> PRT
<213> Artificial sequence

<220>
<223> Human Codon Optimized Coding Region Encoding IBV NP Protein

<400> 38

Ala Thr Gly Thr Cys Thr Ala Ala Cys Ala Thr Gly Gly Ala Cys Ala
1 5 10 15

Thr Cys Gly Ala Cys Thr Cys Thr Ala Thr Ala Ala Ala Cys Ala Cys
20 25 30

Ala Gly Gly Cys Ala Cys Gly Ala Thr Cys Gly Ala Thr Ala Ala Gly
35 40 45

Ala Cys Cys Cys Cys Cys Gly Ala Gly Gly Ala Gly Cys Thr Gly Ala
50 55 60

Cys Ala Cys Cys Cys Gly Gly Cys Ala Cys Thr Thr Cys Ala Gly Gly
65 70 75 80

Cys Gly Cys Cys Ala Cys Cys Ala Gly Ala Cys Cys Cys Ala Thr Ala
85 90 95

Ala Thr Ala Ala Ala Gly Cys Cys Cys Gly Cys Cys Ala Cys Thr Cys
100 105 110

Thr Gly Gly Cys Cys Cys Cys Cys Cys Cys Cys Thr Cys Thr Ala Ala
115 120 125

Cys Ala Ala Gly Ala Gly Gly Ala Cys Gly Ala Gly Gly Ala Ala Cys
130 135 140

Cys Cys Cys Thr Cys Thr Cys Cys Cys Gly Ala Gly Cys Gly Cys Ala
145 150 155 160

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Cys Cys Ala Cys Ala Ala Cys Gly Ala Gly Thr Ala Gly Cys Gly Ala
                165                 170                 175

Gly Ala Cys Gly Gly Ala Cys Ala Thr Cys Gly Gly Cys Ala Gly Gly
            180                 185                 190

Ala Ala Gly Ala Thr Ala Cys Ala Gly Ala Ala Gly Ala Ala Gly Cys
        195                 200                 205

Ala Gly Ala Cys Thr Cys Cys Cys Ala Cys Thr Gly Ala Gly Ala Thr
    210                 215                 220

Thr Ala Ala Gly Ala Ala Gly Thr Cys Cys Gly Thr Gly Thr Ala Thr
225                 230                 235                 240

Ala Ala Gly Ala Thr Gly Gly Thr Gly Gly Thr Thr Ala Ala Gly Cys
                245                 250                 255

Thr Gly Gly Gly Cys Gly Ala Gly Thr Thr Thr Thr Ala Cys Ala Ala
            260                 265                 270

Cys Cys Ala Gly Ala Thr Gly Ala Thr Gly Gly Thr Gly Ala Ala Gly
        275                 280                 285

Gly Cys Cys Gly Gly Cys Cys Thr Gly Ala Ala Cys Gly Ala Thr Gly
    290                 295                 300

Ala Cys Ala Thr Gly Gly Ala Gly Ala Gly Gly Ala Ala Cys Cys Thr
305                 310                 315                 320

Gly Ala Thr Ala Cys Ala Gly Ala Ala Cys Gly Cys Cys Cys Ala Gly
                325                 330                 335

Gly Cys Cys Gly Thr Gly Gly Ala Gly Ala Gly Gly Ala Thr Thr Cys
            340                 345                 350

Thr Gly Cys Thr Gly Gly Cys Cys Gly Cys Cys Ala Cys Cys Gly Ala
        355                 360                 365

Thr Gly Ala Cys Ala Ala Gly Ala Ala Gly Ala Cys Thr Gly Ala Gly
    370                 375                 380

Thr Ala Thr Cys Ala Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala
385                 390                 395                 400

Ala Cys Gly Cys Cys Cys Gly Gly Gly Ala Cys Gly Thr Thr Ala Ala
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                405                 410                 415

Gly Gly Ala Gly Gly Gly Cys Ala Ala Gly Gly Ala Gly Gly Ala Gly
            420                 425                 430

Ala Thr Cys Gly Ala Thr Cys Ala Cys Ala Ala Cys Ala Ala Gly Ala
        435                 440                 445

Cys Ala Gly Gly Cys Gly Gly Cys Ala Cys Thr Thr Thr Cys Thr Ala
    450                 455                 460

Thr Ala Ala Gly Ala Thr Gly Gly Thr Cys Cys Gly Thr Gly Ala Thr
465                 470                 475                 480

Gly Ala Cys Ala Ala Gly Ala Cys Ala Ala Thr Cys Thr Ala Cys Thr
                485                 490                 495

Thr Thr Thr Cys Thr Cys Cys Cys Ala Thr Cys Ala Ala Gly Ala Thr
            500                 505                 510

Cys Ala Cys Ala Thr Thr Cys Cys Thr Gly Ala Ala Gly Gly Ala Gly
        515                 520                 525

Gly Ala Gly Gly Thr Ala Ala Ala Gly Ala Cys Thr Ala Thr Gly Thr
    530                 535                 540

Ala Cys Ala Ala Gly Ala Cys Ala Ala Cys Thr Ala Thr Gly Gly Gly
545                 550                 555                 560

Cys Thr Cys Cys Gly Ala Thr Gly Gly Cys Thr Thr Cys Ala Gly Thr
                565                 570                 575

Gly Gly Cys Cys Thr Gly Ala Ala Cys Cys Ala Cys Ala Thr Ala Ala
            580                 585                 590

Thr Gly Ala Thr Ala Gly Gly Cys Cys Ala Thr Ala Gly Thr Cys Ala
        595                 600                 605

Gly Ala Thr Gly Ala Ala Cys Gly Ala Thr Gly Thr Gly Thr Gly Cys
    610                 615                 620

Thr Thr Cys Cys Ala Gly Ala Gly Ala Ala Gly Cys Ala Ala Gly Gly
625                 630                 635                 640

Gly Cys Cys Thr Gly Ala Ala Gly Ala Gly Gly Gly Thr Cys Gly Gly
                645                 650                 655
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Cys Cys Thr Gly Gly Ala Thr Cys Cys Cys Thr Cys Gly Cys Thr Gly
            660                 665                 670

Ala Thr Thr Ala Gly Thr Ala Cys Cys Thr Thr Cys Gly Cys Cys Gly
        675                 680                 685

Gly Cys Ala Gly Cys Ala Cys Thr Cys Thr Gly Cys Cys Cys Ala Gly
    690                 695                 700

Ala Ala Gly Ala Thr Cys Thr Gly Gly Cys Ala Cys Thr Ala Cys Thr
705                 710                 715                 720

Gly Gly Cys Gly Thr Ala Gly Cys Cys Ala Thr Ala Ala Ala Gly Gly
                725                 730                 735

Gly Cys Gly Gly Cys Gly Gly Cys Ala Cys Ala Cys Thr Gly Gly Thr
            740                 745                 750

Ala Gly Ala Cys Gly Ala Gly Gly Cys Cys Ala Thr Ala Ala Gly Gly
        755                 760                 765

Thr Thr Thr Ala Thr Thr Gly Gly Cys Ala Gly Ala Gly Cys Cys Ala
    770                 775                 780

Thr Gly Gly Cys Cys Gly Ala Cys Cys Gly Cys Gly Gly Cys Cys Thr
785                 790                 795                 800

Gly Cys Thr Gly Ala Gly Ala Gly Ala Thr Ala Thr Cys Ala Ala Gly
                805                 810                 815

Gly Cys Cys Ala Ala Gly Ala Cys Cys Gly Cys Cys Thr Ala Cys Gly
            820                 825                 830

Ala Gly Ala Ala Gly Ala Thr Ala Cys Thr Gly Cys Thr Gly Ala Ala
        835                 840                 845

Cys Cys Thr Gly Ala Ala Gly Ala Ala Cys Ala Ala Gly Thr Gly Cys
    850                 855                 860

Thr Cys Ala Gly Cys Cys Cys Cys Cys Cys Ala Gly Cys Ala Gly Ala
865                 870                 875                 880

Ala Gly Gly Cys Cys Cys Thr Gly Gly Thr Gly Gly Ala Thr Cys Ala
                885                 890                 895
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Gly Gly Thr Gly Ala Thr Cys Gly Gly Cys Ala Gly Thr Ala Gly Ala
            900                 905                 910

Ala Ala Cys Cys Cys Cys Gly Gly Cys Ala Thr Cys Gly Cys Cys Gly
        915                 920                 925

Ala Cys Ala Thr Cys Gly Ala Gly Gly Ala Thr Cys Thr Gly Ala Cys
    930                 935                 940

Thr Cys Thr Gly Cys Thr Gly Gly Cys Cys Ala Gly Ala Ala Gly Cys
945                 950                 955                 960

Ala Thr Gly Gly Thr Ala Gly Thr Cys Gly Thr Ala Ala Gly Ala Cys
                965                 970                 975

Cys Cys Thr Cys Thr Gly Thr Gly Gly Cys Cys Thr Cys Thr Ala Ala
            980                 985                 990

Gly Gly Thr Thr Gly Thr Gly Cys  Thr Gly Cys Cys Cys  Ala Thr Cys
        995                 1000                1005

Thr Cys  Cys Ala Thr Cys Thr  Ala Cys Gly Cys Cys  Ala Ala Gly
    1010                1015                1020

Ala Thr  Thr Cys Cys Cys Cys  Ala Gly Cys Thr Gly  Gly Gly Cys
    1025                1030                1035

Thr Thr  Thr Ala Ala Cys Ala  Cys Thr Gly Ala Gly  Gly Ala Gly
    1040                1045                1050

Thr Ala  Cys Thr Cys Cys Ala  Thr Gly Gly Thr Gly  Gly Gly Cys
    1055                1060                1065

Thr Ala  Thr Gly Ala Gly Gly  Cys Cys Ala Thr Gly  Gly Cys Cys
    1070                1075                1080

Cys Thr  Gly Thr Ala Thr Ala  Ala Cys Ala Thr Gly  Gly Cys Cys
    1085                1090                1095

Ala Cys  Ala Cys Cys Cys Gly  Thr Cys Thr Cys Thr  Ala Thr Cys
    1100                1105                1110

Cys Thr  Gly Cys Gly Gly Ala  Thr Gly Gly Gly Cys  Gly Ala Cys
    1115                1120                1125
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Gly Ala  Thr Gly Cys Cys Ala  Ala Gly Gly Ala Cys  Ala Ala Gly
    1130                1135                1140

Thr Cys  Thr Cys Ala Gly Cys  Thr Gly Thr Thr Thr  Thr Thr Thr
    1145                1150                1155

Ala Thr  Gly Ala Gly Thr Thr  Gly Thr Thr Thr Cys  Gly Gly Cys
    1160                1165                1170

Gly Cys  Cys Gly Cys Cys Thr  Ala Thr Gly Ala Gly  Gly Ala Thr
    1175                1180                1185

Cys Thr  Gly Ala Gly Ala Gly  Thr Cys Cys Thr Gly  Thr Cys Ala
    1190                1195                1200

Gly Cys  Cys Cys Thr Gly Ala  Cys Ala Gly Gly Cys  Ala Cys Thr
    1205                1210                1215

Gly Ala  Gly Thr Thr Cys Ala  Ala Gly Cys Cys Cys  Ala Gly Gly
    1220                1225                1230

Thr Cys  Cys Gly Cys Cys Cys  Thr Gly Ala Ala Gly  Thr Gly Cys
    1235                1240                1245

Ala Ala  Gly Gly Gly Cys Thr  Thr Thr Cys Ala Thr  Gly Thr Gly
    1250                1255                1260

Cys Cys  Cys Gly Cys Cys Ala  Ala Gly Gly Ala Gly  Cys Ala Gly
    1265                1270                1275

Gly Thr  Gly Gly Ala Gly Gly  Gly Cys Ala Thr Gly  Gly Gly Cys
    1280                1285                1290

Gly Cys  Cys Gly Cys Cys Cys  Thr Gly Ala Thr Gly  Ala Gly Cys
    1295                1300                1305

Ala Thr  Cys Ala Ala Gly Cys  Thr Gly Cys Ala Gly  Thr Thr Cys
    1310                1315                1320

Thr Gly  Gly Gly Cys Cys Cys  Cys Cys Ala Thr Gly  Ala Cys Cys
    1325                1330                1335

Cys Gly  Gly Thr Cys Thr Gly  Gly Cys Gly Gly Cys  Ala Ala Cys
    1340                1345                1350

Gly Ala  Gly Gly Thr Cys Thr  Cys Gly Gly Gly Cys  Gly Ala Gly
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    1355                1360                1365

Gly Gly  Cys Gly Gly Cys Ala  Gly Thr Gly Gly Cys  Cys Ala Gly
    1370                1375                1380

Ala Thr  Ala Ala Gly Thr Thr  Gly Cys Ala Gly Cys  Cys Cys Cys
    1385                1390                1395

Gly Thr  Thr Thr Thr Thr Gly  Cys Cys Gly Thr Thr  Gly Ala Gly
    1400                1405                1410

Ala Gly  Ala Cys Cys Cys Ala  Thr Cys Gly Cys Cys  Cys Thr Gly
    1415                1420                1425

Thr Cys  Thr Ala Ala Gly Cys  Ala Gly Gly Cys Cys  Gly Thr Thr
    1430                1435                1440

Ala Gly  Ala Cys Gly Ala Ala  Thr Gly Cys Thr Gly  Ala Gly Thr
    1445                1450                1455

Ala Thr  Gly Ala Ala Cys Gly  Thr Cys Gly Ala Gly  Gly Gly Cys
    1460                1465                1470

Cys Gly  Ala Gly Ala Cys Gly  Cys Cys Gly Ala Thr  Gly Thr Gly
    1475                1480                1485

Ala Ala  Gly Gly Gly Cys Ala  Ala Cys Cys Thr Gly  Cys Thr Gly
    1490                1495                1500

Ala Ala  Gly Ala Thr Gly Ala  Thr Gly Ala Ala Cys  Gly Ala Thr
    1505                1510                1515

Thr Cys  Cys Ala Thr Gly Gly  Cys Cys Ala Ala Gly  Ala Ala Gly
    1520                1525                1530

Ala Cys  Ala Ala Gly Cys Gly  Gly Cys Ala Ala Cys  Gly Cys Cys
    1535                1540                1545

Thr Thr  Cys Ala Thr Thr Gly  Gly Cys Ala Ala Gly  Ala Ala Gly
    1550                1555                1560

Ala Thr  Gly Thr Thr Cys Cys  Ala Gly Ala Thr Ala  Ala Gly Cys
    1565                1570                1575

Gly Ala  Thr Ala Ala Gly Ala  Ala Cys Ala Ala Gly  Gly Thr Thr
    1580                1585                1590
```

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Ala Ala  Cys Cys Cys Cys Ala  Thr Cys Gly Ala Gly  Ala Thr Thr
    1595                 1600                 1605

Cys Cys  Cys Ala Thr Cys Ala  Ala Gly Cys Ala Gly  Ala Cys Cys
    1610                 1615                 1620

Ala Thr  Cys Cys Cys Cys Ala  Ala Cys Thr Thr Cys  Thr Thr Cys
    1625                 1630                 1635

Thr Thr  Cys Gly Gly Cys Ala  Gly Gly Gly Ala Thr  Ala Cys Cys
    1640                 1645                 1650

Gly Cys  Cys Gly Ala Gly Gly  Ala Thr Thr Ala Cys  Gly Ala Thr
    1655                 1660                 1665

Gly Ala  Cys Cys Thr Gly Gly  Ala Cys Thr Ala Cys  Thr Gly Ala
    1670                 1675                 1680
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<210> 39
<211> 552
<212> DNA
<213> Hepatitis B virus

<400> 39
atggacatcg acccttataa agaatttgga gctactgtgg agttactctc gtttttgcct 60

tctgacttct ttccttcagt acgagatctt ctagataccg cctcagctct gtatcgggaa 120

gccttagagt ctcctgagca ttgttcacct caccatactg cactcaggca agcaattctt 180

tgctgggggg aactaatgac tctagctacc tgggtgggtg ttaatttgga agatccagcg 240

tctagagacc tagtagtcag ttatgtcaac actaatatgg gcctaaagtt caggcaactc 300

ttgtggtttc acatttcttg tctcactttt ggaagagaaa cagttataga gtatttggtg 360

tctttcggag tgtggattcg cactcctcca gcttatagac caccaaatgc ccctatccta 420

tcaacacttc cggagactac tgttgttaga cgacgaggca ggtcccctag aagaagaact 480

ccctcgcctc gcagacgaag gtctcaatcg ccgcgtcgca gaagatctca atctcgggaa 540

tctcaatgtt ag 552

<210> 40
<211> 183
<212> PRT
<213> Artificial sequence

<220>
<223> Hepatitus B Virus

<400> 40

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 41
<211> 555
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic HBcAg

<400> 41
atggatatcg atccttataa agaattcgga gctactgtgg agttactctc gtttctcccg 60

agtgacttct ttccttcagt acgagatctt ctggataccg ccagcgcgct gtatcgggaa 120

gccttggagt ctcctgagca ctgcagccct caccatactg ccctcaggca agcaattctt 180

tgctgggggg agctcatgac tctggccacg tgggtgggtg ttaacttgga agatccagct 240

agcagggacc tggtagtcag ttatgtcaac actaatatgg gtttaaagtt caggcaactc 300

ttgtggtttc acattagctg cctcactttc ggccgagaaa cagttctaga atatttggtg 360

tctttcggag tgtggatccg cactcctcca gcttataggc ctccgaatgc ccctatcctg 420

tcgacactcc cggagactac tgttgttaga cgtcgaggca ggtcacctag aagaagaact 480

ccttcgcctc gcaggcgaag gtctcaatcg ccgcggcgcc gaagatctca atctcgggaa 540

tctcaatgtt agtga 555

<210> 42
<211> 183
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic HBcAg

<400> 42

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 43
<211> 2043
<212> DNA
<213> Artificial sequence

<220>
<223> Influenza A Virus NP Gene Fused to Synthetic HBcAg

<400> 43
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aatgccactg aaatcagagc atccgtcgga aaaatgattg gtggaattgg acgattctac 120

atccaaatgt gcaccgaact caaactcagt gattatgagg gacggttgat ccaaaacagc 180

ttaacaatag agagaatggt gctctctgct tttgacgaaa ggagaaataa ataccttgaa 240

gaacatccca gtgcggggaa agatcctaag aaaactggag gacctatata caggagagta 300

aacggaaagt ggatgagaga actcatcctt tatgacaaag aagaaataag gcgaatctgg 360

cgccaagcta ataatggtga cgatgcaacg gctggtctga ctcacatgat gatctggcat 420

tccaatttga atgatgcaac ttatcagagg acaagagctc ttgttcgcac cggaatggat 480

cccaggatgt gctctctgat gcaaggttca actctcccta ggaggtctgg agccgcaggt 540

gctgcagtca aaggagttgg aacaatggtg atggaattgg tcagaatgat caaacgtggg 600

atcaatgatc ggaacttctg gaggggtgag aatggacgaa aaacaagaat tgcttatgaa 660

agaatgtgca acattctcaa agggaaattt caaactgctg cacaaaaagc aatgatggat 720

caagtgagag agagccggaa cccagggaat gctgagttcg aagatctcac ttttctagca 780

cggtctgcac tcatattgag agggtcggtt gctcacaagt cctgcctgcc tgcctgtgtg 840

tatggacctg ccgtagccag tgggtacgac tttgaaaggg agggatactc tctagtcgga 900

atagaccctt tcagactgct tcaaaacagc caagtgtaca gcctaatcag accaaatgag 960

aatccagcac acaagagtca actggtgtgg atggcatgcc attctgccgc atttgaagat 1020

ctaagagtat taagcttcat caaagggacg aaggtgctcc caagagggaa gctttccact 1080

agaggagttc aaattgcttc caatgaaaat atggagacta tggaatcaag tacacttgaa 1140

ctgagaagca ggtactgggc cataaggacc agaagtggag gaaacaccaa tcaacagagg 1200

gcatctgcgg gccaaatcag catacaacct acgttctcag tacagagaaa tctccctttt 1260

gacagaacaa ccgttatggc agcattcagt gggaatacag aggggagaac atctgacatg 1320

aggaccgaaa tcataaggat gatggaaagt gcaagaccag aagatgtgtc tttccagggg 1380

cggggagtct tcgagctctc ggacgaaaag gcagcgagcc cgatcgtgcc ttcctttgac 1440

atgagtaatg aaggatctta tttcttcgga gacaatgcag aggaatacga taatatggat 1500

atcgatcctt ataaagaatt cggagctact gtggagttac tctcgtttct cccgagtgac 1560

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gagtctcctg agcactgcag ccctcaccat actgccctca ggcaagcaat tctttgctgg 1680

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ggagtgtgga tccgcactcc tccagcttat aggcctccga atgcccctat cctgtcgaca 1920

ctcccggaga ctactgttgt tagacgtcga ggcaggtcac ctagaagaag aactccttcg 1980

cctcgcaggc gaaggtctca atcgccgcgg cgccgaagat ctcaatctcg ggaatctcaa 2040

tgt 2043

<210> 44
<211> 2230
<212> DNA
<213> Artificial sequence

<220>
<223> Influenza B Virus NP Gene Fused to Synthetic HBcAg

<400> 44
atgtccaaca tggatattga cagtataaat accggaacaa tcgataaaac accagaagaa 60

ctgactcccg gaaccagtgg ggcaaccaga ccaatcatca agccagcaac ccttgctccg 120

ccaagcaaca aacgaacccg aaatccatct ccagaaagga caaccacaag cagtgaaacc 180

gatatcggaa ggaaaatcca aaagaaacaa accccaacag agataaagaa gagcgtctac 240

aaaatggtgg taaaactggg tgaattctac aaccagatga tggtcaaagc tggacttaat 300

gatgacatgg aaaggaatct aattcaaaat gcacaagctg tggagagaat cctattggct 360

gcaactgatg acaagaaaac tgaataccaa aagaaaagga atgccagaga tgtcaaagaa 420

gggaaggaag aaatagacca caacaagaca ggaggcacct tttataagat ggtaagagat 480

gataaaacca tctacttcag ccctataaaa attacctttt taaaagaaga ggtgaaaaca 540

atgtacaaga ccaccatggg gagtgatggt ttcagtggac taaatcacat tatgattgga 600

cattcacaga tgaacgatgt ctgtttccaa agatcaaagg gactgaaaag ggttggactt 660

gacccttcat taatcagtac ttttgccgga agcacactac ccagaagatc aggtacaact 720

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gcaatggcag acagagggct actgagagac atcaaggcca agacggccta tgaaaagatt 840

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atcggaagta ggaacccagg gattgcagac atagaagacc taactctgct tgccagaagc 960

atggtagttg tcagaccctc tgtagcgagc aaagtggtgc ttcccataag catttatgct 1020

aaaatacctc aactaggatt caataccgaa gaatactcta tggttgggta tgaagccatg 1080

gctctttata atatggcaac acctgtttcc atattaagaa tgggagatga cgcaaaagat 1140

aaatctcaac tattcttcat gtcgtgcttc ggagctgcct atgaagatct aagagtgtta 1200

tctgcactaa cgggcaccga atttaagcct agatcagcac taaaatgcaa gggtttccat 1260

gtcccggcta aggagcaagt agaaggaatg ggggcagctc tgatgtccat caagcttcag 1320

ttctgggccc caatgaccag atctggaggg aatgaagtaa gtggagaagg agggtctggt 1380

caaataagtt gcagccctgt gtttgcagta gaaagaccta ttgctctaag caagcaagct 1440

gtaagaagaa tgctgtcaat gaacgttgaa ggacgtgatg cagatgtcaa aggaaatcta 1500

ctcaaaatga tgaatgattc aatggcaaag aaaaccagtg gaaatgcttt cattgggaag 1560

aaaatgtttc aaatatcaga caaaaacaaa gtcaatccca ttgagattcc aattaagcag 1620

accatcccca atttcttctt tgggagggac acagcagagg attatgatga cctcgattat 1680

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tctttcggag tgtggatccg cactcctcca gcttataggc ctccgaatgc ccctatcctg 2100

tcgacactcc cggagactac tgttgttaga cgtcgaggca ggtcacctag aagaagaact 2160

ccttcgcctc gcaggcgaag gtctcaatcg ccgcggcgcc gaagatctca atctcgggaa 2220

tctcaatgtt 2230

<210> 45

<211> 1305
<212> DNA
<213> Artificial sequence

<220>
<223> Influenza A Virus M1 Fused to Synthetic HBcAg

<400> 45
atgagtcttc taaccgaggt cgaaacgtac gtactctcta tcatcccgtc aggccccctc 60

aaagccgaga tcgcacagag acttgaagat gtctttgcag ggaagaacac tgatcttgag 120

gttctcatgg aatggctaaa gacaagacca atcctgtcac ctctgactaa ggggatttta 180

ggatttgtgt tcacgctcac cgtgcccagt gagcgaggac tgcagcgtag acgctttgtc 240

caaaatgccc ttaatgggaa cggggatcca ataacatgg acaaagcagt taaactgtat 300

aggaagctca agagggagat aacattccat ggggccaaag aaatctcact cagttattct 360

gctggtgcac ttgccagttg tatgggcctc atatacaaca ggatgggggc tgtgaccact 420

gaagtggcat ttggcctggt atgtgcaacc tgtgaacaga ttgctgactc ccagcatcgg 480

tctcataggc aaatggtgac aacaaccaat ccactaatca gacatgagaa cagaatggtt 540

ttagccagca ctacagctaa ggctatggag caaatggctg gatcgagtga gcaagcagca 600

gaggccatgg aggttgctag tcaggctaga caaatggtgc aagcgatgag aaccattggg 660

actcatccta gctccagtgc tggtctgaaa aatgatcttc ttgaaaattt gcaggcctat 720

cagaaacgaa tgggggtgca gatgcaacgg ttcaagatgg atatcgatcc ttataaagaa 780

ttcggagcta ctgtggagtt actctcgttt ctcccgagtg acttctttcc ttcagtacga 840

gatcttctgg ataccgccag cgcgctgtat cgggaagcct tggagtctcc tgagcactgc 900

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gtcaacacta atatgggttt aaagttcagg caactcttgt ggtttcacat tagctgcctc 1080

actttcggcc gagaaacagt tctagaatat ttggtgtctt tcggagtgtg gatccgcact 1140

cctccagctt ataggcctcc gaatgcccct atcctgtcga cactcccgga gactactgtt 1200

gttagacgtc gaggcaggtc acctagaaga agaactcctt cgcctcgcag gcgaaggtct 1260

caatcgccgc ggcgccgaag atctcaatct cgggaatctc aatgt 1305

<210> 46
<211> 1581
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for TPANP from VR4700

<400> 46
atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgcccagcg ctagaggatc gggaatggcg tcccaaggca ccaaacggtc ttacgaacag 120

atggagactg atggagaacg ccagaatgcc actgaaatca gagcatccgt cggaaaaatg 180

attggtggaa ttggacgatt ctacatccaa atgtgcaccg aactcaaact cagtgattat 240

gagggacggt tgatccaaaa cagcttaaca atagagagaa tggtgctctc tgcttttgac 300

gaaaggagaa ataaatacct ggaagaacat cccagtgcgg ggaaagatcc taagaaaact 360

ggaggaccta tatacaggag agtaaacgga aagtggatga gagaactcat cctttatgac 420

aaagaagaaa taaggcgaat ctggcgccaa gctaataatg gtgacgatgc aacggctggt 480

ctgactcaca tgatgatctg gcattccaat ttgaatgatg caacttatca gaggacaaga 540

gctcttgttc gcaccggaat ggatcccagg atgtgctctc tgatgcaagg ttcaactctc 600

cctaggaggt ctggagccgc aggtgctgca gtcaaaggag ttggaacaat ggtgatggaa 660

ttggtcagga tgatcaaacg tgggatcaat gatcggaact tctggagggg tgagaatgga 720

cgaaaaacaa gaattgctta tgaaagaatg tgcaacattc tcaaagggaa atttcaaact 780

gctgcacaaa aagcaatgat ggatcaagtg agagagagcc ggaacccagg gaatgctgag 840

ttcgaagatc tcacttttct agcacggtct gcactcatat tgagagggtc ggttgctcac 900

aagtcctgcc tgcctgcctg tgtgtatgga cctgccgtag ccagtgggta cgactttgaa 960

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tacagcctaa tcagaccaaa tgagaatcca gcacacaaga gtcaactggt gtggatggca 1080

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tcagtacaga gaaatctccc ttttgacaga acaaccatta tggcagcatt caatgggaat 1380

acagagggaa gaacatctga catgaggacc gaaatcataa ggatgatgga aagtgcaaga 1440

ccagaagatg tgtctttcca ggggcgggga gtcttcgagc tctcggacga aaaggcagcg 1500

agcccgatcg tgccttcctt tgacatgagt aatgaaggat cttatttctt cggagacaat 1560

gcagatgagt acgacaatta a 1581

<210> 47
<211> 333
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for TPAM2 DeltaTM from VR4707

<400> 47
atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgcccagcg ctagaggatc gggaatgagt cttctgaccg aggtcgaaac ccctatcaga 120

aacgaatggg ggtgcagatg caacgattca agtgatcctg gcggcggcga tcggcttttt 180

ttcaaatgca tttatcggcg ctttaaatac ggcttgaaaa gagggccttc taccgaagga 240

gtgccagagt ctatgaggga agaatatcgg aaggaacagc agaatgctgt ggatgttgac 300

gatagccatt ttgtcagcat cgagctggag taa 333

<210> 48
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify TPAM2 Fragment

<400> 48
gccgaatcca tggatgcaat gaag 24

<210> 49
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify TPAM2 Fragment

<400> 49
ggtgccttgg gacgccatat cacttgaatc gttgca 36

<210> 50
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene

<400> 50
tgcaacgatt caagtgatat ggcgtcccaa ggcacc 36

<210> 51
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene

<400> 51
gccgtcgact taattgtcgt actc 24

<210> 52
<211> 1653
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for TPAM2NP from VR4710

<400> 52
atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgcccagcg ctagaggatc gggaatgagt cttctgaccg aggtcgaaac ccctatcaga 120

aacgaatggg ggtgcagatg caacgattca agtgatatgg cgtcccaagg caccaaacgg 180

tcttacgaac agatggagac tgatggagaa cgccagaatg ccactgaaat cagagcatcc 240

gtcggaaaaa tgattggtgg aattggacga ttctacatcc aaatgtgcac cgaactcaaa 300

ctcagtgatt atgagggacg gttgatccaa aacagcttaa caatagagag aatggtgctc 360

tctgcttttg acgaaaggag aaataaatac ctggaagaac atcccagtgc ggggaaagat 420

cctaagaaaa ctggaggacc tatatacagg agagtaaacg gaaagtggat gagagaactc 480

atcctttatg acaaagaaga aataaggcga atctggcgcc aagctaataa tggtgacgat 540

gcaacggctg gtctgactca catgatgatc tggcattcca atttgaatga tgcaacttat 600

cagaggacaa gagctcttgt tcgcaccgga atggatccca ggatgtgctc tctgatgcaa 660

ggttcaactc tccctaggag gtctggagcc gcaggtgctg cagtcaaagg agttggaaca 720

atggtgatgg aattggtcag gatgatcaaa cgtgggatca atgatcggaa cttctggagg 780

ggtgagaatg gacgaaaaac aagaattgct tatgaaagaa tgtgcaacat tctcaaaggg 840

aaatttcaaa ctgctgcaca aaaagcaatg atggatcaag tgagagagag ccggaaccca 900

gggaatgctg agttcgaaga tctcactttt ctagcacggt ctgcactcat attgagaggg 960

tcggttgctc acaagtcctg cctgcctgcc tgtgtgtatg gacctgccgt agccagtggg 1020

tacgactttg aaagagaggg atactctcta gtcggaatag acccttcag actgcttcaa 1080

aacagccaag tgtacagcct aatcagacca aatgagaatc cagcacacaa gagtcaactg 1140

gtgtggatgg catgccattc tgccgcattt gaagatctaa gagtattaag cttcatcaaa 1200

gggacgaagg tgctcccaag agggaagctt tccactagag gagttcaaat tgcttccaat 1260

gaaaatatgg agactatgga atcaagtaca cttgaactga gaagcaggta ctgggccata 1320

aggaccagaa gtggaggaaa caccaatcaa cagagggcat ctgcgggcca aatcagcata 1380

caacctacgt tctcagtaca gagaaatctc ccttttgaca gaacaaccat tatggcagca 1440

ttcaatggga atacagaggg aagaacatct gacatgagga ccgaaatcat aaggatgatg 1500

gaaagtgcaa gaccagaaga tgtgtctttc caggggcggg gagtcttcga gctctcggac 1560

gaaaaggcag cgagcccgat cgtgccttcc tttgacatga gtaatgaagg atcttatttc 1620

ttcggagaca atgcagatga gtacgacaat taa 1653

<210> 53
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the HA Gene

<400> 53
gggctagcgc cgccaccatg aagaccatca ttgct 35

<210> 54
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the HA Gene

<400> 54
ccgtcgactc aaatgcaaat gttgca 26

<210> 55
<211> 1701
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for HA H3N2 from VR4750

<400> 55
atgaagacca tcattgcttt gagctacatt ttctgtctgg ctctcggcca agaccttcca 60

ggaaatgaca acaacacagc aacgctgtgc ctgggacatc atgcggtgcc aaacggaaca 120

ctagtgaaaa caatcacaga tgatcagatt gaagtgacta atgctactga gctagttcag 180

agctcctcaa cggggaaaat atgcaacaat cctcatcgaa tccttgatgg aatagactgc 240

acactgatag atgctctatt gggggaccct cattgtgatg tttttcaaaa tgagacatgg 300

gacctttttcg ttgaacgcag caaagctttc agcaactgtt acccttatga tgtgccagat 360

tatgcccccc ttaggtcact agttgcctcg tcaggcactc tggagtttat cactgagggt 420

ttcacttgga ctggggtcac tcagaatggg ggaagcagtg cttgcaaaag gggacctggt 480

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aacgtgacta tgccaaacaa tgacaatttt gacaaactat acatttgggg ggttcaccac 600

ccgagcacga accaagaaca aaccagcctg tatgttcaag catcagggag agtcacagtc 660

tctaccagga gaagccagca aactataatc ccgaatatcg agtccagacc ctgggtaagg 720

ggtctgtcta gtagaataag catctattgg acaatagtta agccgggaga cgtactggta 780

attaatagta atgggaacct aatcgctcct cggggttatt tcaagatgcg cactgggaaa 840

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aatggaagca ttcccaatga caagcccttt caaaacgtaa acaaaatcac gtatggagca 960

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gagaaacaaa ctagaggcct attcggcgca atagcaggtt tcatagaaaa tggttgggag 1080

ggaatgatag acggttggta cggtttcagg catcaaaatt ctgagggcac aggacaagca 1140

gcagatctta aaagcactca agcagccatc gaccaaatca atgggaaatt gaacaggata 1200

atcaagaaga cgaacgagaa attccatcaa atcgaaaagg aattctcaga agtagaaggg 1260

agaattcagg acctcgagaa atacgttgaa gacactaaaa tagatctctg gtcttacaat 1320

gcggagcttc ttgtcgctct ggagaatcaa catacaattg acctgactga ctcggaaatg 1380

aacaagctgt ttgaaaaaac aaggaggcaa ctgagggaaa atgctgaaga catgggcaat 1440

ggttgcttca aaatatacca caaatgtgac aacgcttgca tagagtcaat cagaactggg 1500

acttatgacc atgatgtata cagagacgaa gcattaaaca accggtttca gatcaaaggt 1560

gttgaactga agtctggata caaagactgg atcctgtgga tttcctttgc catatcatgc 1620

tttttgcttt gtgttgtttt gctggggttc atcatgtggg cctgccagaa aggcaacatt 1680

aggtgcaaca tttgcatttg a 1701

<210> 56
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the HA Gene

<400> 56
gggctagcgc cgccaccatg aaggcaaacc tactg 35

<210> 57
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the HA Gene

<400> 57

ccgtcgactc agatgcatat tctgca 26

<210> 58
<211> 1701
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for HA H1N1 from VR4752

<400> 58
atgaaggcaa acctactggt cctgttatgt gcacttgcag ctgcagatgc agacacaata 60

tgtataggct accatgcgaa caattcaacc gacactgttg acacagtgct cgagaagaat 120

gtgacagtga cacactctgt taacctgctc gaagacagcc acaacggaaa actatgtaga 180

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aacccagaat gcgacccact gcttccagtg agatcatggt cctacattgt agaaacacca 300

aactctgaga atggaatatg ttatccagga gatttcatcg actatgagga gctgagggag 360

caattgagct cagtgtcatc attcgaaaga ttcgaaatat ttcccaaaga aagctcatgg 420

cccaaccaca acacaaccaa aggagtaacg gcagcatgct cccatgcggg gaaaagcagt 480

ttttacagaa atttgctatg gctgacggag aaggagggct catacccaaa gctgaaaaat 540

tcttatgtga acaagaaagg gaaagaagtc cttgtactgt ggggtattca tcacccgtct 600

aacagtaagg atcaacagaa tatctatcag aatgaaaatg cttatgtctc tgtagtgact 660

tcaaattata acaggagatt taccccggaa atagcagaaa gacccaaagt aagagatcaa 720

gctgggagga tgaactatta ctggaccttg ctaaaacccg gagacacaat aatatttgag 780

gcaaatggaa atctaatagc accaaggtat gctttcgcac tgagtagagg ctttgggtcc 840

ggcatcatca cctcaaacgc atcaatgcat gagtgtaaca cgaagtgtca aacacccctg 900

ggagctataa acagcagtct ccctttccag aatatacacc cagtcacaat aggagagtgc 960

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gaattgttag ttctactgga aaatgaaagg actctggatt tccatgactc aaatgtgaag 1380

aatctgtatg agaaagtaaa aagccaatta aagaataatg ccaaagaaat cggaaatgga 1440

tgttttgagt tctaccacaa gtgtgacaat gaatgcatgg aaagtgtaag aaatgggact 1500

tatgattatc ccaaatattc agaagagtca aagttgaaca gggaaaaggt agatggagtg 1560

aaattggaat caatggggat ctatcagatt ctggcgatct actcaactgt cgccagttca 1620

ctggtgcttt tggtctccct gggggcaatc agtttctgga tgtgttctaa tggatctttg 1680

cagtgcagaa tatgcatctg a 1701

<210> 59
<211> 1050
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for the M2M1 Fusion from VR4755

<400> 59
atgagcctgc tgaccgaggt ggagaccccc atcagaaacg agtggggctg cagatgcaac 60

gacagcagcg acccccctggt ggtggccgcc agcatcatcg gcatcctgca cctgatcctg 120

tggatcctgg acagactgtt cttcaagtgc atctacagac tgttcaagca cggcctgaag 180

agaggcccca gcaccgaggg cgtgcccgag agcatgagag aggagtacag aaaggagcag 240

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gagtggctga agaccagacc catcctgagc cccctgacca agggcatcct gggcttcgtg 480

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aagagagaga tcaccttcca cggcgccaag gagatcgccc tgagctacag cgccggcgcc 660

ctggccagct gcatgggcct gatctacaac agaatgggcg ccgtgaccac cgaggtggcc 720

ttcggcctgg tgtgcgccac ctgcgagcag atcgccgaca gccagcacag aagccacaga 780

cagatggtgg ccaccaccaa ccccctgatc agacacgaga acagaatggt gctggccagc 840

accaccgcca aggccatgga gcagatggcc ggcagcagcg agcaggccgc cgaggccatg 900

gagatcgcca gccaggccag acagatggtg caggccatga gagccatcgg cacccacccc 960

agcagcagcg ccggcctgaa ggacgacctg ctggagaacc tgcagaccta ccagaagaga 1020

atgggcgtgc agatgcagag attcaagtga 1050

<210> 60
<211> 982
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for Fragment 7 from VR4756

<400> 60
atgagccttc taaccgaggt cgaaacgtat gttctctcta tcgttccatc aggccccctc 60

aaagccgaaa tcgcgcagag acttgaagat gtctttgctg ggaaaaacac agatcttgag 120

gctctcatgg aatggctaaa gacaagacca atcctgtcac ctctgactaa ggggattttg 180

gggtttgtgt tcacgctcac cgtgcccagt gagcgaggac tgcagcgtag acgctttgtc 240

caaaatgccc tcaatgggaa tggggatcca ataacatgg acagagcagt taaactatat 300

agaaaactta agagggagat tacattccat ggggccaaag aaatagcact cagttattct 360

gctggtgcac ttgccagttg catgggcctc atatacaaca gaatgggggc tgtaaccact 420

gaagtggcct ttggcctggt atgtgcaaca tgtgaacaga ttgctgactc ccagcacagg 480

tctcataggc aaatggtggc aacaaccaat ccattaataa ggcatgagaa cagaatggtt 540

ttggccagca ctacagctaa ggctatggag caaatggctg gatcaagtga gcaggcagcg 600

gaggccatgg aaattgctag tcaggccagg caaatggtgc aggcaatgag agccattggg 660

actcatccta gctccagtgc tggtctaaaa gatgatcttc ttgaaaattt gcagacctat 720

cagaaacgaa tgggggtgca gatgcaacga ttcaagtgac ccgcttgttg ttgctgcgag 780

tatcattggg atcttgcact tgatattgtg gattcttgat cgtctttttt tcaaatgcat 840

ctatcgactc ttcaaacacg gtctgaaaag agggccttct acggaaggag tacctgagtc 900

tatgagggaa gaatatcgaa aggaacagca gaatgctgtg gatgctgacg acagtcattt 960

tgtcagcata gagctggagt aa 982

<210> 61
<211> 982
<212> DNA
<213> Artificial sequence

<220>
<223> Codon Optimized Segment 7 from VR4763

<400> 61
atgagcctgc tgaccgaggt cgaaacgtat gttctctcta tcgtgcccag cggccccctg 60

aaggccgaga tcgcccagag actggaggac gtgttcgccg gcaagaacac cgacctggag 120

gccctgatgg agtggctgaa gaccagaccc atcctgagcc ccctgaccaa gggcatcctg 180

ggcttcgtgt tcaccctgac cgtgcccagc gagagaggcc tgcagagaag aagattcgtg 240

cagaacgccc tgaacggcaa cggcgacccc aacaacatgg acagagccgt gaagctgtac 300

agaaagctga agagagagat caccttccac ggcgccaagg agatcgccct gagctacagc 360

gccggcgccc tggccagctg catgggcctg atctacaaca gaatgggcgc cgtgaccacc 420

gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag ccagcacaga 480

agccacagac agatggtggc caccaccaac cccctgatca gacacgagaa cagaatggtg 540

ctggccagca ccaccgccaa ggccatggag cagatggccg gcagcagcga gcaggccgcc 600

gaggccatgg agatcgccag ccaggccaga cagatggtgc aggccatgag agccatcggc 660

acccacccca gcagcagcgc cggcctgaaa gatgatcttc ttgaaaattt gcagacctat 720

cagaaacgaa tgggggtgca gatgcaacga ttcaagtgac cccctggtgg tggccgccag 780

catcatcggc atcctgcacc tgatcctgtg gatcctggac agactgttct tcaagtgcat 840

ctacagactg ttcaagcacg gcctgaagag aggccccagc accgagggcg tgcccgagag 900

catgagagag gagtacagaa aggagcagca gaacgccgtg gacgccgacg acagccactt 960

cgtgagcatc gagctggagt ga 982

<210> 62
<211> 1569
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for eM2NP Codon Optimized by Contract

<400> 62
atgagcttgc tcactgaagt cgagacacca atcagaaacg aatggggatg tagatgcaac 60

gatagctcag acatggcctc ccagggaacc aaaagaagct atgaacagat ggagactgac 120

ggagagagac agaacgccac agagatcaga gctagtgtag gaaagatgat agacggtatc 180

gggcgatttt acattcaaat gtgtacggaa ttgaaactca gcgactatga aggcagactt 240

atccagaact cactcacaat tgagcgcatg gtactcagtg catttgatga aagaaggaat 300

aggtacctcg aagaacaccc cagcgccggc aaagatccca agaagactgg cggcccaatt 360

tacagaagag tggacggtaa gtggatgaga gagctggtat tgtacgataa agaagaaatt 420

agaagaatct ggaggcaagc aaacaatgga gaggatgcta cagctggcct gacccacatg 480

atgatttggc atagtaacct gaatgatacc acctaccagc ggacaagggc tctcgttcga 540

accgggatgg atccccgcat gtgctcattg atgcagggta gtacactccc gaggaggtca 600

ggcgcggccg gtgcagccgt gaaaggaatc ggcactatgg taatggaatt gataagaatg 660

attaaaaggg ggattaatga caggaacttt tggagaggag aaaatggacg caaaacaagg 720

agtgcgtatg aacggatgtg caatattttg aaaggaaaat tccaaactgc agcacagcgc 780

gccatgatgg atcaggtacg agaaagtcgc aacccaggta atgctgaaat agaggacctt 840

atatttctcg cccggagtgc tctcatactt agaggaagcg tggcccataa aagttgtctc 900

cccgcatgcg tatacggtcc cgctgtgtct tccggatacg attttgaaaa agagggatat 960

tcattggtgg gaatcgaccc ttttaagctg cttcagaact cacaggttta cagtttgatt 1020

agaccaaacg agaacccagc ccacaaatca caactcgtgt ggatggcatg ccactctgcc 1080

gctttcgaag atctgagact gctctcattt attagaggca ctaaagtgag cccgagggga 1140

aaactgagca cacgaggagt acagatagca tctaacgaaa atatggataa tatgggatct 1200

agcacactcg aattgaggtc acgatactgg gctattagaa cacggagcgg agggaacacc 1260

aaccagcaga gagcatccgc cggtcagata agcgttcagc ctacattttc agtacaacga 1320

aacctgccat ttgaaaagag tacagtgatg gccgcattta ctggcaacac cgagggacga 1380

acaagcgaca tgagagcaga gattattaga atgatggaag gagctaaacc agaggaggtt 1440

tcatttagag gaaggggagt cttcgaattg tccgatgaga aagccacaaa tcccatagta 1500

cctagcttcg acatgtccaa cgaaggctct tacttttttg gtgacaatgc cgaagagtac 1560

gacaattga 1569

<210> 63
<211> 1569
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for eM2NP Codon Optimized by Applicants

<400> 63
atgagcctgc tgaccgaggt ggagaccccc atcagaaacg agtggggctg cagatgcaac 60

gacagcagcg acatggccag ccagggcacc aagagaagct acgagcagat ggagaccgac 120

ggcgagagac agaacgccac cgagatcaga gccagcgtgg gcaagatgat cgacggcatc 180

ggcagattct acatccagat gtgcaccgag ctgaagctga gcgactacga gggcagactg 240

atccagaaca gcctgaccat cgagagaatg gtgctgagcg ccttcgacga gagaagaaac 300

agatacctgg aggagcaccc cagcgccggc aaggacccca agaagaccgg cggccccatc 360

tacagaagag tggacggcaa gtggatgaga gagctggtgc tgtacgacaa ggaggagatc 420

agaagaatct ggagacaggc caacaacggc gaggacgcca ccgccggcct gacccacatg 480

atgatctggc acagcaacct gaacgacacc acctaccaga gaaccagagc cctggtgcgg 540

accggcatgg accccagaat gtgcagcctg atgcagggca gcaccctgcc cagaagaagc 600

ggcgccgccg gcgccgccgt gaagggcatc ggcaccatgg tgatggagct gatcagaatg 660

atcaagagag gcatcaacga cagaaacttc tggagaggcg agaacggcag aaagaccaga 720

agcgcctacg agagaatgtg caacatcctg aagggcaagt tccagaccgc cgcccagaga 780

gccatgatgg accaggtccg ggagagcaga aaccccggca acgccgagat cgaggacctg 840

atcttcctgg ccagaagcgc cctgatcctg agaggcagcg tggcccacaa gagctgcctg 900

cccgcctgcg tgtacggccc cgccgtgagc agcggctacg acttcgagaa ggagggctac 960

agcctggtgg gcatcgaccc cttcaagctg ctgcagaaca gccaggtgta cagcctgatc 1020

agacccaacg agaaccccgc ccacaagagc cagctggtgt ggatggcctg ccacagcgcc 1080

gccttcgagg acctgagact gctgagcttc atcagaggca ccaaggtgtc ccccagaggc 1140

aagctgagca ccagaggcgt gcagatcgcc agcaacgaga acatggacaa catgggcagc 1200

agcaccctgg agctgagaag cagatactgg gccatcagaa ccagaagcgg cggcaacacc 1260

aaccagcaga gagccagcgc cggccagatc agcgtgcagc ccaccttcag cgtgcagaga 1320

aacctgccct tcgagaagag caccgtgatg gccgccttca ccggcaacac cgagggcaga 1380

accagcgaca tgagagccga gatcatcaga atgatggagg gcgccaagcc cgaggaggtg 1440

tccttcagag gcagaggcgt gttcgagctg agcgacgaga aggccaccaa ccccatcgtg 1500

cctagcttcg acatgagcaa cgagggcagc tacttcttcg gcgacaacgc cgaggagtac 1560

gacaactga 1569

<210> 64
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the M2 Gene

<400> 64
gccgaattcg ccaccatgag cctgctgacc 30

<210> 65
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify the M2 Gene

<400> 65
gccgtcgact gatcactcca gctcgatgct cac 33

<210> 66
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for M2 Gene from VR4759

<400> 66

atgagcctgc tgaccgaggt ggagaccccc atcagaaacg agtggggctg cagatgcaac 60

gacagcagcg acccccctggt ggtggccgcc agcatcatcg gcatcctgca cctgatcctg 120

tggatcctgg acagactgtt cttcaagtgc atctacagac tgttcaagca cggcctgaag 180

agaggcccca gcaccgaggg cgtgcccgag agcatgagag aggagtacag aaaggagcag 240

cagaacgccg tggacgccga cgacagccac ttcgtgagca tcgagctgga gtga 294

<210> 67
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used Amplify M1 Gene from VR4755

<400> 67
gccgaattcg ccaccatgtc cctgctgaca gaagtg 36

<210> 68
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify M1 Gene from VR4755

<400> 68
gccgtcgact gatcacttga atctctgcat c 31

<210> 69
<211> 759
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for M1 Gene from VR4760

<400> 69
atgtccctgc tgacagaagt ggaaacatac gtgctgagca tcgtgcccag cggcccccctg 60

aaggccgaga tcgcccagag actggaggac gtgttcgccg gcaagaacac cgacctggag 120

gccctgatgg agtggctgaa gaccagaccc atcctgagcc ccctgaccaa gggcatcctg 180

ggcttcgtgt tcaccctgac cgtgcccagc gagagaggcc tgcagagaag aagattcgtg 240

cagaacgccc tgaacggcaa cggcgacccc aacaacatgg accgggccgt gaagctgtac 300

cggaagctga agagagagat caccttccac ggcgccaagg agatcgccct gagctacagc 360

gccggcgccc tggccagctg catgggcctg atctacaaca gaatgggcgc cgtgaccacc 420

gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag ccagcacaga 480

agccacagac agatggtggc caccaccaac cccctgatca gacacgagaa cagaatggtg 540

ctggccagca ccaccgccaa ggccatggag cagatggccg gcagcagcga gcaggccgcc 600

gaggccatgg agatcgccag ccaggccaga cagatggtgc aggccatgag agccatcggc 660

acccacccca gcagcagcgc cggcctgaag gacgacctgc tggagaacct gcagacctac 720

cagaagagaa tgggcgtgca gatgcagaga ttcaagtga 759

<210> 70
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene from VR4757

<400> 70
gccgaattcg ccaccatggc ctcccaggga accaaaag 38

<210> 71
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene from VR4757

<400> 71
gccgtcgact gatcaattgt cgtactcttc 30

<210> 72
<211> 1497
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for NP Codon Optimized by Contract

<400> 72
atggcctccc agggaaccaa aagaagctat gaacagatgg agactgacgg agagagacag 60

aacgccacag agatcagagc tagtgtagga aagatgatag acggtatcgg gcgattttac 120

attcaaatgt gtacggaatt gaaactcagc gactatgaag gcagacttat ccagaactca 180

ctcacaattg agcgcatggt actcagtgca tttgatgaaa gaaggaatag gtacctcgaa 240

gaacacccca gcgccggcaa agatcccaag aagactggcg gcccaattta cagaagagtg 300

gacggtaagt ggatgagaga gctggtattg tacgataaag aagaaattag aagaatctgg 360

aggcaagcaa acaatggaga ggatgctaca gctggcctga cccacatgat gatttggcat 420

agtaacctga atgataccac ctaccagcgg acaagggctc tcgttcgaac cgggatggat 480

ccccgcatgt gctcattgat gcagggtagt acactcccga ggaggtcagg cgcggccggt 540

gcagccgtga aaggaatcgg cactatggta atggaattga taagaatgat taaaaggggg 600

attaatgaca ggaacttttg gagaggagaa aatggacgca aaacaaggag tgcgtatgaa 660

cggatgtgca atattttgaa aggaaaattc caaactgcag cacagcgcgc catgatggat 720

caggtacgag aaagtcgcaa cccaggtaat gctgaaatag aggaccttat atttctcgcc 780

cggagtgctc tcatacttag aggaagcgtg gcccataaaa gttgtctccc cgcatgcgta 840

tacggtcccg ctgtgtcttc cggatacgat tttgaaaaag agggatattc attggtggga 900

atcgaccctt ttaagctgct tcagaactca caggtttaca gtttgattag accaaacgag 960

aacccagccc acaaatcaca actcgtgtgg atggcatgcc actctgccgc tttcgaagat 1020

ctgagactgc tctcatttat tagaggcact aaagtgagcc cgaggggaaa actgagcaca 1080

cgaggagtac agatagcatc taacgaaaat atggataata tgggatctag cacactcgaa 1140

ttgaggtcac gatactgggc tattagaaca cggagcggag ggaacaccaa ccagcagaga 1200

gcatccgccg gtcagataag cgttcagcct acattttcag tacaacgaaa cctgccattt 1260

gaaaagagta cagtgatggc cgcatttact ggcaacaccg agggacgaac aagcgacatg 1320

agagcagaga ttattagaat gatggaagga gctaaaccag aggaggtttc atttagagga 1380

aggggagtct tcgaattgtc cgatgagaaa gccacaaatc ccatagtacc tagcttcgac 1440

atgtccaacg aaggctctta ctttttggt gacaatgccg aagagtacga caattga 1497

<210> 73
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene from VR4758

<400> 73
gccgaattcg ccaccatggc cagccagggc accaag 36

<210> 74
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Used to Amplify NP Gene from VR4758

<400> 74
gccgtcgact gatcagttgt cgtactcc 28

<210> 75
<211> 1497
<212> DNA
<213> Artificial sequence

<220>
<223> Open Reading Frame for NP Codon Optimized by Applicants from VR4762

<400> 75
atggccagcc agggcaccaa gagaagctac gagcagatgg agaccgacgg cgagagacag 60

aacgccaccg agatcagagc cagcgtgggc aagatgatcg acggcatcgg cagattctac 120

atccagatgt gcaccgagct gaagctgagc gactacgagg gcagactgat ccagaacagc 180

ctgaccatcg agagaatggt gctgagcgcc ttcgacgaga gaagaaacag atacctggag 240

gagcacccca gcgccggcaa ggaccccaag aagaccggcg gccccatcta cagaagagtg 300

gacggcaagt ggatgagaga gctggtgctg tacgacaagg aggagatcag aagaatctgg 360

agacaggcca acaacggcga ggacgccacc gccggcctga cccacatgat gatctggcac 420

agcaacctga acgacaccac ctaccagaga accagagccc tggtgcggac cggcatggac 480

cccagaatgt gcagcctgat gcagggcagc accctgccca gaagaagcgg cgccgccggc 540

gccgccgtga agggcatcgg caccatggtg atggagctga tcagaatgat caagagaggc 600

atcaacgaca gaaacttctg gagaggcgag aacggcagaa agaccagaag cgcctacgag 660

agaatgtgca acatcctgaa gggcaagttc cagaccgccg cccagagagc catgatggac 720

caggtccggg agagcagaaa ccccggcaac gccgagatcg aggacctgat cttcctggcc 780

agaagcgccc tgatcctgag aggcagcgtg gcccacaaga gctgcctgcc cgcctgcgtg 840

tacggccccg ccgtgagcag cggctacgac ttcgagaagg agggctacag cctggtgggc 900

atcgaccccct tcaagctgct gcagaacagc caggtgtaca gcctgatcag acccaacgag 960

aaccccgccc acaagagcca gctggtgtgg atggcctgcc acagcgccgc cttcgaggac 1020

ctgagactgc tgagcttcat cagaggcacc aaggtgtccc ccagaggcaa gctgagcacc 1080

agaggcgtgc agatcgccag caacgagaac atggacaaca tgggcagcag caccctggag 1140

ctgagaagca gatactgggc catcagaacc agaagcggcg gcaacaccaa ccagcagaga 1200

gccagcgccg gccagatcag cgtgcagccc accttcagcg tgcagagaaa cctgcccttc 1260

gagaagagca ccgtgatggc cgccttcacc ggcaacaccg agggcagaac cagcgacatg 1320

agagccgaga tcatcagaat gatggagggc gccaagcccg aggaggtgtc cttcagaggc 1380

agaggcgtgt tcgagctgag cgacgagaag gccaccaacc ccatcgtgcc tagcttcgac 1440

atgagcaacg agggcagcta cttcttcggc gacaacgccg aggagtacga caactga 1497

<210> 76
<211> 498
<212> PRT
<213> Artificial sequence

<220>
<223> NP Consensus Sequence

<400> 76

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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 Lys Met
            20                  25                  30

Ile Asp Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
        35                  40                  45

Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu
    50                  55                  60

Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Arg Tyr Leu Glu
65                  70                  75                  80

Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile
                85                  90                  95

Tyr Arg Arg Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp
            100                 105                 110

Lys Glu Glu Ile Arg 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
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 Ile 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 Lys Thr Arg Ser Ala Tyr Glu Arg Met Cys Asn
    210                 215                 220
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Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
225                 230                 235                 240

Gln Val Arg Glu Ser 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 Pro Ala Val Ser 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 Val Tyr Ser Leu Ile Arg Pro Asn Glu
305                 310                 315                 320

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 Leu Leu Ser Phe Ile Arg Gly Thr Lys Val
            340                 345                 350

Ser Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
        355                 360                 365

Glu Asn Met Asp Asn Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
    370                 375                 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385                 390                 395                 400

Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
                405                 410                 415

Asn Leu Pro Phe Glu Lys Ser Thr Val Met Ala Ala Phe Thr Gly Asn
            420                 425                 430

Thr Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
        435                 440                 445

Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Arg Gly Arg Gly Val Phe
    450                 455                 460

Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
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465 470 475 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495

Asp Asn

<210> 77
<211> 252
<212> PRT
<213> Artificial sequence

<220>
<223> M1 Gene Consensus Sequence

<400> 77

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 Asn 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 Gly Ala
100 105 110

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

Gly Leu Ile Tyr Asn Arg Met Gly Ala 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 Ala 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 Ile Ala Ser Gln
        195                 200                 205

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

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

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
                245                 250
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<210> 78
<211> 97
<212> PRT
<213> Artificial sequence

<220>
<223> M2 Gene Consensus Sequence

<400> 78

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Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe
        35                  40                  45

Lys Cys Ile Tyr Arg Leu Phe Lys His Gly Leu Lys Arg Gly Pro Ser
    50                  55                  60

Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
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Gln Asn Ala Val Asp Ala Asp Asp Ser His Phe Val Ser Ile Glu Leu
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Glu
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tggatcctgg acagactgtt cttcaagtgc atctacagac tgttcaagca cggcctgaag 180

agaggcccca gcaccgaggg cgtgcccgag agcatgagag aggagtacag aaaggagcag 240

cagaacgccg tggacgccga cgacagccac ttcgtgagca tcgagctgga gtga 294

<210> 81
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> H2Kd Binding Peptide

<400> 81

Thr Tyr Gln Arg Thr Arg Ala Leu Val
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<223> RSV Promoter from Plasmid VCL1005

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<210> 85
<211> 19
<212> DNA
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<220>
<223> Primer WNVpst rev

<400> 85
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<210> 86
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<223> VR4772, M2 Insert Replacing WNV Insert from VR6430

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