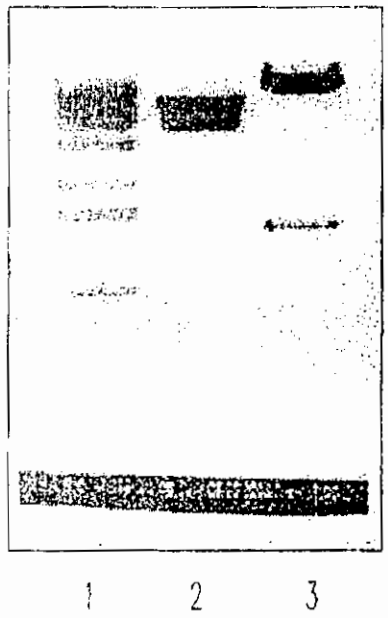

1
2
3

Fig. 1A

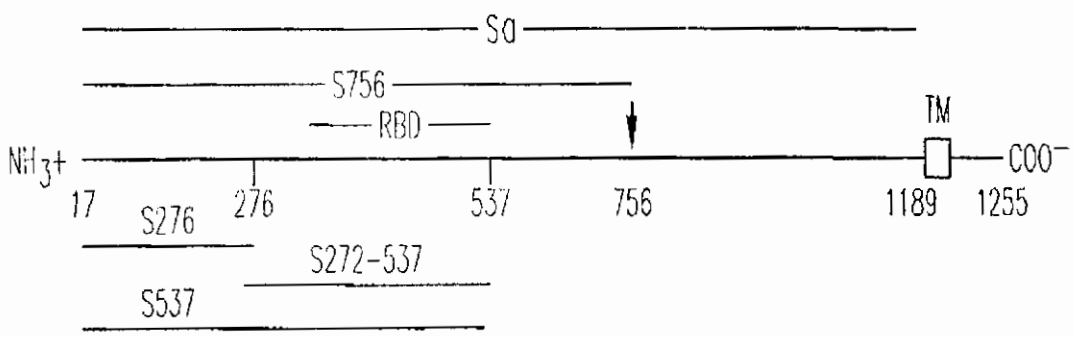

Sa
S756
RBD
TM
NH3+
COO−
17
276
537
756
1189
1255
S276
S272-537
S537

Fig. 1B

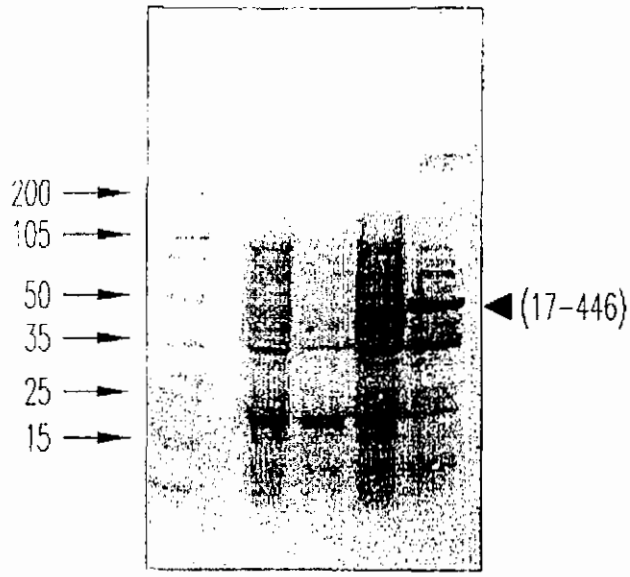

200
105
50
35
25
15
(17-446)

Fig. 2

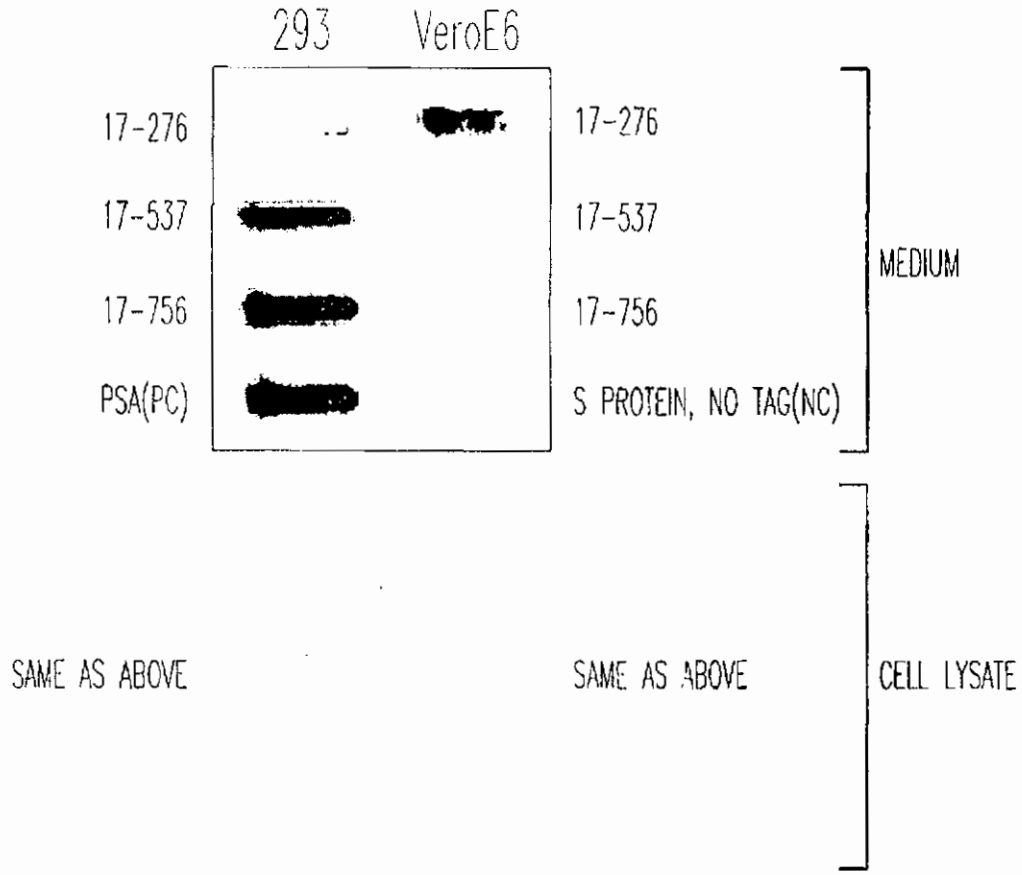

293
VeroE6
17-276
17-537
17-756
PSA(PC)
17-276
17-537
17-756
S PROTEIN, NO TAG(NC)
MEDIUM
SAME AS ABOVE
SAME AS ABOVE
CELL LYSATE

Fig. 3

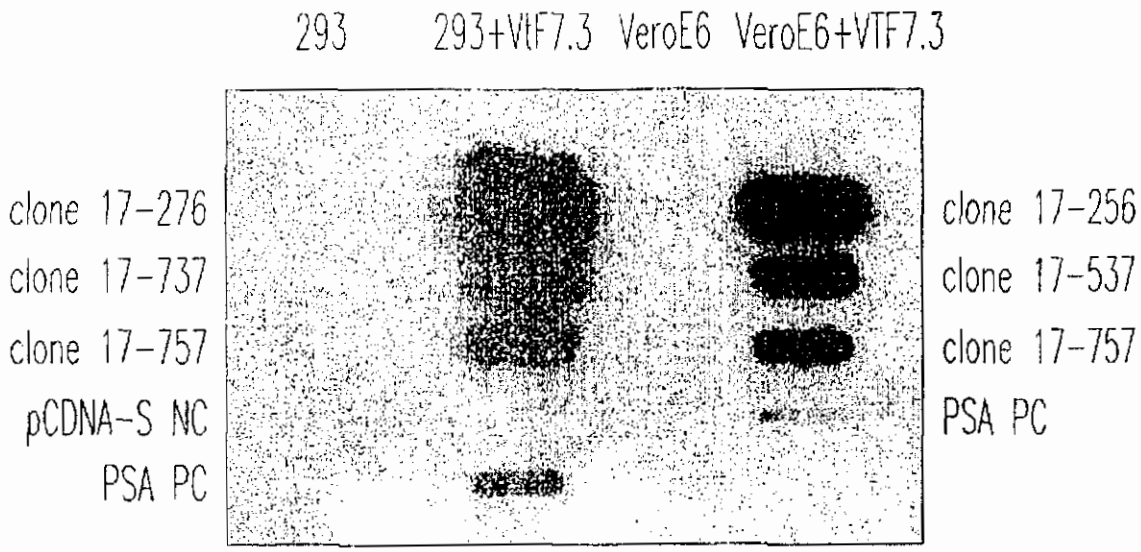

293
293+VtF7.3
VeroE6
VeroE6+VTF7.3
clone 17-276
clone 17-737
clone 17-757
pCDNA-S NC
PSA PC
clone 17-256
clone 17-537
clone 17-757
PSA PC

Fig. 4A

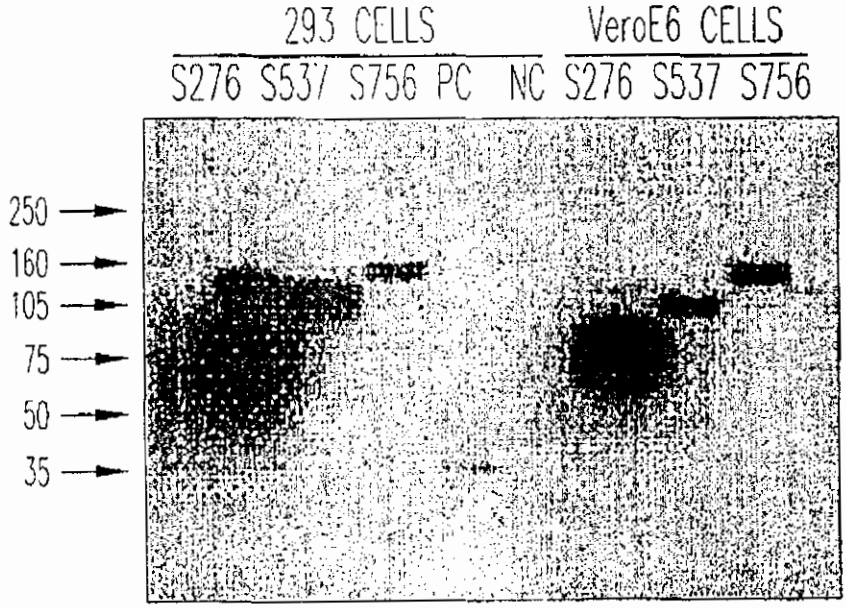

293 CELLS
VeroE6 CELLS
S276 S537 S756 PC NC S276 S537 S756
250
160
105
75
50
35

Fig. 4B

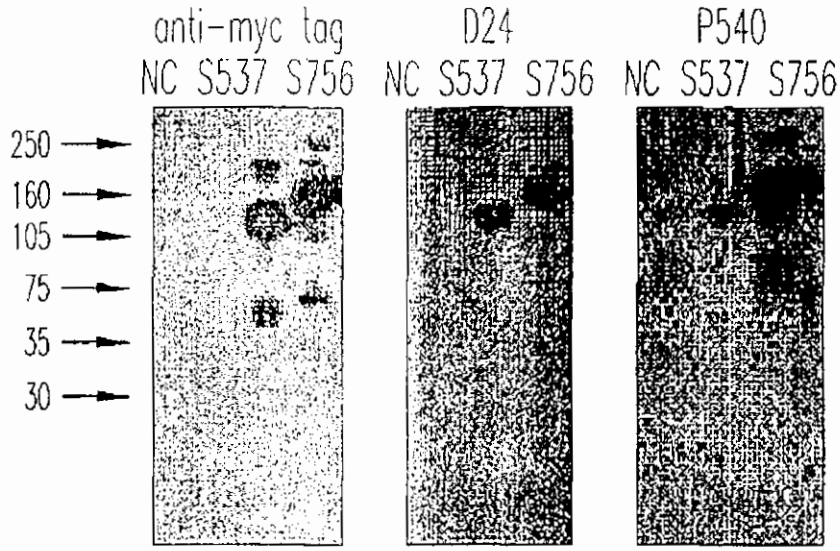

anti-myc tag
NC S537 S756
D24
NC S537 S756
P540
NC S537 S756
250
160
105
75
35
30

Fig. 4C

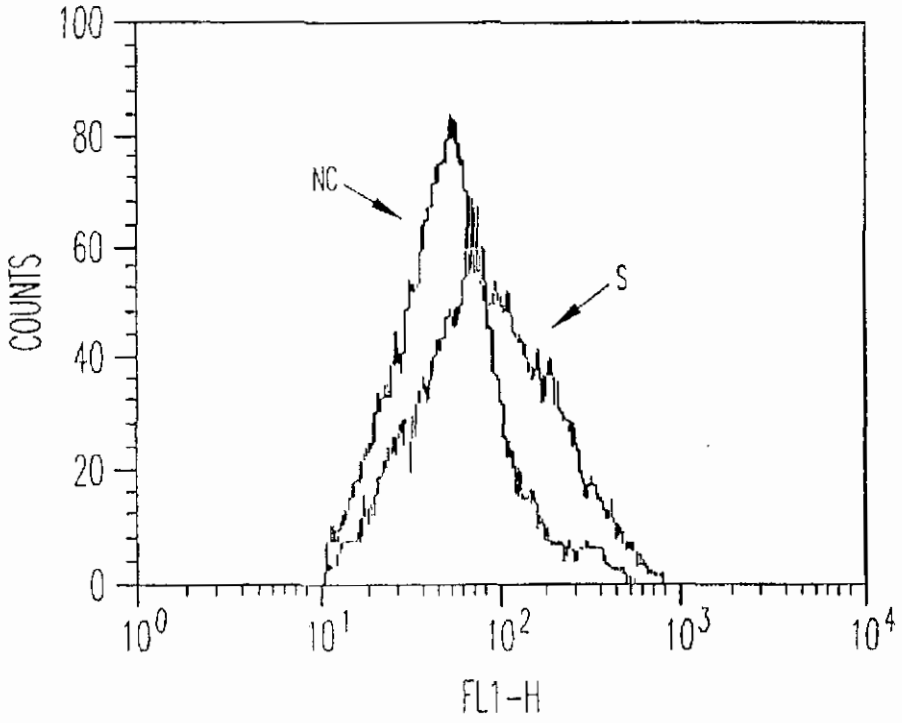

100
80
60
40
20
0
COUNTS
NC
S
10^0
10^1
10^2
10^3
10^4
FL1-H

Fig. 5

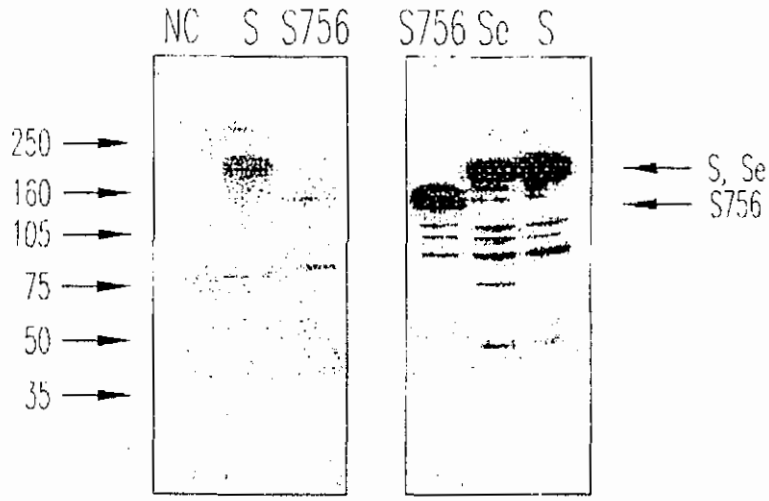


Fig. 6A Fig. 6B

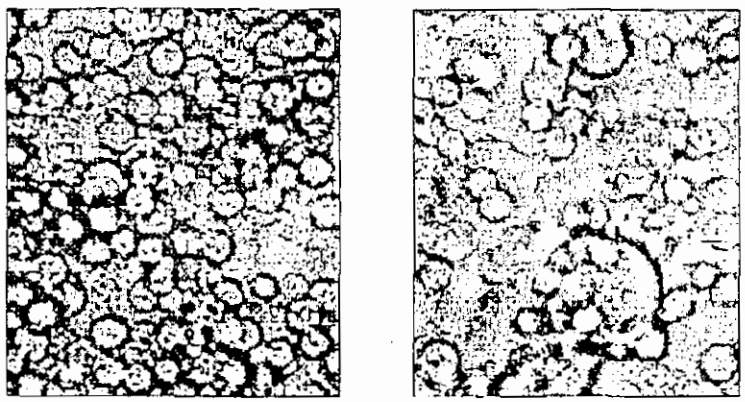


Fig. 7A Fig. 7B

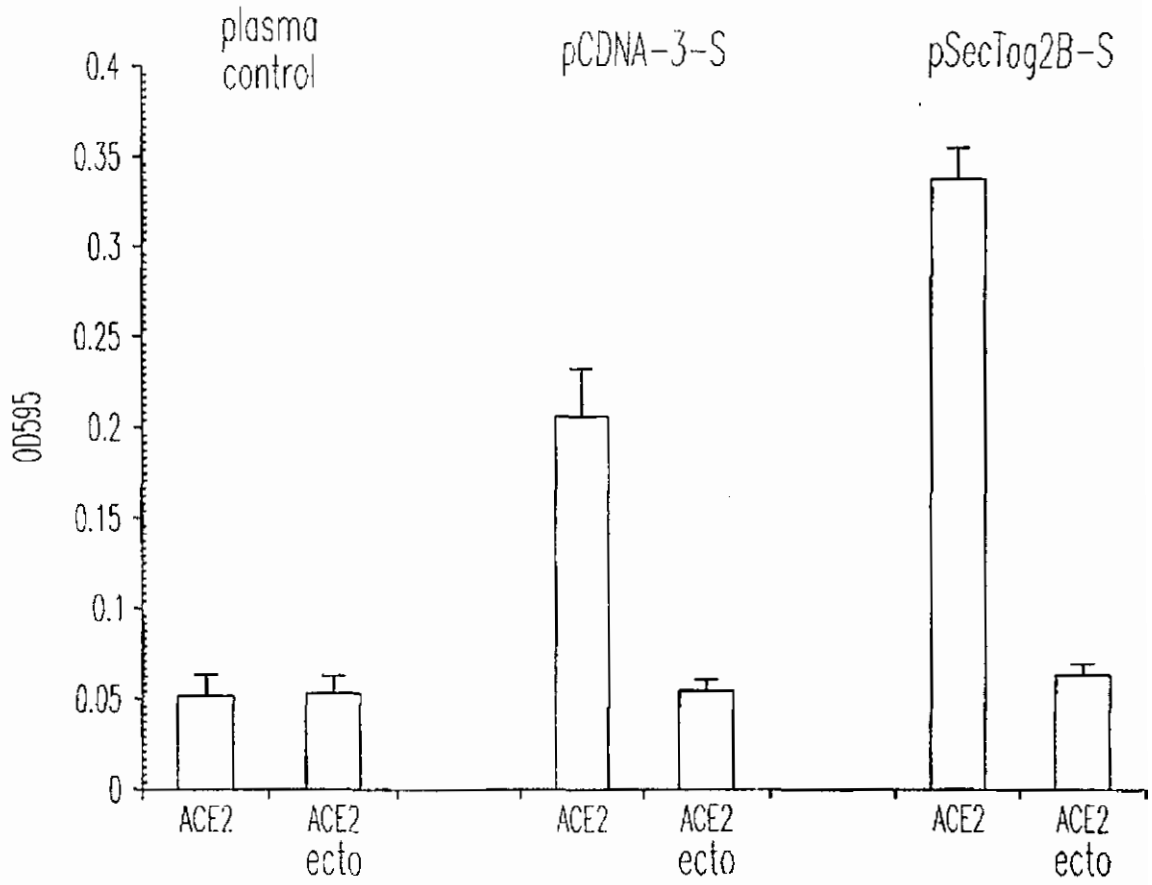

plasma control
pCDNA-3-S
pSecTag2B-S
OD595
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
ACE2
ACE2 ecto
ACE2
ACE2 ecto
ACE2
ACE2 ecto

Fig. 7C

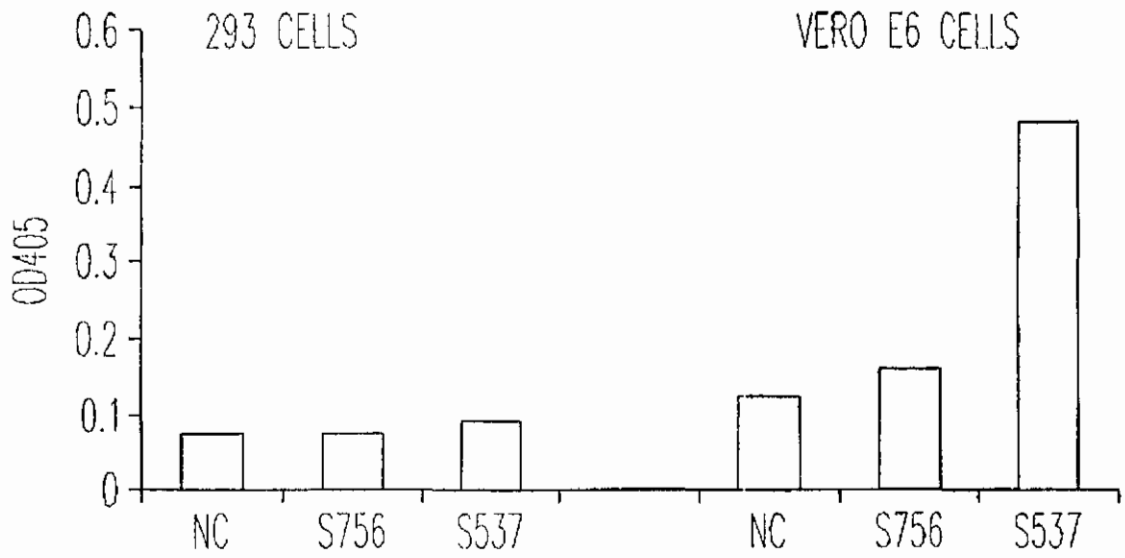


Fig. 8A

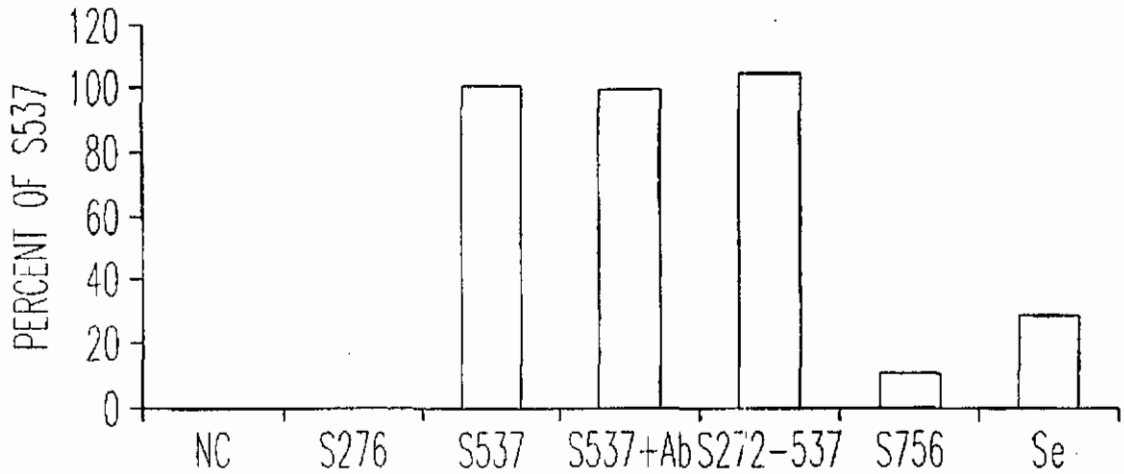


Fig. 8B

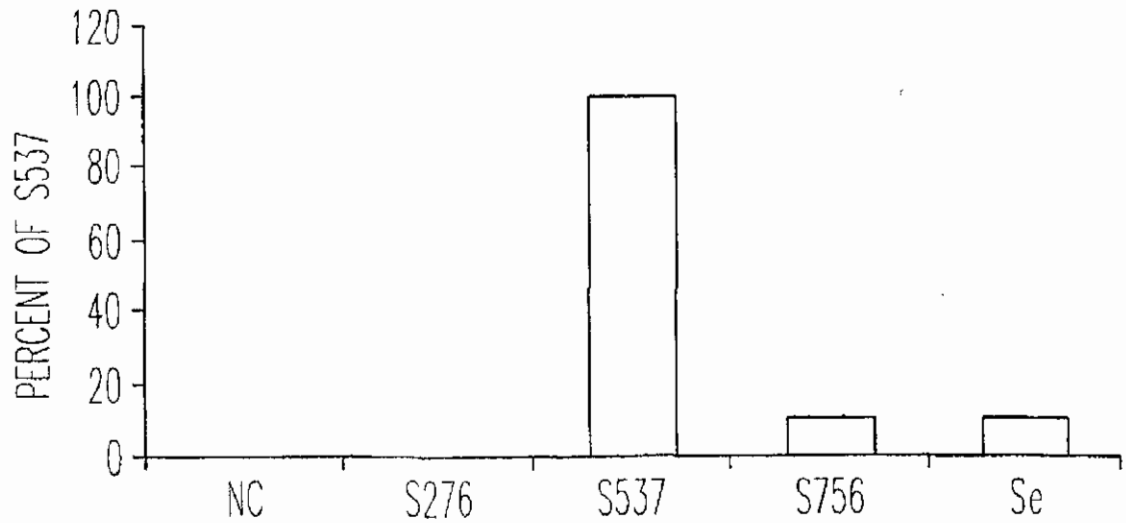


Fig. 8C

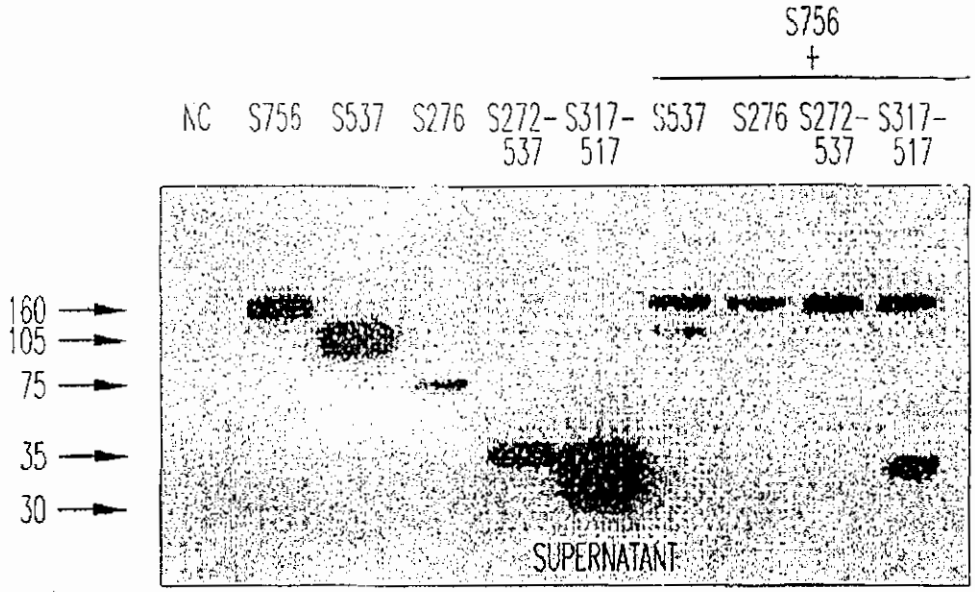


Fig. 9A

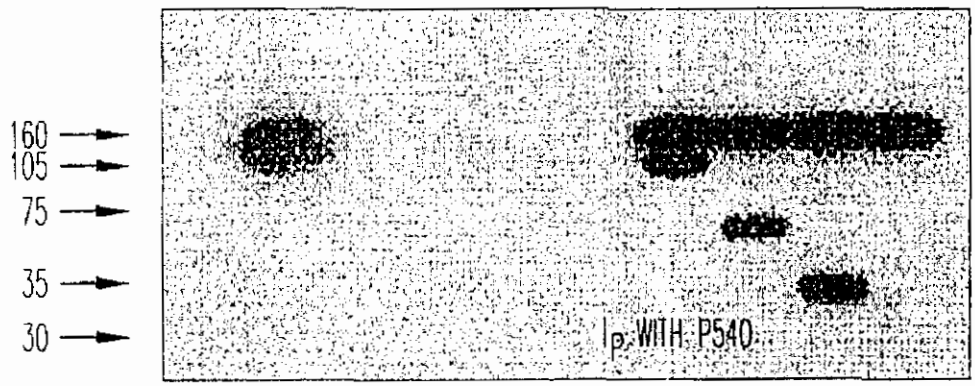


Fig. 9B

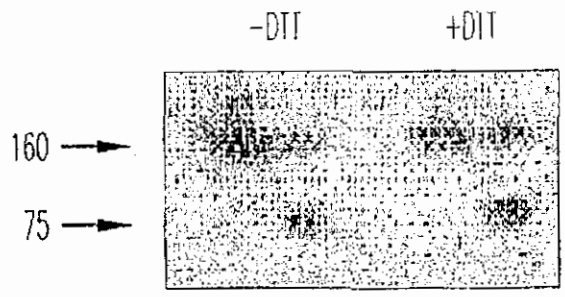


Fig. 9C

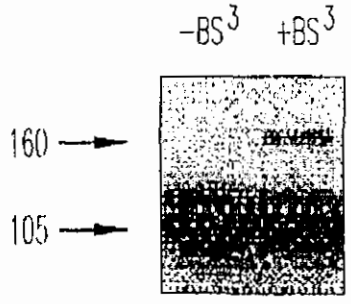


Fig. 9D

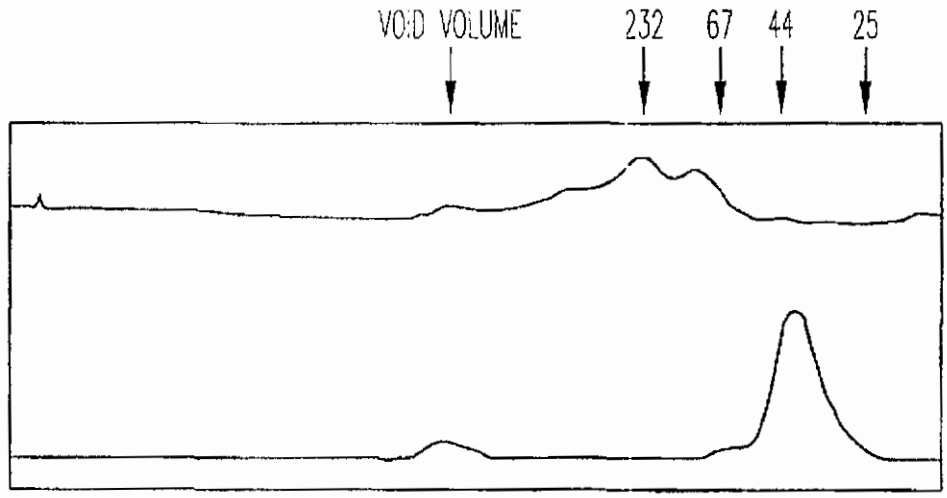


Fig. 10A

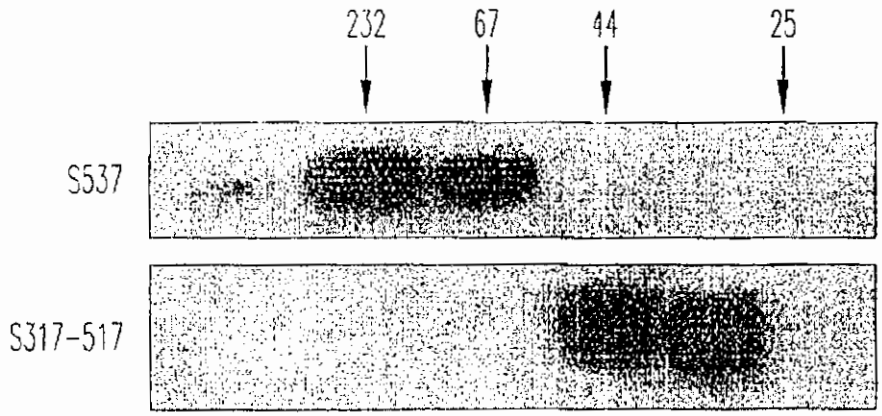


Fig. 10B

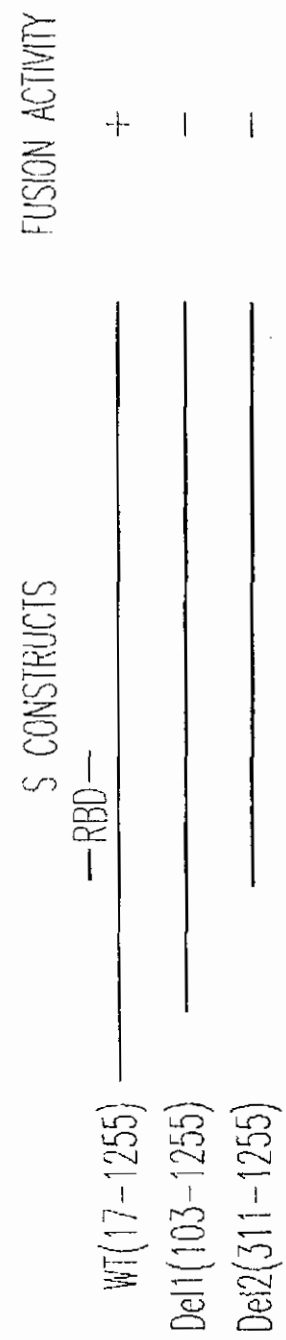

S CONSTRUCTS
FUSION ACTIVITY
RBD
WT(17-1255)
Del1(103-1255)
Del2(311-1255)
+
-
-

Fig. 11A

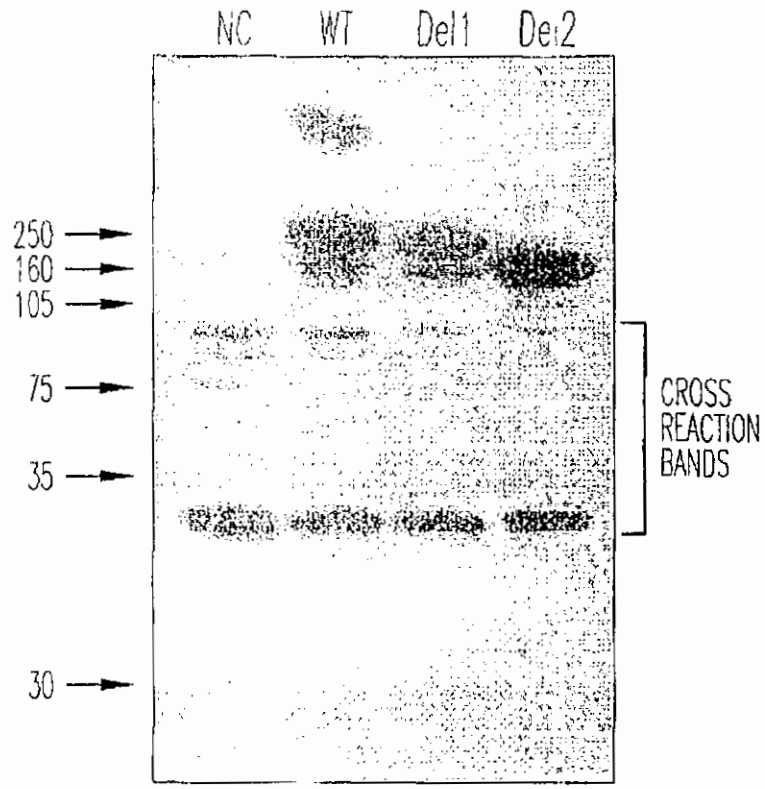


Fig. 11B

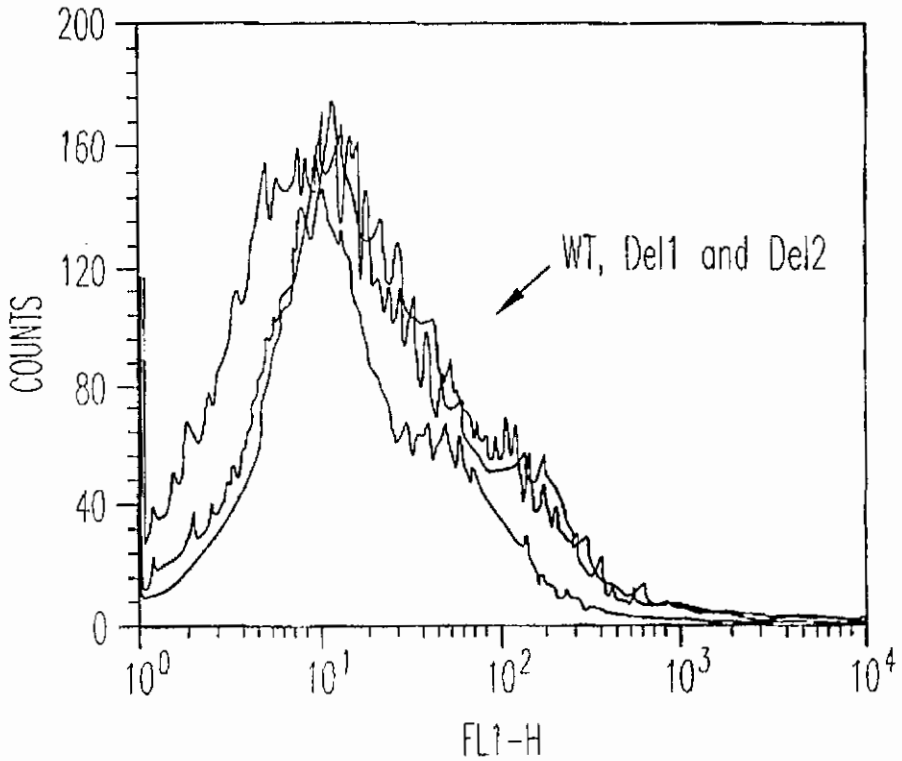


Fig. 11C

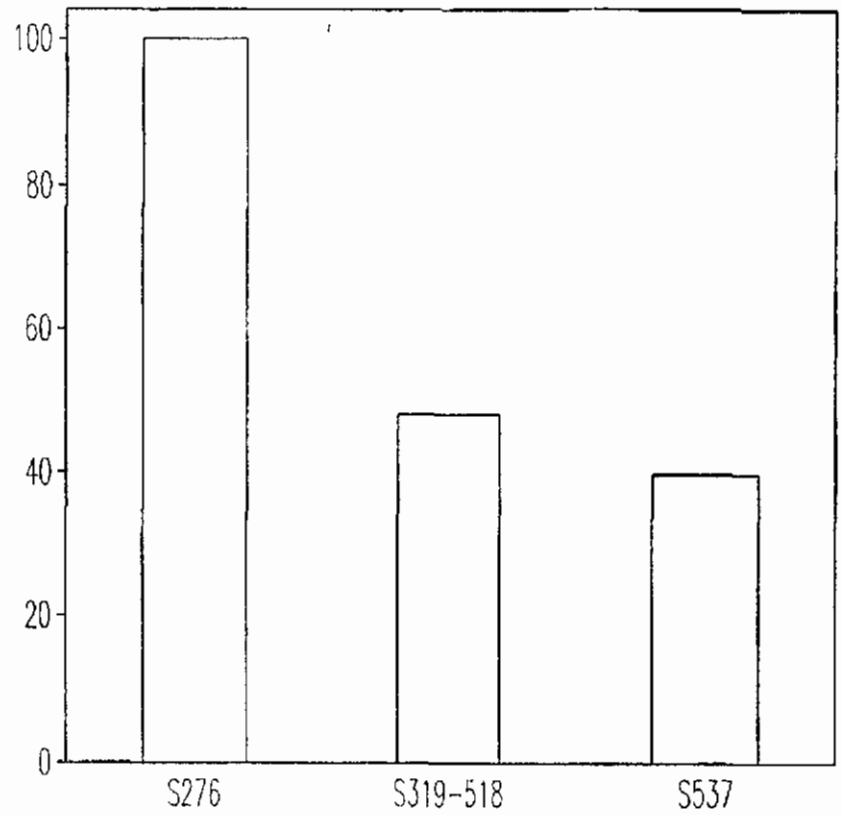


Fig. 12A

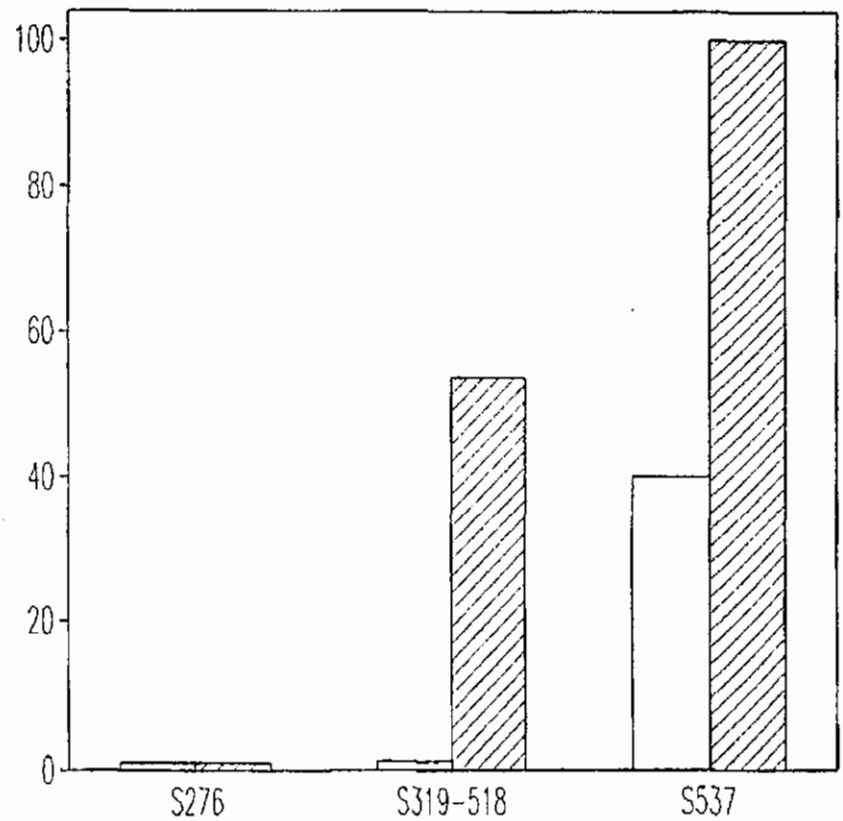


Fig. 12B

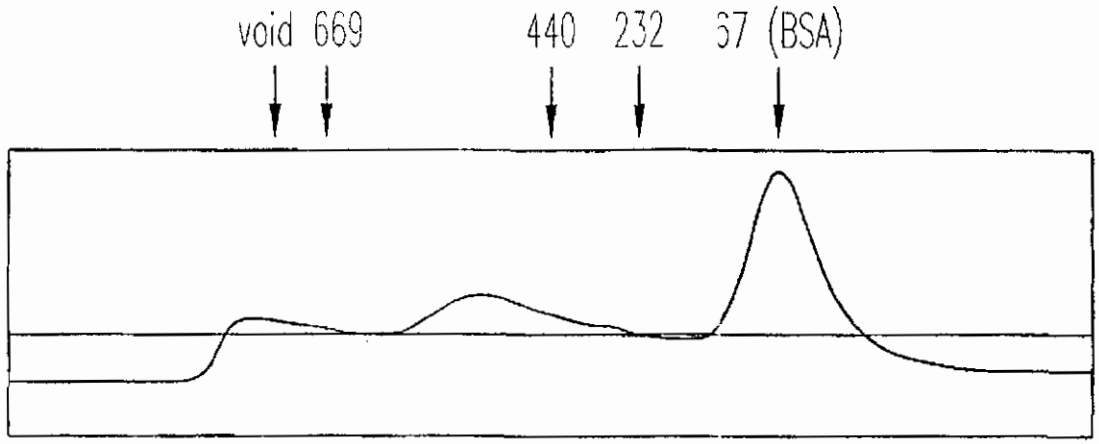


Fig. 13A

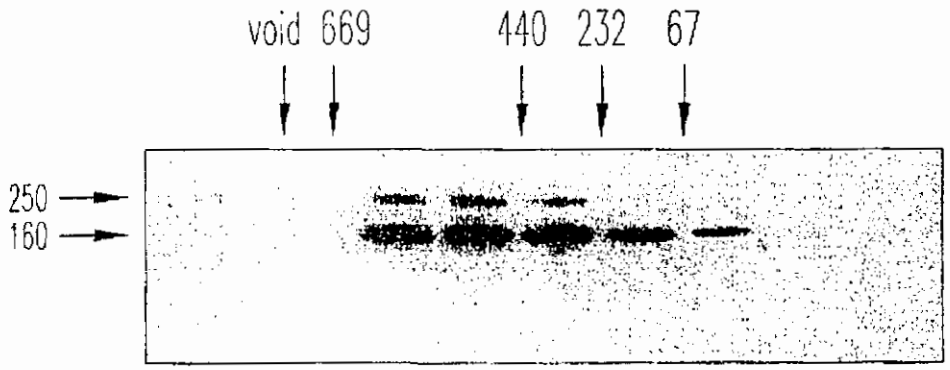


Fig. 13B

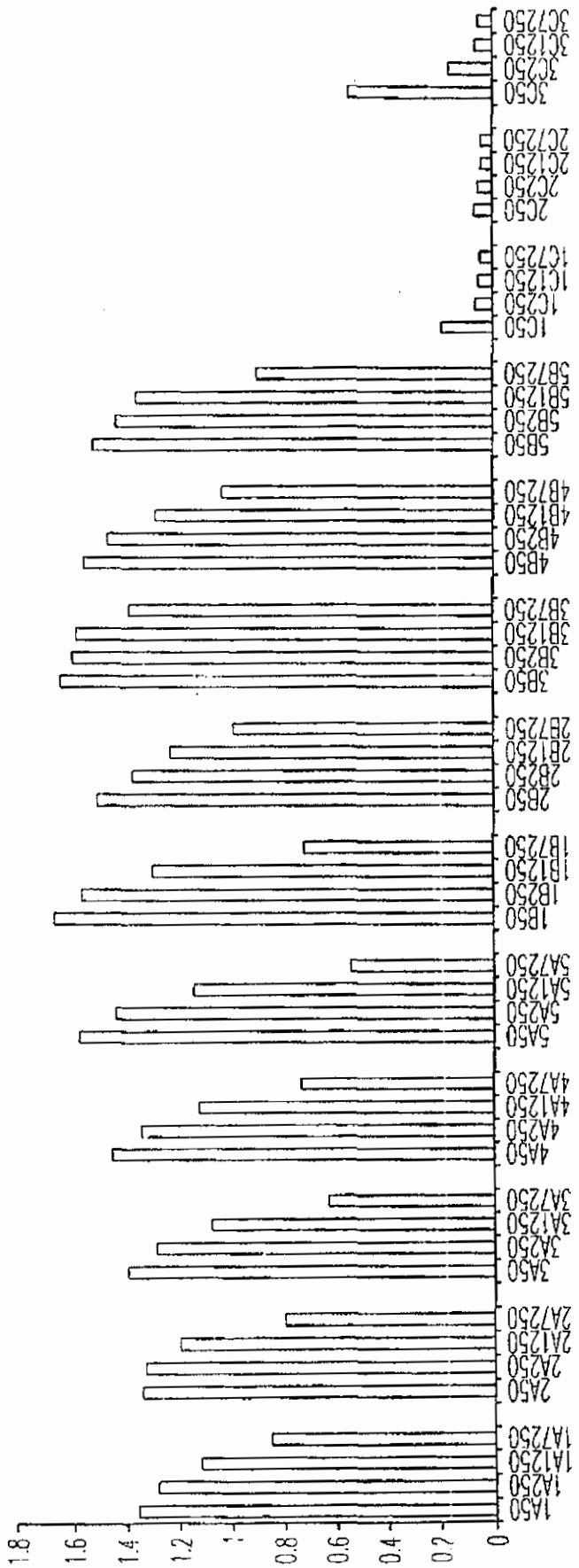

1A50
1A250
1A1250
1A7250
2A50
2A250
2A1250
2A7250
3A50
3A250
3A1250
3A7250
4A50
4A250
4A1250
4A7250
5A50
5A250
5A1250
5A7250
1B50
1B250
1B1250
1B7250
2B50
2B250
2B1250
2B7250
3B50
3B250
3B1250
3B7250
4B50
4B250
4B1250
4B7250
5B50
5B250
5B1250
5B7250
1C50
1C250
1C1250
1C7250
2C50
2C250
2C1250
2C7250
3C50
3C250
3C1250
3C7250
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8

Fig. 14A

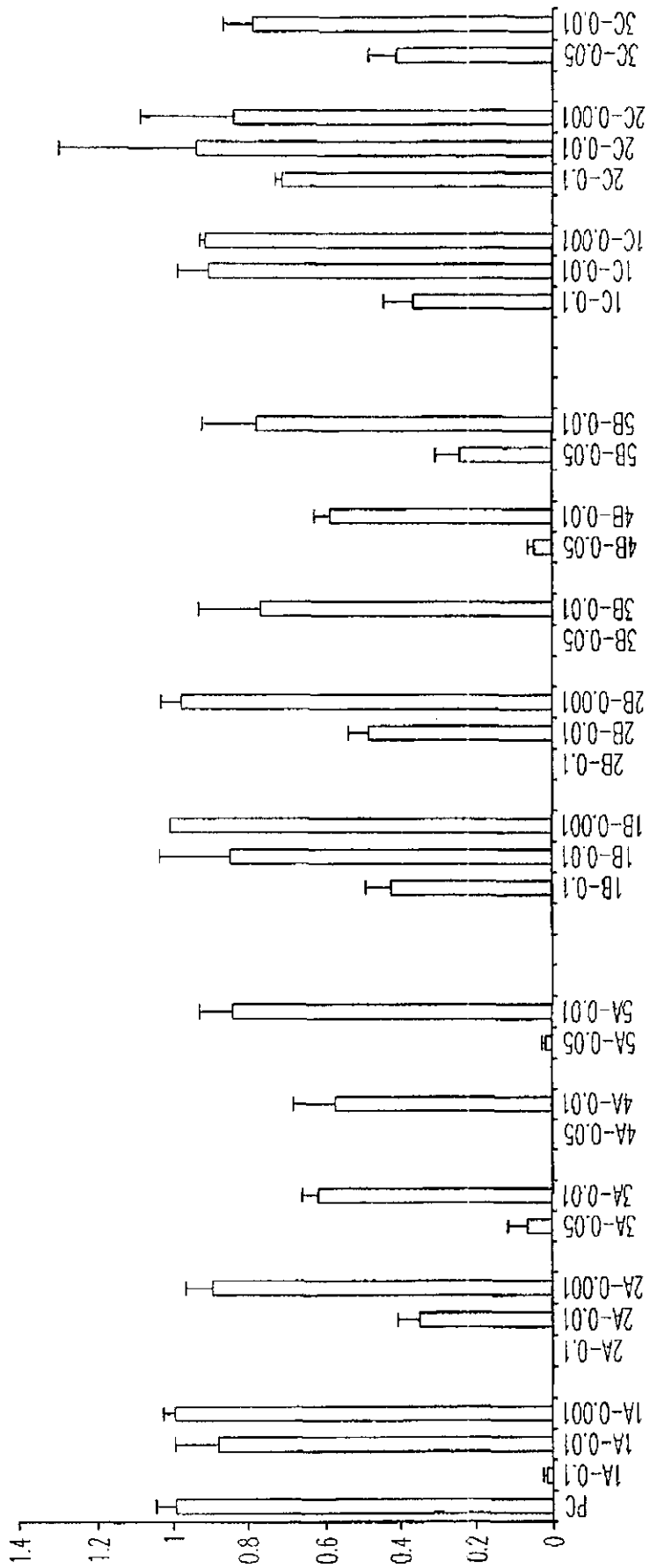

PC
1A-0.1
1A-0.01
1A-0.001
2A-0.1
2A-0.01
2A-0.001
3A-0.05
3A-0.01
4A-0.05
4A-0.01
5A-0.05
5A-0.01
1B-0.1
1B-0.01
1B-0.001
2B-0.1
2B-0.01
2B-0.001
3B-0.05
3B-0.01
4B-0.05
4B-0.01
5B-0.05
5B-0.01
1C-0.1
1C-0.01
1C-0.001
2C-0.1
2C-0.01
2C-0.001
3C-0.05
3C-0.01
0
0.2
0.4
0.6
0.8
1
1.2
1.4

Fig. 14B

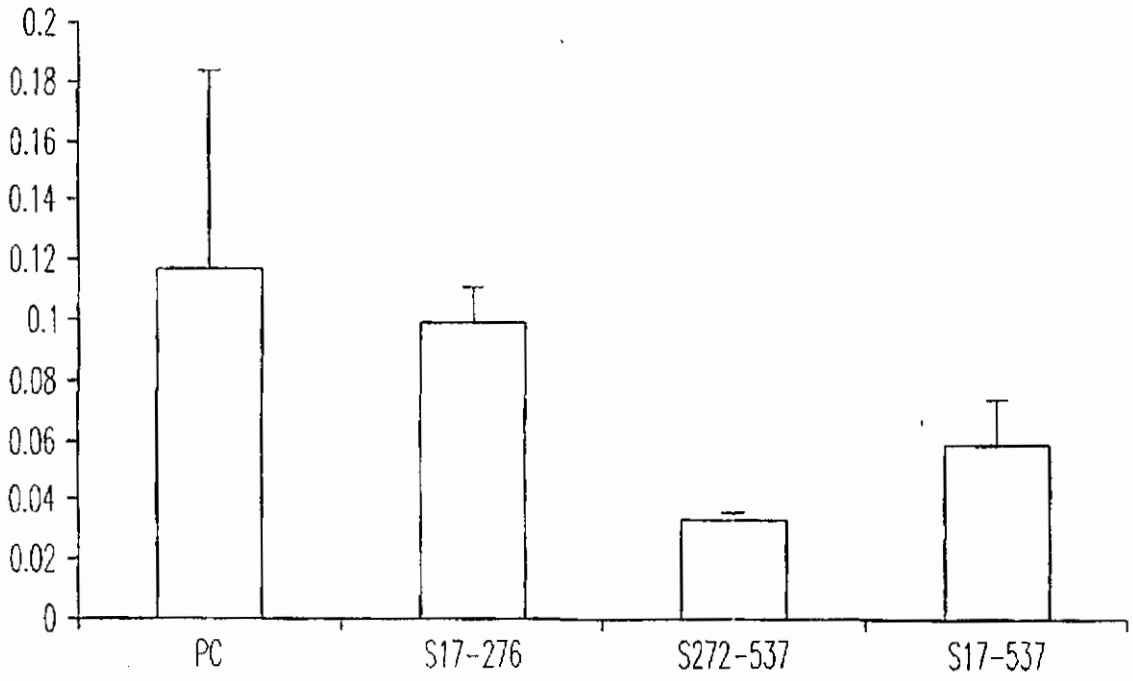

0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
PC
S17-276
S272-537
S17-537

Fig. 15

SEQUENCE LISTING

<110> National Institutes of Health
Dimitrov, Dimiter S.
Xiao, Xiaodong

<120> Soluble Fragments of the SARS-CoV Spike Glycoprotein

<130> 1662.024WO1

<150> US 60/489,166
<151> 2003-07-21

<150> US 60/524,642
<151> 2003-11-25

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1255
<212> PRT
<213> SARS coronavirus

<400> 1

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

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

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
820 825 830
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
835 840 845
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
850 855 860
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865 870 875 880
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
885 890 895
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
900 905 910
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
915 920 925
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
930 935 940
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945 950 955 960
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
965 970 975
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
980 985 990
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
995 1000 1005
Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp Phe
1010 1015 1020
Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala Pro His
1025 1030 1035 1040
Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln Glu Arg Asn
1045 1050 1055
Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys Ala Tyr Phe Pro
1060 1065 1070
Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser Trp Phe Ile Thr Gln
1075 1080 1085
Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr Thr Asp Asn Thr Phe Val
1090 1095 1100
Ser Gly Asn Cys Asp Val Val Ile Gly Ile Ile Asn Asn Thr Val Tyr
1105 1110 1115 1120
Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys
1125 1130 1135

Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser
1140 1145 1150
Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu
1155 1160 1165
Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu
1170 1175 1180
Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu
1185 1190 1195 1200
Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu
1205 1210 1215
Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys
1220 1225 1230
Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
1235 1240 1245
Gly Val Lys Leu His Tyr Thr
1250 1255

<210> 2
<211> 3768
<212> DNA
<213> SARS coronavirus

<400> 2
atgtttattt tcttattatt tcttactctc actagtggta gtgaccttga ccggtgcacc 60
acttttgatg atgttcaagc tcctaattac actcaacata cttcatctat gaggggggtt 120
tactatcctg atgaaatttt tagatcagac actctttatt taactcagga tttatttctt 180
ccattttatt ctaatgttac agggtttcat actattaatc atacgtttgg caaccctgtc 240
ataccttta aggatggtat ttattttgct gccacagaga aatcaaatgt tgtccgtggt 300
tgggtttttg gttctaccat gaacaacaag tcacagtcgg tgattattat taacaattct 360
actaatgttg ttatacgagc atgtaacttt gaattgtgtg acaaccctt ctttgctgtt 420
tctaaaccca tgggtacaca gacacatact atgatattcg ataatgcatt taattgcact 480
ttcgagtaca tatctgatgc cttttcgctt gatgtttcag aaaagtcagg taattttaaa 540
cacttacgag agtttgtgtt taaaaataaa gatgggtttc tctatgttta taagggctat 600
caacctatag atgtagttcg tgatctacct tctggtttta acactttgaa acctattttt 660
aagttgcctc ttggtattaa cattacaaat ttcagagcca ttcttacagc cttttcacct 720
gctcaagaca tttggggcac gtcagctgca gcctattttg ttggctattt aaagccaact 780
acatttatgc tcaagtatga tgaaaatggt acaatcacag atgctgttga ttgttctcaa 840
aatccacttg ctgaactcaa atgctctgtt aagagctttg agattgacaa aggaatttac 900
cagacctcta atttcagggt tgttcctca ggagatgttg tgagattccc taatattaca 960
aacttgtgtc cttttggaga ggttttaat gctactaaat tccottctgt ctatgcatgg 1020
gagagaaaaa aaatttctaa ttgtgttgct gattactctg tgctctacaa ctcaacattt 1080
ttttcaacct ttaagtgcta tggcgtttct gccactaagt tgaatgatct ttgcttctcc 1140

aatgtctatg cagattcttt tgtagtcaag ggagatgatg taagacaaat agcgccagga 1200
caaactggtg ttattgctga ttataattat aaattgccag atgattttcat gggttgtgtc 1260
cttgcttgga atactaggaa cattgatgct acttcaactg gtaattataa ttataaatat 1320
aggtatctta gacatggcaa gcttaggccc tttgagagag acattatctaa tgtgcctttc 1380
tcccctgatg gcaaaccttg caccccacct gctcttaatt gttattggcc attaaatgat 1440
tatggttttt acaccactac tggcattggc taccaacctt acagagttgt agtactttct 1500
tttgaacttt taaatgcacc ggccacggtt tgtggaccaa aattatccac tgaccttatt 1560
aagaaccagt gtgtcaattt taattttaat ggactcactg gtactggtgt gttaactcct 1620
tcttcaaaga gatttcaacc atttcaacaa tttggccgtg atgtttctga tttcactgat 1680
tccgttcgag atcctaaaac atctgaaata ttagacattt caccttgcgc ttttgggggt 1740
gtaagtgtaa ttacacctgg aacaaatgct tcatctgaag ttgctgttct atatcaagat 1800
gttaactgca ctgatgtttc tacagcaatt catgcagatc aactcacacc agcttggcgc 1860
atatattcta ctggaaacaa tgtattccag actcaagcag gctctcttat aggagctgag 1920
catgtcgaca cttcttatga gtgcgacatt cctattggag ctgccatttg tgctagttac 1980
catacagttt ctttattacg tagtactagc caaaaatcta ttgtggctta tactatgtct 2040
ttaggtgctg atagttcaat tgcttactct aataacacca ttgctatacc tactaacttt 2100
tcaattagca ttactacaga agtaatgcct gtttctatgg ctaaaacctc cgtagattgt 2160
aatatgtaca tctgcggaga ttctactgaa tgtgctaatt tgcttctcca atatggtagc 2220
ttttgcacac aactaaatcg tgcactctca ggtattgctg ctgaacagga tcgcaacaca 2280
cgtgaagtgt tcgctcaagt caaacaaatg tacaaaaccc caactttgaa atattttggt 2340
ggttttaatt tttcacaaat attacctgac cctctaaagc caactaagag gtcttttatt 2400
gaggacttgc tctttaataa ggtgacactc gctgatgctg gttcatgaa gcaatatggc 2460
gaatgcctag gtgatattaa tgctagagat ctcatttgtg cgcagaagtt caatggactt 2520
acagtgttgc cacctctgct cactgatgat atgattgctg cctacactgc tgctctagtt 2580
agtggtactg ccactgctgg atggacattt ggtgctggcg ctgctcttca aatacctttt 2640
gctatgcaaa tggcatatag gttcaatggc attggagtta cccaaaatgt tctctatgag 2700
aaccaaaaac aaatcgccaa ccaatttaac aaggcgatta gtcaaattca agaatcactt 2760
acaacaacat caactgcatt gggcaagctg caagacgttg ttaaccagaa tgctcaagca 2820
ttaaacacac ttgttaaaca acttagctct aattttggtg caatttcaag tgtgctaaat 2880
gatatccttt cgcgacttga taaagtcgag gcggaggtac aaattgacag gttaattaca 2940
ggcagacttc aaagccttca aacctatgta acacaacaac taatcagggc tgctgaaatc 3000
agggcttctg ctaatcttgc tgctactaaa atgtctgagt gtgttcttgg acaatcaaaa 3060
agagttgact tttgtggaaa gggctaccac cttatgtcct tcccacaagc agccccgcat 3120
ggtgttgtct tcctacatgt cacgtatgtg ccatcccagg agaggaactt caccacagcg 3180
accagcaattt gtcatgaagg caaagcatac ttccctcgtg aaggtgtttt tgtgtttaat 3240
ggcacttctt ggtttattac acagaggaac ttctttttctc cacaaataat tactacagac 3300
aatacatttg tctcaggaaa ttgtgatgtc gttattggca tcattaacaa cacagtttat 3360
gatcctctgc aacctgagct cgactcattc aaagaagagc tggacaagta cttcaaaaat 3420
catacatcac cagatgttga tcttggcgac atttcaggca ttaacgcttc tgtcgtcaac 3480
attcaaaaag aaattgaccg cctcaatgag gtcgctaaaa atttaaatga atcactcatt 3540
gaccttcaag aattgggaaa atatgagcaa tatattaaat ggccctggta tgtttggctc 3600
ggcttcattg ctggactaat tgccatcgtc atggttacaa tcttgctttg ttgcatgact 3660

agttgttgca gttgcctcaa gggtgcatgc tcttgtggtt cttgctgcaa gtttgatgag 3720
gatgactctg agccagttct caagggtgtc aaattacatt acacataa 3768

<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 3
agtcggatcc ggtaggctta tcattagag 29

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 4
ccatcagggg agaaaggcac 20

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 5
gtgcctttct cccctgatgg 20

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 6
5gaagagcagc gccagcacc 19

<210> 7
<211> 19
<212> DNA
10<213> Artificial Sequence

<220>
<223> A synthetic primer

15<400> 7
ggtgctggcg ctgctcttc 19

<210> 8
<211> 28
20<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer
25
<400> 8
actgtctaga gttcgtttat gtgtaatg 28

<210> 9
30<211> 29
<212> DNA
<213> Artificial Sequence

<220>
35<223> A synthetic primer

<400> 9
agtcggatcc gaccggtgca ccacttttg 29

40

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 10
agtcgggccc ctgttcagca gcaatacc 28

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 11
actgggatcc gaagtgttcg ctcaagtc 28

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 12
actgtctaga ttgctcatat tttccc 26

<210> 13
<211> 740
<212> PRT
<213> SARS coronavirus

<400> 13
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15

10

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu Gln
740

<210> 14
<211> 429
<212> PRT
<213> SARS coronavirus

<400> 14
Glu Val Phe Ala Gln Val Lys Gln Met Tyr Lys Thr Pro Thr Leu Lys
1 5 10 15
Tyr Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Leu Lys
20 25 30
Pro Thr Lys Arg Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr
35 40 45
Leu Ala Asp Ala Gly Phe Met Lys Gln Tyr Gly Glu Cys Leu Gly Asp
50 55 60
Ile Asn Ala Arg Asp Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr
65 70 75 80
Val Leu Pro Pro Leu Leu Thr Asp Asp Met Ile Ala Ala Tyr Thr Ala
85 90 95
Ala Leu Val Ser Gly Thr Ala Thr Ala Gly Trp Thr Phe Gly Ala Gly
100 105 110
Ala Ala Leu Gln Ile Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn
115 120 125
Gly Ile Gly Val Thr Gln Asn Val Leu Tyr Glu Asn Gln Lys Gln Ile
130 135 140
Ala Asn Gln Phe Asn Lys Ala Ile Ser Gln Ile Gln Glu Ser Leu Thr
145 150 155 160
Thr Thr Ser Thr Ala Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn
165 170 175
Ala Gln Ala Leu Asn Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly
180 185 190
Ala Ile Ser Ser Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val
195 200 205

Glu Ala Glu Val Gln Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser
210 215 220
Leu Gln Thr Tyr Val Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg
225 230 235 240
Ala Ser Ala Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly
245 250 255
Gln Ser Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser
260 265 270
Phe Pro Gln Ala Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr
275 280 285
Val Pro Ser Gln Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His
290 295 300
Glu Gly Lys Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly
305 310 315 320
Thr Ser Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile
325 330 335
Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
340 345 350
Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser
355 360 365
Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp
370 375 380
Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile
385 390 395 400
Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu
405 410 415
Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr Glu Gln
420 425

<210> 15
<211> 1170
<212> PRT
<213> SARS coronavirus

<400> 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu Gln Asp Glu Val Phe Ala Gln Val Lys Gln Met Tyr Lys
740 745 750
Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu
755 760 765
Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile Glu Asp Leu Leu
770 775 780
Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met Lys Gln Tyr Gly
785 790 795 800
Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile Cys Ala Gln Lys
805 810 815
Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr Asp Asp Met Ile
820 825 830
Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala Thr Ala Gly Trp
835 840 845
Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe Ala Met Gln Met
850 855 860
Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn Val Leu Tyr Glu
865 870 875 880
Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala Ile Ser Gln Ile
885 890 895
Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly Lys Leu Gln Asp
900 905 910
Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu Val Lys Gln Leu
915 920 925
Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn Asp Ile Leu Ser
930 935 940
Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp Arg Leu Ile Thr
945 950 955 960
Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln Gln Leu Ile Arg
965 970 975
Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala Thr Lys Met Ser
980 985 990
Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp Phe Cys Gly Lys Gly
995 1000 1005
Tyr His Leu Met Ser Phe Pro Gln Ala Ala Pro His Gly Val Val Phe
1010 1015 1020
Leu His Val Thr Tyr Val Pro Ser Gln Glu Arg Asn Phe Thr Thr Ala
1025 1030 1035 1040
Pro Ala Ile Cys His Glu Gly Lys Ala Tyr Phe Pro Arg Glu Gly Val
1045 1050 1055

Phe Val Phe Asn Gly Thr Ser Trp Phe Ile Thr Gln Arg Asn Phe Phe
1060 1065 1070
Ser Pro Gln Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys
1075 1080 1085
Asp Val Val Ile Gly Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln
1090 1095 1100
Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1105 1110 1115 1120
His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1125 1130 1135
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala
1140 1145 1150
Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
1155 1160 1165
Glu Gln
1170

<210> 16
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic k chain leader sequence

<400> 16
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp
20

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic myc epitope

<400> 17
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic histidine tag

<400> 18
His His His His His His
1 5

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 19
ctagctcgag caacagcatc tgtg 24

<210> 20
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 20
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95

Val Val Arg Gly
100

<210> 21
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 21
Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln Ser Val Ile Ile
1 5 10 15
Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys Asn Phe Glu Leu
20 25 30
Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met Gly Thr Gln Thr
35 40 45
His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr Phe Glu Tyr Ile
50 55 60
Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser Gly Asn Phe Lys
65 70 75 80
His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly Phe Leu Tyr Val
85 90 95
Tyr Lys Gly Tyr
100

<210> 22
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 22
Gln Pro Ile Asp Val Val Arg Asp Leu Pro Ser Gly Phe Asn Thr Leu
1 5 10 15
Lys Pro Ile Phe Lys Leu Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg
20 25 30
Ala Ile Leu Thr Ala Phe Ser Pro Ala Gln Asp Ile Trp Gly Thr Ser
35 40 45
Ala Ala Ala Tyr Phe Val Gly Tyr Leu Lys Pro Thr Thr Phe Met Leu
50 55 60
Lys Tyr Asp Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ser Gln
65 70 75 80
Asn Pro Leu Ala Glu Leu Lys Cys Ser Val Lys Ser Phe Glu Ile Asp
85 90 95

Lys Gly Ile Tyr
100

<210> 23
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 23
Gln Thr Ser Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe
1 5 10 15
Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr
20 25 30
Lys Phe Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys
35 40 45
Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe
50 55 60
Lys Cys Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser
65 70 75 80
Asn Val Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln
85 90 95
Ile Ala Pro Gly
100

<210> 24
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 24
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
1 5 10 15
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
20 25 30
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
35 40 45
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
50 55 60
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
65 70 75 80
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
85 90 95

Val Val Leu Ser
100

<210> 25
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 25
Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser
1 5 10 15
Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu
20 25 30
Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe
35 40 45
Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp
50 55 60
Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys Ala Phe Gly Gly
65 70 75 80
Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val
85 90 95
Leu Tyr Gln Asp
100

<210> 26
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 26
Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
1 5 10 15
Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
20 25 30
Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
35 40 45
Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
50 55 60
Leu Leu Arg Ser Thr Ser Gln Lys Ser Ile Val Ala Tyr Thr Met Ser
65 70 75 80
Leu Gly Ala Asp Ser Ser Ile Ala Tyr Ser Asn Asn Thr Ile Ala Ile
85 90 95

Pro Thr Asn Phe
100

<210> 27
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 27
Ser Ile Ser Ile Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr
1 5 10 15
Ser Val Asp Cys Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala
20 25 30
Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala
35 40 45
Leu Ser Gly Ile Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe
50 55 60
Ala Gln Val Lys Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly
65 70 75 80
Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys
85 90 95
Arg Ser Phe Ile
100

<210> 28
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 28
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
1 5 10 15
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
20 25 30
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
35 40 45
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
50 55 60
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
65 70 75 80
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
85 90 95

Val Leu Tyr Glu
100

<210> 29
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 29
Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala Ile Ser Gln Ile
1 5 10 15
Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly Lys Leu Gln Asp
20 25 30
Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu Val Lys Gln Leu
35 40 45
Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn Asp Ile Leu Ser
50 55 60
Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp Arg Leu Ile Thr
65 70 75 80
Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln Gln Leu Ile Arg
85 90 95
Ala Ala Glu Ile
100

<210> 30
<211> 100
<212> PRT
<213> SARS coronavirus

<400> 30
Arg Ala Ser Ala Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu
1 5 10 15
Gly Gln Ser Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met
20 25 30
Ser Phe Pro Gln Ala Ala Pro His Gly Val Val Phe Leu His Val Thr
35 40 45
Tyr Val Pro Ser Gln Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys
50 55 60
His Glu Gly Lys Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn
65 70 75 80
Gly Thr Ser Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile
85 90 95

Ile Thr Thr Asp
100

<210> 31
<211> 90
<212> PRT
<213> SARS coronavirus

<400> 31
Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Ile Asn
1 5 10 15
Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu
20 25 30
Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu
35 40 45
Gly Asp Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu
50 55 60
Ile Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile
65 70 75 80
Asp Leu Gln Glu Leu Gly Lys Tyr Glu Gln
85 90

<210> 32
<211> 200
<212> PRT
<213> SARS coronavirus

<400> 32
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190
Phe Leu Tyr Val Tyr Lys Gly Tyr
195 200

<210> 33
<211> 200
<212> PRT
<213> SARS coronavirus

<400> 33
Gln Pro Ile Asp Val Val Arg Asp Leu Pro Ser Gly Phe Asn Thr Leu
1 5 10 15
Lys Pro Ile Phe Lys Leu Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg
20 25 30
Ala Ile Leu Thr Ala Phe Ser Pro Ala Gln Asp Ile Trp Gly Thr Ser
35 40 45
Ala Ala Ala Tyr Phe Val Gly Tyr Leu Lys Pro Thr Thr Phe Met Leu
50 55 60
Lys Tyr Asp Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ser Gln
65 70 75 80
Asn Pro Leu Ala Glu Leu Lys Cys Ser Val Lys Ser Phe Glu Ile Asp
85 90 95
Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Val Pro Ser Gly Asp
100 105 110
Val Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val
115 120 125
Phe Asn Ala Thr Lys Phe Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys
130 135 140
Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe
145 150 155 160
Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp
165 170 175

Leu Cys Phe Ser Asn Val Tyr Ala Asp Ser Phe Val Val Lys Gly Asp
180 185 190
Asp Val Arg Gln Ile Ala Pro Gly
195 200

<210> 34
<211> 200
<212> PRT
<213> SARS coronavirus

<400> 34
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
1 5 10 15
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
20 25 30
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
35 40 45
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
50 55 60
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
65 70 75 80
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
85 90 95
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
100 105 110
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
115 120 125
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
130 135 140
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
145 150 155 160
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
165 170 175
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
180 185 190
Glu Val Ala Val Leu Tyr Gln Asp
195 200

<210> 35
<211> 200
<212> PRT
<213> SARS coronavirus

<400> 35

Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
1 5 10 15

Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
20 25 30

Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
35 40 45

Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
50 55 60

Leu Leu Arg Ser Thr Ser Gln Lys Ser Ile Val Ala Tyr Thr Met Ser
65 70 75 80

Leu Gly Ala Asp Ser Ser Ile Ala Tyr Ser Asn Asn Thr Ile Ala Ile
85 90 95

Pro Thr Asn Phe Ser Ile Ser Ile Thr Thr Glu Val Met Pro Val Ser
100 105 110

Met Ala Lys Thr Ser Val Asp Cys Asn Met Tyr Ile Cys Gly Asp Ser
115 120 125

Thr Glu Cys Ala Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln
130 135 140

Leu Asn Arg Ala Leu Ser Gly Ile Ala Ala Glu Gln Asp Arg Asn Thr
145 150 155 160

Arg Glu Val Phe Ala Gln Val Lys Gln Met Tyr Lys Thr Pro Thr Leu
165 170 175

Lys Tyr Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Leu
180 185 190

Lys Pro Thr Lys Arg Ser Phe Ile
195 200

<210> 36

<211> 200

<212> PRT

<213> SARS coronavirus

<400> 36

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
1 5 10 15

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
20 25 30

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
35 40 45

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
50 55 60

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
65 70 75 80
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
85 90 95
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
100 105 110
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
115 120 125
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
130 135 140
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
145 150 155 160
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
165 170 175
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
180 185 190
Gln Leu Ile Arg Ala Ala Glu Ile
195 200

<210> 37
<211> 190
<212> PRT
<213> SARS coronavirus

<400> 37
Arg Ala Ser Ala Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu
1 5 10 15
Gly Gln Ser Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met
20 25 30
Ser Phe Pro Gln Ala Ala Pro His Gly Val Val Phe Leu His Val Thr
35 40 45
Tyr Val Pro Ser Gln Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys
50 55 60
His Glu Gly Lys Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn
65 70 75 80
Gly Thr Ser Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile
85 90 95
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile
100 105 110
Gly Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
115 120 125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro
130 135 140
Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val Val Asn
145 150 155 160
Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn
165 170 175
Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr Glu Gln
180 185 190

<210> 38
<211> 400
<212> PRT
<213> SARS coronavirus

<400> 38
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205

30

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400

<210> 39
<211> 600
<212> PRT
<213> SARS coronavirus

<400> 39
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
405 410 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
420 425 430
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
435 440 445
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450 455 460
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590
Glu Val Ala Val Leu Tyr Gln Asp
595 600

<210> 40
<211> 800
<212> PRT
<213> SARS coronavirus

<400> 40
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
405 410 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
420 425 430
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
435 440 445
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450 455 460
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800

<210> 41
<211> 1000
<212> PRT
<213> SARS coronavirus

<400> 41
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220

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

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
820 825 830
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
835 840 845
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
850 855 860
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865 870 875 880
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
885 890 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
900 905 910
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
915 920 925
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
930 935 940
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945 950 955 960
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
965 970 975
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
980 985 990
Gln Leu Ile Arg Ala Ala Glu Ile
995 1000

<210> 42
<211> 1190
<212> PRT
<213> SARS coronavirus

<400> 42
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160

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

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
820 825 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
835 840 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
850 855 860

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865 870 875 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
885 890 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
900 905 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
915 920 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
930 935 940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945 950 955 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
965 970 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
980 985 990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
995 1000 1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp Phe
1010 1015 1020

Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala Pro His
1025 1030 1035 1040

Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln Glu Arg Asn
1045 1050 1055

Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys Ala Tyr Phe Pro
1060 1065 1070

Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser Trp Phe Ile Thr Gln
1075 1080 1085

Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr Thr Asp Asn Thr Phe Val
1090 1095 1100

Ser Gly Asn Cys Asp Val Val Ile Gly Ile Ile Asn Asn Thr Val Tyr
1105 1110 1115 1120

Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys
1125 1130 1135

Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser
1140 1145 1150

Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu
1155 1160 1165

Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu
1170 1175 1180
Leu Gly Lys Tyr Glu Gln
1185 1190

<210> 43
<211> 84
<212> PRT
<213> SARS coronavirus

<400> 43
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly

<210> 44
<211> 184
<212> PRT
<213> SARS coronavirus

<400> 44
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr
180

<210> 45
<211> 384
<212> PRT
<213> SARS coronavirus

<400> 45
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380

<210> 46
<211> 584
<212> PRT
<213> SARS coronavirus

<400> 46
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp
580

<210> 47
<211> 784
<212> PRT
<213> SARS coronavirus

<400> 47
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
740 745 750

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
755 760 765
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
770 775 780

<210> 48
<211> 984
<212> PRT
<213> SARS coronavirus

<400> 48
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
195 200 205
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
210 215 220
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
225 230 235 240

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
245 250 255
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
740 745 750
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
755 760 765
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
770 775 780
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
785 790 795 800
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
805 810 815
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
820 825 830
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
835 840 845
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
850 855 860
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
865 870 875 880
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
885 890 895
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
900 905 910

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
915 920 925
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
930 935 940
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
945 950 955 960
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
965 970 975
Gln Leu Ile Arg Ala Ala Glu Ile
980

<210> 49
<211> 1174
<212> PRT
<213> SARS coronavirus

<400> 49
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
130 135 140
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
145 150 155 160
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
165 170 175
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
180 185 190

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

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
740 745 750
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
755 760 765
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
770 775 780
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
785 790 795 800
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
805 810 815
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
820 825 830
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
835 840 845
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
850 855 860

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
865 870 875 880
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
885 890 895
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
900 905 910
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
915 920 925
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
930 935 940
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
945 950 955 960
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
965 970 975
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
980 985 990
Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp Phe
995 1000 1005
Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala Pro His
1010 1015 1020
Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln Glu Arg Asn
1025 1030 1035 1040
Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys Ala Tyr Phe Pro
1045 1050 1055
Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser Trp Phe Ile Thr Gln
1060 1065 1070
Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr Thr Asp Asn Thr Phe Val
1075 1080 1085
Ser Gly Asn Cys Asp Val Val Ile Gly Ile Ile Asn Asn Thr Val Tyr
1090 1095 1100
Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys
1105 1110 1115 1120
Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser
1125 1130 1135
Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu
1140 1145 1150
Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu
1155 1160 1165
Leu Gly Lys Tyr Glu Gln
1170

<210> 50
<211> 260
<212> PRT
<213> SARS coronavirus

<400> 50

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

<210> 51
<211> 430
<212> PRT
<213> SARS coronavirus

<400> 51

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

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly
420 425 430

<210> 52
<211> 521
<212> PRT
<213> SARS coronavirus

<400> 52
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
1 5 10 15
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
20 25 30
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
35 40 45
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
50 55 60
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
65 70 75 80
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
85 90 95
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
100 105 110
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
115 120 125

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

60

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val
515 520

<210> 53
<211> 777
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence of amino acids 17-757 of SEQ ID NO:1 plus an N-terminal mouse K chain leader sequence and a C-terminal myc epitope and a polyhistidine tag

<400> 53
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala
20 25 30
Pro Asn Tyr Thr Gln His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro
35 40 45
Asp Glu Ile Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe
50 55 60
Leu Pro Phe Tyr Ser Asn Val Thr Gly Phe His Thr Ile Asn His Thr
65 70 75 80
Phe Gly Asn Pro Val Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala
85 90 95
Thr Glu Lys Ser Asn Val Val Arg Gly Trp Val Phe Gly Ser Thr Met
100 105 110
Asn Asn Lys Ser Gln Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val
115 120 125
Val Ile Arg Ala Cys Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala
130 135 140
Val Ser Lys Pro Met Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn
145 150 155 160
Ala Phe Asn Cys Thr Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp
165 170 175

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

Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln
515 520 525
Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr
530 535 540
Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val
545 550 555 560
Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu
565 570 575
Asp Ile Ser Pro Cys Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly
580 585 590
Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys
595 600 605
Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp
610 615 620
Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys
625 630 635 640
Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro
645 650 655
Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg
660 665 670
Ser Thr Ser Gln Lys Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala
675 680 685
Asp Ser Ser Ile Ala Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn
690 695 700
Phe Ser Ile Ser Ile Thr Thr Glu Val Met Pro Val Ser Met Ala Lys
705 710 715 720
Thr Ser Val Asp Cys Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys
725 730 735
Ala Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg
740 745 750
Ala Leu Ser Gly Ile Ala Ala Glu Gln Glu Gln Lys Leu Ile Ser Glu
755 760 765
Glu Asp Leu His His His His His His
770 775

<210> 54
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence of amino acids 17-276 of SEQ ID NO:1 plus an

N-terminal mouse K chain leader sequence and a C-terminal myc epitope and a polyhistidine tag

<400> 54

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

<210> 55
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 17-537 of SEQ ID NO:1 plus an N-terminal mouse K chain leader sequence and a C-terminal myc epitope and a polyhistidine tag

<400> 55

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala
20 25 30
Pro Asn Tyr Thr Gln His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro
35 40 45
Asp Glu Ile Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe
50 55 60
Leu Pro Phe Tyr Ser Asn Val Thr Gly Phe His Thr Ile Asn His Thr
65 70 75 80
Phe Gly Asn Pro Val Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala
85 90 95
Thr Glu Lys Ser Asn Val Val Arg Gly Trp Val Phe Gly Ser Thr Met
100 105 110
Asn Asn Lys Ser Gln Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val
115 120 125
Val Ile Arg Ala Cys Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala
130 135 140
Val Ser Lys Pro Met Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn
145 150 155 160
Ala Phe Asn Cys Thr Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp
165 170 175
Val Ser Glu Lys Ser Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe
180 185 190
Lys Asn Lys Asp Gly Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile
195 200 205
Asp Val Val Arg Asp Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile
210 215 220
Phe Lys Leu Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu
225 230 235 240

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

<210> 56
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 17-756 of SEQ ID NO:1 without a signal peptide at the N-terminus

<400> 56

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

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
260 265 270
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
275 280 285
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
290 295 300
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
305 310 315 320
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
325 330 335
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
340 345 350
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
355 360 365
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
370 375 380
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
385 390 395 400
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
405 410 415
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
420 425 430
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
435 440 445
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
450 455 460
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
465 470 475 480
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
485 490 495
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
500 505 510
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
515 520 525
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
530 535 540
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
545 550 555 560
Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
565 570 575
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
580 585 590

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
595 600 605
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
610 615 620
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
625 630 635 640
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
645 650 655
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
660 665 670
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
675 680 685
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
690 695 700
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
705 710 715 720
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
725 730 735
Ala Ala Glu

<210> 57
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 272-537 of SEQ ID NO:1

<400> 57
Ile Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys
1 5 10 15
Cys Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser
20 25 30
Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Asn Ile Thr
35 40 45
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
50 55 60
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
65 70 75 80
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
85 90 95

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
100 105 110
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
115 120 125
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
130 135 140
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
145 150 155 160
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
165 170 175
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
180 185 190
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
195 200 205
Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
210 215 220
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
225 230 235 240
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
245 250 255
Phe Asn Gly Leu Thr Gly Thr Gly Val
260 265

<210> 58
<211> 17
<212> PRT
<213> SARS coronavirus

<400> 58
Asp Val Gln Ala Pro Asn Tyr Thr Gln His Thr Ser Ser Met Arg Gly
1 5 10 15
Cys

<210> 59
<211> 15
<212> PRT
<213> SARS coronavirus

<400> 59
Pro Ser Ser Lys Arg Phe Gln Pro Gln Gln Phe Gly Arg Asp Cys
1 5 10 15

<210> 60
<211> 16
<212> PRT
<213> SARS coronavirus

<400> 60
Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15

<210> 61
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 303-537 of SEQ ID NO:1 containing the receptor binding domain

<400> 61
Ser Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn
1 5 10 15
Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe
20 25 30
Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala
35 40 45
Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys
50 55 60
Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val
65 70 75 80
Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala
85 90 95
Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp
100 105 110
Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala
115 120 125
Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly
130 135 140
Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro
145 150 155 160
Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu
165 170 175

Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr
180 185 190
Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val
195 200 205
Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn
210 215 220
Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly Val
225 230 235

<210> 62
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 319-517 of SEQ ID NO:1 containing the receptor binding domain

<400> 62
Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe
1 5 10 15
Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala
20 25 30
Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Ihr Phe Lys Cys
35 40 45
Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val
50 55 60
Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala
65 70 75 80
Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp
85 90 95
Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala
100 105 110
Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly
115 120 125
Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro
130 135 140
Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu
145 150 155 160
Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr
165 170 175

Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val
180 185 190
Cys Gly Pro Lys Leu Ser Thr
195

<210> 63
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic sequence of amino acids 319-518 of SEQ ID NO:1 containing the receptor binding domain

<400> 63
Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe
1 5 10 15
Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala
20 25 30
Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys
35 40 45
Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val
50 55 60
Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala
65 70 75 80
Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp
85 90 95
Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala
100 105 110
Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly
115 120 125
Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro
130 135 140
Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu
145 150 155 160
Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr
165 170 175
Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val
180 185 190
Cys Gly Pro Lys Leu Ser Thr Asp
195 200

<210> 64
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 64
gatcggatcc ggtacaatca cag 23

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic primer

<400> 65
gatcgggccc gacacactgg ttc 23