SEQUENCE LISTING

<110> NEC Soft, Ltd

<120> Nucleic acid molecules which bind to Influenza virus and use thereof.

<130> 1010004889WO01

<150> JP 2012-126861
<151> 2012-06-04

<160> 53

<170> PatentIn version 3.5

<210> 1
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 1
ggttagcccg tcccgagata accttggggt ctttgggtgg ggttggtgtg gtcttaacac 60

acggcggctg tag 73

<210> 2
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 2
ggttagcccg tcccgagata acggtctcgg ctcggttctt tcggaaatgt tgcttaacac 60

acggcggctg tag 73

<210> 3
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 3
ggttagcccg tcccgagata acgggtttcg acttgatcgg acttaagcac cgcttaacac 60

acggcggctg tag 73

<210> 4
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 4
ggttagcccg tcccgagata acgggtggtt ggggggggcct tttctggttt tgtcttaaca 60

cacggcggct gtag 74

<210> 5
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 5
ggttagcccg tcccgagata actctcggct tggttcgtct gcgaaatgtt acttaacaca 60

cggcggctgt ag 72

<210> 6
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 6
cctgcaccca gtgtcccaca cgtgtatggg ttttttatgg ttaggtaggg gcggcttgac 60

ggagaggagg acgg 74

<210> 7
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 7
cctgcaccca gtgtccccgg cgtttggttg gcgtgaacca tttttaagtt ctgcgtgtga 60

cggagaggag gacgg 75

<210> 8
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 8
cctgcaccca gtgtcccgtc gttggtgttt ttttggcttt tagggtaggt gtggcttgac 60

ggagaggagg acgg 74

<210> 9
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 9
cctgcaccca gtgtccctcg cttctttttt tgggttgggg tgggcgggtt cctgtcggac 60

ggagaggagg acgg 74

<210> 10
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 10
cctgcaccca gtgtcccccc ctgtgtcggg cgggccgttc agggttttgg gtgggggtga 60

cggagaggag gacgg 75

<210> 11
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 11
ggttagcccg tcccgagata acctgtgttg ggggtgggag ggtttttggg gtcttaacac 60

acggcggctg tag 73

<210> 12
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 12
ggttagcccg tcccgagata actcggggtg tttgatggtt tggtctggtt ggcttaacac 60

acggcggctg tag 73

<210> 13
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 13
ggtttggtct ggttgg 16

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 14
gtggtttggt ctggttggac 20

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 15
cgtttggttt ggtctggttg gcaacg 26

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 16
cgttatggtt tggtctggtt ggctaacg 28

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 17
gtgtttgatg gtttggtctg gttggcttaa cac 33

<210> 18
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 18
ggttagcccg tcccgagata actcggtgtg ttgggtttgg gttgggttgg gtcttaacac 60

acggcggctg tag 73

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 19
gggtttgggt tgggttggg 19

<210> 20
<211> 87

<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 20
atatatatgc ccaccctctc gctgtacggt tgatgcgcgt ttctttctct ttatattgct 60

gggtgccgcc tccaaggtca aaaaaaa 87

<210> 21
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 21
gggcaccctc tcgctgtacg gttgatgcac gtttctttct ctttatattg ctgggtgccc 60

<210> 22
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 22
atatatatgc ccaccctctc gctggcggct ctgttctgtt ctcgtctcct tgatttctgt 60

gggcagccgc ctccaaggtc aaaaaaaa 88

<210> 23
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 23
ggggcccacc ctctcgctgg cggctctgtt ctgttctcgt ctccttgatt tctgtgggcc 60

cc 62

<210> 24
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 24
atatatatcc tgcacccagt gtcccgtgtg caattcagtt ggggttattt tgggagggcg 60

ggggttgacg gagaggagga cggaaaaaaa a 91

<210> 25
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 25
ttggggttat tttgggaggg cgggggtt 28

<210> 26
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 26
cctgcaccca gtgtcccttt cctcgttggg ggtggtggtg ggtttcggtt catgggtggg 60

acggagagga ggacgg 76

<210> 27
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 27
tcctcgttgg gggtggtggt gggtttcggt tcatgggtgg gacggagagg a 51

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

<220>
<223> aptamer

<400> 28
cctgcaccca gtgtcccgtg ctccgggggt tgggcgtggt gggtctgtcg ggtttcggac 60

ggagaggagg acgg 74

<210> 29
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 29
cctgcaccca gtgtccctgg gtcggctaat ttggcatttg gggtggtttg gggggggac 60

ggagaggagg acgg 74

<210> 30
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 30
cctgcaccca gtgtccctgt gtgctggtgt ggggtggttt gggggggga cggagaggag 60

gacgg 65

<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<220>
<221> misc_feature
<222> (20)..(20)
<223> n represents one ore more any bases

<400> 31
gggtttgggt tgggttgggn gggtttgggt tgggttggg 39

<210> 32
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 32
gggtttgggt tgggttgggt ttttttttgg gtttgggttg ggttggg 47

<210> 33
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 33
gggtttgggt tgggttgggt ttttgggttt gggttgggtt ggg 43

<210> 34
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<220>
<221> misc_feature
<222> (23)..(23)
<223> n represents random 30-mer sequence.

<400> 34
ggttagcccg tcccgagata acncttaaca cacggcggct gtag 44

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<220>
<221> misc_feature
<222> (13)..(13)
<223> n represents random 40-mer sequence.

<400> 35
acccagtgtc ccngacggag aggaggacgg 30

<210> 36
<211> 337
<212> PRT
<213> Influenza virus/A/Anhui/1/2005

<400> 36

Met Glu Lys Ile Val Leu Leu Leu Ala Ile 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 Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp 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 Asn 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 Asp His Glu Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile

165 170 175

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

Gly Ile His His Ser 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 Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

Arg Met Asp 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 Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile 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 Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

Pro

<210> 37
<211> 338
<212> PRT
<213> Influenza virus/A/goose-Guiyang/337/2006

<400> 37

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

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Val 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 Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asp 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 Asp 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 Pro Asn His Glu Ala Ser
130 135 140

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

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Ser 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 Ile Lys Leu Tyr Gln
195 200 205

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

Leu Val Pro Thr Ile Ala Thr Arg Ser 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 Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

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

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

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

Thr Leu

<210> 38
<211> 523
<212> PRT
<213> Influenza virus/A/Anhui/1/2005

<400> 38

```
Met Glu Lys Ile Val Leu Leu Leu Ala Ile 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 Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp 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 Asn 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 Asp His Glu Ala Ser
    130                 135                 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
145                 150                 155                 160

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

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

Gly Ile His His Ser 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 Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

Arg Met Asp 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 Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile 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 Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

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

Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn Glu Gln
355 360 365

Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp
370 375 380

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

Phe Glu Ala Val Gly Arg Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu
405 410 415

Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr
420 425 430

Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe
435 440 445

His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu
450 455 460

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

Lys Cys Asp Asn Glu Cys Met Glu Ser Val Arg Asn Gly Thr Tyr Asp
485 490 495

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

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

<210> 39
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 39
cggcgtttgg ttggcgtgaa ccatttttaa gtt 33

<210> 40
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 40
aattaaccct cactaaaggg ctgagtctca aaaccgcaat acactggttg tatggtcgaa 60

taagttaa 68

<210> 41
<211> 344
<212> PRT
<213> Influenza virus/A/california/04/2009

<400> 41

Met Lys Ala Ile Leu Val Val Leu Leu Tyr Thr Phe Ala Thr Ala Asn
1 5 10 15

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

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

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

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

Ser Asn Lys Gly Val Thr Ala Ala Cys Pro His Ala Gly Ala Lys Ser
145                 150                 155                 160

Phe Tyr Lys Asn Leu Ile Trp Leu Val Lys Lys Gly Asn Ser Tyr Pro
                165                 170                 175

Lys Leu Ser Lys Ser Tyr Ile Asn Asp Lys Gly Lys Glu Val Leu Val
            180                 185                 190

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

Tyr Gln Asn Ala Asp Thr Tyr Val Phe Val Gly Ser Ser Arg Tyr Ser
    210                 215                 220

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

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

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

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

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

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

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

Asn Ile Pro Ser Ile Gln Ser Arg
            340
```

<210> 42
<211> 343
<212> PRT
<213> Influenza virus/A/Brisbane/59/2007

<400> 42

```
Met Lys Val Lys Leu Leu Val Leu Leu Cys Thr Phe Thr Ala Thr Tyr
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 Asn Ser His Asn Gly Lys Leu Cys Leu Leu Lys Gly Ile
    50                  55                  60

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

Asn Pro Glu Cys Glu Leu Leu Ile Ser Lys Glu Ser Trp Ser Tyr Ile
                85                  90                  95

Val Glu Lys Pro Asn Pro Glu Asn Gly Thr Cys Tyr Pro Gly His Phe
            100                 105                 110

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

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

Val Thr Gly Val Ser Ala Ser Cys Ser His Asn Gly Glu Ser Ser Phe
145                 150                 155                 160

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

Leu Ser Lys Ser Tyr Ala Asn Asn Lys Glu Lys Glu Val Leu Val Leu
            180                 185                 190

Trp Gly Val His His Pro Pro Asn Ile Gly Asp Gln Lys Ala Leu Tyr
        195                 200                 205

His Thr Glu Asn Ala Tyr Val Ser Val Val Ser Ser His Tyr Ser Arg
    210                 215                 220

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

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

Ile Phe Glu Ala Asn Gly Asn Leu Ile Ala Pro Arg Tyr Ala Phe Ala
            260                 265                 270
```

Leu Ser Arg Gly Phe Gly Ser Gly Ile Ile Asn Ser Asn Ala Pro Met
275 280 285

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

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

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

Ile Pro Ser Ile Gln Ser Arg
340

<210> 43
<211> 345
<212> PRT
<213> Influenza virus/A/Aichi/2/1968

<400> 43

Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Ala Leu Gly
1 5 10 15

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

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

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

Gly Lys Ile Cys Asn Asn Pro His Arg Ile Leu Asp Gly Ile Asp Cys
65 70 75 80

Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His Cys Asp Val Phe Gln
85 90 95

Asn Glu Thr Trp Asp Leu Phe Val Glu Arg Ser Lys Ala Phe Ser Asn
100 105 110

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

Ala Ser Ser Gly Thr Leu Glu Phe Ile Thr Glu Gly Phe Thr Trp Thr
130 135 140

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

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

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

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

Ser Leu Tyr Val Gln Ala Ser Gly Arg Val Thr Val Ser Thr Arg Arg
210 215 220

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

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

Asp Val Leu Val Ile Asn Ser Asn Gly Asn Leu Ile Ala Pro Arg Gly
260 265 270

Tyr Phe Lys Met Arg Thr Gly Lys Ser Ser Ile Met Arg Ser Asp Ala
275 280 285

Pro Ile Asp Thr Cys Ile Ser Glu Cys Ile Thr Pro Asn Gly Ser Ile
290 295 300

Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Lys Ile Thr Tyr Gly Ala
305 310 315 320

Cys Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Gly Met
325 330 335

Arg Asn Val Pro Glu Lys Gln Thr Arg
340 345

<210> 44
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense

<400> 44
cccaaaccca acccaaccca aaaacccaaa cccaacccaa cccttttt 48

<210> 45
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<220>
<221> misc_feature
<222> (34)..(34)
<223> n represents one or more any bases.

<400> 45
gtgtttgatg gtttggtctg gttggcttaa cacngtgttt gatggtttgg tctggttggc 60

ttaacac 67

<210> 46
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 46
gggtttgggt tgggttggga tatatatagg gtttgggttg ggttggg 47

<210> 47
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 47
gggtttgggt tgggttgggg attggaatta aggcgtgtgg ggtttgggtt gggttggg 58

<210> 48
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 48
gtgtttgatg gtttggtctg gttggcttaa cactttttt ttgtgtttga tggtttggtc 60

tggttggctt aacac 75

<210> 49
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 49
gtgtttgatg gtttggtctg gttggcttaa cacttttgt gtttgatggt ttggtctggt 60

tggcttaaca c 71

<210> 50
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<220>
<221> misc_feature
<222> (20)..(20)
<223> n represents one or more any bases.

<220>
<221> misc_feature
<222> (40)..(40)
<223> n represents one or more any bases.

<400> 50
gggtttgggt tgggttgggn gggtttgggt tgggttgggn gggtttgggt tgggttggg 59

<210> 51
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 51
gggtttgggt tgggttgggt ttttttttgg gtttgggttg ggttgggttt ttttttgggt 60

ttgggttggg ttggg 75

<210> 52
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 52
gaattcagtc ggacagcggg gttcccatgc ggatgttata aagcagtcgc ttataaggga 60

tggacgaata tcgtctccc 79

<210> 53
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> aptamer

<400> 53
gaattcagtc ggacagcggg ggggaattct agcagtacac ctcgagaatt atagccagga 60

tggacgaata tcgtctccc 79