

SEQUENCE LISTING

<110> IgNova GmbH
 <120> Antibody that binds specifically to the SARS CoV 2 spike protein
 <130> ID 47828
 <160> 41
 <170> PatentIn version 3.5
 <210> 1
 <211> 1273
 <212> PRT
 <213> artificial sequence
 <220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer
 <400> 1

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
 20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
 35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
 65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
210 215 220

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

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
325 330 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala

340

345

350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 355 360 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 370 375 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 385 390 395 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 405 410 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 420 425 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 435 440 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 450 455 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 465 470 475 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 485 490 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 500 505 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 515 520 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 530 535 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 545 550 555 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
565 570 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
580 585 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
595 600 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
610 615 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625 630 635 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
645 650 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
660 665 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
675 680 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
690 695 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705 710 715 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
725 730 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
740 745 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
755 760 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln

770

775

780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 785 790 795 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 805 810 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 820 825 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 835 840 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 850 855 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 865 870 875 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 900 905 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 915 920 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 930 935 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 945 950 955 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 980 985 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
995 1000 1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn
1010 1015 1020

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1025 1030 1035

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1040 1045 1050

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1055 1060 1065

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1070 1075 1080

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1085 1090 1095

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1100 1105 1110

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1115 1120 1125

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1130 1135 1140

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1145 1150 1155

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1160 1165 1170

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
1175 1180 1185

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu

1190

1195

1200

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu
 1205 1210 1215

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
 1220 1225 1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235 1240 1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
 1250 1255 1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
 1265 1270

<210> 2

<211> 1198

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 2

Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
 1 5 10 15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
 20 25 30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr
 35 40 45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
 50 55 60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
 65 70 75 80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
85 90 95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
100 105 110

Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val
115 120 125

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
130 135 140

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

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
165 170 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
180 185 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu
195 200 205

Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
210 215 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
225 230 235 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
245 250 255

Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
260 265 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
275 280 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
290 295 300

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

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
325 330 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
340 345 350

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
355 360 365

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
370 375 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
385 390 395 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
405 410 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
420 425 430

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
435 440 445

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
450 455 460

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
465 470 475 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
485 490 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
500 505 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
515 520 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
530 535 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
545 550 555 560

Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser
565 570 575

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
580 585 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
595 600 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
610 615 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His
625 630 635 640

Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys
645 650 655

Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val
660 665 670

Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn
675 680 685

Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr
690 695 700

Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser
705 710 715 720

Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn
725 730 735

Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu
740 745 750

Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala
755 760 765

Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly
770 775 780

Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg
785 790 795 800

Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala
805 810 815

Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg
820 825 830

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

Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala
850 855 860

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

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

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

Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser
915 920 925

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

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

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

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

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

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1010 1015 1020

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1025 1030 1035

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1040 1045 1050

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1055 1060 1065

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1070 1075 1080

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1085 1090 1095

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1100 1105 1110

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1115 1120 1125

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1130 1135 1140

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1145 1150 1155

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
1160 1165 1170

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
1175 1180 1185

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro
1190 1195

<210> 3

<211> 273

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 3

Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
1 5 10 15

Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
20 25 30

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
35 40 45

Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
50 55 60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65 70 75 80

Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
85 90 95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
100 105 110

Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly

115

120

125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
 130 135 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
 145 150 155 160

Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
 165 170 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
 180 185 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
 195 200 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn
 210 215 220

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys
 225 230 235 240

Phe Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp
 245 250 255

Ala Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys
 260 265 270

Ser

<210> 4

<211> 201

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 4

Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr
1 5 10 15

Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys
20 25 30

Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe
35 40 45

Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr
50 55 60

Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln
65 70 75 80

Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu
85 90 95

Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu
100 105 110

Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg
115 120 125

Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr
130 135 140

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

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
165 170 175

Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro
180 185 190

Ala Thr Val Cys Gly Pro Lys Lys Ser
195 200

<210> 5

<211> 127

<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 5

Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr Gln
1 5 10 15

Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser
20 25 30

Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser Val Ala Tyr
35 40 45

Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile Ser Val Thr
50 55 60

Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val Asp Cys Thr
65 70 75 80

Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu Leu Leu Gln
85 90 95

Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr Gly Ile Ala
100 105 110

Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln Val Lys
115 120 125

<210> 6
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 6

Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser Phe Ile Glu Asp Leu
1 5 10 15

Leu

<210> 7
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 7

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
1 5 10 15

Ile Ala

<210> 8
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 8

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
1 5 10

<210> 9
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 9

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro
1 5 10

<210> 10
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 10

Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu
1 5 10

<210> 11
<211> 1273
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 11

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
210 215 220

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

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys

325

330

335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 340 345 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 355 360 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 370 375 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 385 390 395 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 405 410 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 420 425 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 435 440 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 450 455 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 465 470 475 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 485 490 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 500 505 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 515 520 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 530 535 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545 550 555 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
565 570 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
580 585 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
595 600 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
610 615 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625 630 635 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
645 650 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
660 665 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Ala Ser Val Ala
675 680 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
690 695 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705 710 715 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
725 730 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
740 745 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr

755

760

765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 770 775 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 785 790 795 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Ala Ser
 805 810 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 820 825 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 835 840 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 850 855 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 865 870 875 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 900 905 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 915 920 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 930 935 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 945 950 955 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
980 985 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
995 1000 1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn
1010 1015 1020

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1025 1030 1035

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1040 1045 1050

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1055 1060 1065

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1070 1075 1080

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1085 1090 1095

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1100 1105 1110

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1115 1120 1125

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1130 1135 1140

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1145 1150 1155

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1160 1165 1170

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu

1175

1180

1185

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
 1190 1195 1200

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu
 1205 1210 1215

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
 1220 1225 1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235 1240 1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
 1250 1255 1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
 1265 1270

<210> 12

<211> 1198

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 12

Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
 1 5 10 15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
 20 25 30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr
 35 40 45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
 50 55 60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
65 70 75 80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
85 90 95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
100 105 110

Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val
115 120 125

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
130 135 140

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

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
165 170 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
180 185 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu
195 200 205

Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
210 215 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
225 230 235 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
245 250 255

Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
260 265 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
275 280 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
290 295 300

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

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
325 330 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
340 345 350

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
355 360 365

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
370 375 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
385 390 395 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
405 410 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
420 425 430

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
435 440 445

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
450 455 460

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
465 470 475 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
485 490 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
500 505 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
515 520 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
530 535 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
545 550 555 560

Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser
565 570 575

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
580 585 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
595 600 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
610 615 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His
625 630 635 640

Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys
645 650 655

Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Ala Ser Val
660 665 670

Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn
675 680 685

Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr
690 695 700

Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser
705 710 715 720

Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn
725 730 735

Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu
740 745 750

Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala
755 760 765

Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly
770 775 780

Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Ala
785 790 795 800

Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala
805 810 815

Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg
820 825 830

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

Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala
850 855 860

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

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

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

Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser
915 920 925

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

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

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

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

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

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1010 1015 1020

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1025 1030 1035

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1040 1045 1050

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1055 1060 1065

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1070 1075 1080

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1085 1090 1095

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1100 1105 1110

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1115 1120 1125

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1130 1135 1140

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1145 1150 1155

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
1160 1165 1170

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
1175 1180 1185

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro
1190 1195

<210> 13

<211> 127

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 13

Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr Gln
1 5 10 15

Thr Gln Thr Asn Ser Pro Arg Arg Ala Ala Ser Val Ala Ser Gln Ser
20 25 30

Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser Val Ala Tyr
35 40 45

Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile Ser Val Thr
50 55 60

Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val Asp Cys Thr
65 70 75 80

Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu Leu Leu Gln
85 90 95

Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr Gly Ile Ala

100

105

110

Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln Val Lys
 115 120 125

<210> 14

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 14

Leu Pro Asp Pro Ser Lys Pro Ser Lys Ala Ser Phe Ile Glu Asp Leu
 1 5 10 15

Leu

<210> 15

<211> 18

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 15

Gln Thr Asn Ser Pro Arg Arg Ala Ala Ser Val Ala Ser Gln Ser Ile
 1 5 10 15

Ile Ala

<210> 16

<211> 3816

<212> DNA

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 16

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tgctgaacc tgaccaccag gactcaactg cctccagctt acaccaacag cttcacccgt	180
ggtgtctact accccgacaa ggtgttccgt tcctccgtgc tgcactctac ccaggacctg	240
ttcctgcctt tcttctccaa cgtgacctgg ttccacgcta tccacgtgtc cgggtactaac	300
ggcaccaagc gtttcgacaa ccccggtgctg cttttcaacg acggcgtgta cttcgcttcc	360
accgagaagt ccaacatcat ccgtggctgg atcttcggta ctaccctgga ctccaagact	420
cagtcctgc tgatcgtgaa caacgctacc aacgtggta tcaaagtgtg cgagttccag	480
ttctgcaacg accccttctt gggcgtttac taccacaaga acaacaagtc ctggatggaa	540
tccgagttcc gtgtgtactc ctccgctaac aactgcacct tcgagtacgt gtcccagcct	600
ttcctgatgg acctcgaggg caagcagggc aacttcaaga acctgcgcga gttcgtgttc	660
aagaacatcg acggctactt caagatctac tccaagcaca cccctatcaa cctcgtgcgt	720
gacctgcctc agggcttctc tgctctggaa cctctgggtg acctgccaat cggtatcaac	780
atcacccgtt tccagactct gctggctctg caccgttctt acttgacccc tggcgactcc	840
tcttctggat ggactgctgg tgctgctgcc tactacgtgg gttacctgca gcctcgtacc	900
ttcctgctga agtacaacga gaacggaacc atcaccgacg ctgtggactg cgctctggac	960
cctttgtccg agactaagtg caccctgaag tccttcaccg tcgagaaggg catctaccag	1020
acctccaact tccgtgtgca gcccaccgag tccatcgtgc gtttccctaa catcaccaac	1080
ttgtgcccct tcggcgaggt gttcaacgct actcgtttcg cttccgtgta cgcttggaac	1140
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agcaccttca agtgctacgg tgtctcccct accaagctga acgacctgtg cttcaccaac	1260
gtctacgtg actccttcgt gatccgtggc gacgaagtgc gtcagatcgc tcctgggtcaa	1320
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gcctggaact ccaacaacct ggactctaaa gtcggcggca actacaatta cctgtaccgt	1440
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gctggttcta ccccttgcaa cgggtgctgag ggcttcaact gctacttccc actgcagtcc	1560
tacggtttcc agcctaccaa cggcgtcggg taccagcctt accgtgtggg ggtgctgtcc	1620

ttcgaactgc tgcacgctcc tgctactgtg tgcgggtccca agaaatccac caacctgggtc	1680
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tctaacaaga agttcctgcc attccagcaa ttcggccgtg atatcgctga caccactgac	1800
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gtgaactgca ccgaagtgcc cgtgggtatt cacgctgacc agctgactcc aacctggcgc	1980
gtgtactcca ccggttccaa cgtgttccag acacgtgctg gttgcctgat cggtgctgag	2040
cacgtcaaca actcctacga gtgcgacatc cccatcggcg ctggtatctg cgcttcctac	2100
cagactcaga ccaactctcc tgctggcgct ggttccgtgg cttcccagtc catcattgct	2160
tacactatgt ccctgggtgc tgagaactcc gtcgcttact ctaacaactc tatcgctatc	2220
cccaccaact tcaccatctc cgtcaccacc gagatcctgc ctgtgtccat gaccaagacc	2280
tccgtggact gcacatgta catctgcggc gactccaccg agtgctctaa cctgctgttg	2340
cagtacggtt ctttctgcac ccagctgaac cgtgctctga ccggtatcgc tgtcgagcag	2400
gacaagaaca cccaagaggt gttcgtcaa gtgaagcaga tctacaagac ccctcctatc	2460
aaggacttcg gcggtttcaa cttctcccag atcttgcccg atccttctaa gccctccaag	2520
cgctccttca tcgaggatct gctgtttaac aaagtgacct tggctgacgc tggcttcac	2580
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tccgctctgc tcgctggcac tatcacctcc ggatggactt tcggagctgg tgccgctctg	2760
cagatcccct tcgctatgca gatggcttac cgtttcaacg gtatcggtgt caccagaac	2820
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tctgtcctga acgacatcct gtccaggctg gaccctcctg aggctgaagt gcaaactgcac	3060
cgtctgatca ccggctgtct gcagtctctg cagacctacg tgaccagca gttgatccgc	3120
gctgctgaga tccgtgcttc cgctaacctg gctgctacca agatgtccga gtgcgtgctg	3180
ggacagtcca agcgtgttga cttctgcggc aagggttacc acctgatgag cttccctcag	3240

tccgctcctc acggtgtcgt gttcttgac gtcacctacg tgcccgtca agagaagaac 3300
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 ttcgtgtcca acggcaccca ttggttcgtc acccagcgca acttctacga gccccagatc 3420
 atcactaccg acaacacctt cgtgtccggc aactgacgac tcgtcatcgg tatcgttaac 3480
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<210> 17
 <211> 1272
 <212> PRT
 <213> artificial sequence

<220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 17

Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
 1 5 10 15

Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
 20 25 30

Ala His Ser Ala Phe Ala Ala Asp Cys Val Asn Leu Thr Thr Arg Thr
 35 40 45

Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe Thr Arg Gly Val Tyr Tyr
 50 55 60

Pro Asp Lys Val Phe Arg Ser Ser Val Leu His Ser Thr Gln Asp Leu
 65 70 75 80

Phe Leu Pro Phe Phe Ser Asn Val Thr Trp Phe His Ala Ile His Val

85

90

95

Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn Pro Val Leu Pro Phe
 100 105 110

Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu Lys Ser Asn Ile Ile Arg
 115 120 125

Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys Thr Gln Ser Leu Leu
 130 135 140

Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys Val Cys Glu Phe Gln
 145 150 155 160

Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr His Lys Asn Asn Lys
 165 170 175

Ser Trp Met Glu Ser Glu Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys
 180 185 190

Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu Met Asp Leu Glu Gly Lys
 195 200 205

Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val Phe Lys Asn Ile Asp
 210 215 220

Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro Ile Asn Leu Val Arg
 225 230 235 240

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

Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr Leu Leu Ala Leu His Arg
 260 265 270

Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly Ala
 275 280 285

Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe Leu Leu Lys
 290 295 300

Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ala Leu Asp
305 310 315 320

Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser Phe Thr Val Glu Lys
325 330 335

Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Gln Pro Thr Glu Ser Ile
340 345 350

Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe
355 360 365

Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile
370 375 380

Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe
385 390 395 400

Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu
405 410 415

Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu
420 425 430

Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn
435 440 445

Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser
450 455 460

Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg
465 470 475 480

Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr
485 490 495

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
500 505 510

Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly

515

520

525

Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
 530 535 540

His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val
 545 550 555 560

Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
 565 570 575

Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro Phe Gln Gln Phe Gly
 580 585 590

Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg Asp Pro Gln Thr Leu
 595 600 605

Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly Gly Val Ser Val Ile
 610 615 620

Thr Pro Gly Thr Asn Thr Ser Asn Gln Val Ala Val Leu Tyr Gln Asp
 625 630 635 640

Val Asn Cys Thr Glu Val Pro Val Ala Ile His Ala Asp Gln Leu Thr
 645 650 655

Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn Val Phe Gln Thr Arg
 660 665 670

Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn Asn Ser Tyr Glu Cys
 675 680 685

Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr Gln Thr Gln Thr
 690 695 700

Asn Ser Pro Ala Gly Ala Gly Ser Val Ala Ser Gln Ser Ile Ile Ala
 705 710 715 720

Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser Val Ala Tyr Ser Asn Asn
 725 730 735

Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile Ser Val Thr Thr Glu Ile
740 745 750

Leu Pro Val Ser Met Thr Lys Thr Ser Val Asp Cys Thr Met Tyr Ile
755 760 765

Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu Leu Leu Gln Tyr Gly Ser
770 775 780

Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr Gly Ile Ala Val Glu Gln
785 790 795 800

Asp Lys Asn Thr Gln Glu Val Phe Ala Gln Val Lys Gln Ile Tyr Lys
805 810 815

Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu
820 825 830

Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser Phe Ile Glu Asp Leu Leu
835 840 845

Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Ile Lys Gln Tyr Gly
850 855 860

Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp Leu Ile Cys Ala Gln Lys
865 870 875 880

Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr Asp Glu Met Ile
885 890 895

Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly Thr Ile Thr Ser Gly Trp
900 905 910

Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe Ala Met Gln Met
915 920 925

Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn Val Leu Tyr Glu
930 935 940

Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn Ser Ala Ile Gly Lys Ile

945		950		955		960
Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala Leu Gly Lys Leu Gln Asp						
		965		970		975
Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu Val Lys Gln Leu						
		980		985		990
Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn Asp Ile Leu Ser						
		995		1000		1005
Arg Leu Asp Pro Pro Glu Ala Glu Val Gln Ile Asp Arg Leu Ile						
		1010		1015		1020
Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln Gln Leu						
		1025		1030		1035
Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala Thr						
		1040		1045		1050
Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp Phe						
		1055		1060		1065
Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala Pro						
		1070		1075		1080
His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu						
		1085		1090		1095
Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala						
		1100		1105		1110
His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp						
		1115		1120		1125
Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr						
		1130		1135		1140
Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile						
		1145		1150		1155

Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser
1160 1165 1170

Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro
1175 1180 1185

Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val Val
1190 1195 1200

Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys Asn
1205 1210 1215

Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr Glu
1220 1225 1230

Gln Tyr Ile Lys Trp Pro Gly Tyr Ile Pro Glu Ala Pro Arg Asp
1235 1240 1245

Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
1250 1255 1260

Thr Phe Leu His His His His His His
1265 1270

<210> 18
<211> 2151
<212> DNA
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 18
atgctgctgg tcaaccagtc tcaccagggt ttcaacaaag aacacacctc caagatggtg 60
tccgccatcg tgctgtacgt gctgttggct gctgctgctc actccgcttt cgctgctgac 120
tgcgtgaacc tgaccaccag gactcaactg cctccagctt acaccaacag cttcaccctg 180
gggtgtctact accccgacaa ggtgttccgt tcctccgtgc tgcactctac ccaggacctg 240
ttcctgcctt tcttctccaa cgtgacctgg ttccacgcta tccacgtgtc cggtactaac 300
ggcaccaagc gtttcgacaa ccccgctgctg cttttcaacg acggcgtgta cttcgcttcc 360

accgagaagt ccaacatcat ccgtggctgg atcttcggta ctaccctgga ctccaagact	420
cagtccctgc tgatcgtgaa caacgctacc aacgtgggtca tcaaagtgtg cgagttccag	480
ttctgcaacg accccttcct gggcggtttac taccacaaga acaacaagtc ctggatggaa	540
tccgagttcc gtgtgtactc ctccgctaac aactgcacct tcgagtacgt gtcccagcct	600
ttcctgatgg acctcgaggg caagcagggc aacttcaaga acctgcgcga gttcgtgttc	660
aagaacatcg acggctactt caagatctac tccaagcaca cccctatcaa cctcgtgcgt	720
gacctgcctc agggcttctc tgctctggaa cctctgggtg acctgccaat cggtatcaac	780
atcacccgtt tccagactct gctggctctg caccgttcct acttgacccc tggcgactcc	840
tcttctggat ggactgctgg tgctgctgcc tactacgtgg gttacctgca gcctcgtacc	900
ttcctgctga agtacaacga gaacggaacc atcacgcacg ctgtggactg cgctctggac	960
cctttgtccg agactaagtg caccctgaag tccttcaccg tcgagaaggg catctaccag	1020
acctccaact tccgtgtgca gcccaccgag tccatcgtgc gtttccctaa catcaccaac	1080
ttgtgcccct tcggcgaggt gttcaacgct actcgtttcg cttccgtgta cgcttggaac	1140
cgcaagcgca tctctaactg cgtggccgac tactccgtcc tgtacaactc cgcttccttc	1200
agcaccttca agtgctacgg tgtctcccct accaagctga acgacctgtg cttcaccaac	1260
gtctacgctg actccttcgt gatccgtggc gacgaagtgc gtcagatcgc tcctgggtcaa	1320
accggcaaga tcgctgacta caactacaag ctgcccgcg acttcaccgg ttgcgtgac	1380
gcctggaact ccaacaacct ggactctaaa gtcggcggca actacaatta cctgtaccgt	1440
ctgttccgca agtccaacct gaagcctttc gagcgtgaca tctctaccga gatctaccag	1500
gctggttcta ccccttgcaa cgggtgtcgag ggcttcaact gctacttccc actgcagtcc	1560
tacggtttcc agcctaccaa cggcgtcgggt taccagcctt accgtgtggt ggtgctgtcc	1620
ttcgaactgc tgcacgctcc tgctactgtg tgcgggtcca agaaatccac caacctggtc	1680
aagaacaaat gcgtgaactt caacttcaac ggcctgaccg gcaccggtgt cctgaccgag	1740
tctaacaaga agttcctgcc attccagcaa ttcggccgtg atatcgctga caccactgac	1800
gctgtgcgcg accctcagac tctggaaatc ctggacatca ccccatgcag cttcgggtggt	1860
gtctccgtga tcaccctgg tactaacacc tctaaccagg tggccgttct gtaccaggac	1920
gtgaactgca ccgaagtgcc cgtggctatt cacgctgacc agctgactcc aacctggcgc	1980

gtgtactcca ccggttccaa cgtgttccag acacgtgctg gttgcctgat cgggtgctgag 2040
cacgtcaaca actcctacga gtgcgacatc cccatcggcg ctggtatctg cgcttcctac 2100
cagactcaga ccaactctcc tgctggcgct ggtcaccacc atcaccacca c 2151

<210> 19
<211> 717
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 19

Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
1 5 10 15

Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
20 25 30

Ala His Ser Ala Phe Ala Ala Asp Cys Val Asn Leu Thr Thr Arg Thr
35 40 45

Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe Thr Arg Gly Val Tyr Tyr
50 55 60

Pro Asp Lys Val Phe Arg Ser Ser Val Leu His Ser Thr Gln Asp Leu
65 70 75 80

Phe Leu Pro Phe Phe Ser Asn Val Thr Trp Phe His Ala Ile His Val
85 90 95

Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn Pro Val Leu Pro Phe
100 105 110

Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu Lys Ser Asn Ile Ile Arg
115 120 125

Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys Thr Gln Ser Leu Leu
130 135 140

Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys Val Cys Glu Phe Gln
145 150 155 160

Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr His Lys Asn Asn Lys
165 170 175

Ser Trp Met Glu Ser Glu Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys
180 185 190

Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu Met Asp Leu Glu Gly Lys
195 200 205

Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val Phe Lys Asn Ile Asp
210 215 220

Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro Ile Asn Leu Val Arg
225 230 235 240

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

Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr Leu Leu Ala Leu His Arg
260 265 270

Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly Ala
275 280 285

Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe Leu Leu Lys
290 295 300

Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ala Leu Asp
305 310 315 320

Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser Phe Thr Val Glu Lys
325 330 335

Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Gln Pro Thr Glu Ser Ile
340 345 350

Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe

355

360

365

Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile
 370 375 380

Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe
 385 390 395 400

Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu
 405 410 415

Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu
 420 425 430

Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn
 435 440 445

Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser
 450 455 460

Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg
 465 470 475 480

Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr
 485 490 495

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
 500 505 510

Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly
 515 520 525

Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
 530 535 540

His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val
 545 550 555 560

Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
 565 570 575

Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro Phe Gln Gln Phe Gly
580 585 590

Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg Asp Pro Gln Thr Leu
595 600 605

Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly Gly Val Ser Val Ile
610 615 620

Thr Pro Gly Thr Asn Thr Ser Asn Gln Val Ala Val Leu Tyr Gln Asp
625 630 635 640

Val Asn Cys Thr Glu Val Pro Val Ala Ile His Ala Asp Gln Leu Thr
645 650 655

Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn Val Phe Gln Thr Arg
660 665 670

Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn Asn Ser Tyr Glu Cys
675 680 685

Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr Gln Thr Gln Thr
690 695 700

Asn Ser Pro Ala Gly Ala Gly His His His His His His
705 710 715

<210> 20
<211> 807
<212> DNA
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 20
atgctgctgg tcaaccagtc tcaccagggt ttcaacaaag aacacacctc caagatggtg 60
tccgccatcg tgctgtacgt gctgttggct gctgctgctc actccgcttt cgctgctgat 120
cgtgtgcagc ctaccgagtc catcgtgcgt ttccccaaca tcaccaactt gtgccccttc 180
ggcgagggtgt tcaacgctac ccgtttcgct tccgtgtacg cttggaaccg caagcgcac 240

tctaactgcg tggccgacta ctccgtcctg tacaactccg cttccttcag caccttcaag 300
tgctacgggtg tctcccctac caagctgaac gacctgtgct tcaccaacgt ctacgctgac 360
tccttcgtga tccgtggcga cgaagtgcgt cagatcgctc ctggtcaaac cggcaagatc 420
gctgactaca actacaagct gcccgcgcac ttcaccggtt gcgtgatcgc ctggaactcc 480
aacaacctgg actccaaagt cgggtggcaac tacaattacc tgtaccgcct gttccgcaag 540
tccaacctga agcctttcga gcgtgacatc tccaccgaga tctaccaggc tggttctacc 600
ccttgcaacg gtgtcgaggg cttcaactgc tacttccac tgcatccta cggtttccag 660
cctaccaacg gcgtgggtta ccagccttac cgtgtggtgg tgctgtcctt cgaactgctg 720
cacgctcctg ctactgtgtg cgggtccaag aaatccacca acctggtcaa gaacaaatgc 780
gtgaacttcc accaccacca tcaccac 807

<210> 21
<211> 269
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 21

Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
1 5 10 15

Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
20 25 30

Ala His Ser Ala Phe Ala Ala Asp Arg Val Gln Pro Thr Glu Ser Ile
35 40 45

Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe
50 55 60

Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile
65 70 75 80

Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe

85

90

95

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

Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu
 115 120 125

Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn
 130 135 140

Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser
 145 150 155 160

Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg
 165 170 175

Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr
 180 185 190

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
 195 200 205

Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly
 210 215 220

Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
 225 230 235 240

His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val
 245 250 255

Lys Asn Lys Cys Val Asn Phe His His His His His His
 260 265

<210> 22

<211> 957

<212> DNA

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or

concatemer

<400> 22

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atgctgctgg tcaaccagtc tcaccagggt ttcaacaaag aacacacctc caagatgggtg      60
tccgccatcg tgctgtacgt gctgttggct gctgctgctc actccgcttt cgctgctgat      120
cgtgtgcagc ctaccgagtc catcgtgcgt ttccccaaca tcaccaactt gtgccccttc      180
ggcgagggtgt tcaacgctac ccgtttcgct tccgtgtacg cttggaaccg caagcgcac      240
tctaactgcg tggccgacta ctccgtcctg tacaactccg cttccttcag caccttcaag      300
tgctacgggtg tctcccctac caagctgaac gacctgtgct tcaccaacgt ctacgctgac      360
tccttcgtga tccgtggcga cgaagtgcgt cagatcgctc ctggtcaaac cggcaagatc      420
gctgactaca actacaagct gcccgcagc ttcaccgggt gcgtgatcgc ctggaactcc      480
aacaacctgg actccaaagt cgggtggcaac tacaattacc tgtaccgcct gttccgcaag      540
tccaacctga agcctttcga gcgtgacatc tccaccgaga tctaccaggc tggttctacc      600
ccttgcaacg gtgtcgaggg cttcaactgc tacttccac tgcatccta cggtttccag      660
cctaccaacg gcgtgggtta ccagccttac cgtgtgggtg tgctgtcctt cgaactgctg      720
cacgctcctg ctactgtgtg cgggtccaag aaatccacca acctggtcaa gaacaaatgc      780
gtgaacttca acttcaacgg cctgaccggc accggtgtcc tgaccgagtc taacaagaag      840
ttcctgcctt tccagcaatt cggccgtgat atcgtgaca ccaccgacgc tgtgcgtgac      900
cctcagactc tggaaatcct ggacatcacc ccttgctctc accaccacca tcaccac      957

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<210> 23

<211> 319

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 23

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Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
1             5             10            15

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Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
20            25            30

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Ala His Ser Ala Phe Ala Ala Asp Arg Val Gln Pro Thr Glu Ser Ile
35 40 45

Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe
50 55 60

Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile
65 70 75 80

Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe
85 90 95

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

Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu
115 120 125

Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn
130 135 140

Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser
145 150 155 160

Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg
165 170 175

Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr
180 185 190

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
195 200 205

Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly
210 215 220

Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
225 230 235 240

His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val

245

250

255

Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
 260 265 270

Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro Phe Gln Gln Phe Gly
 275 280 285

Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg Asp Pro Gln Thr Leu
 290 295 300

Glu Ile Leu Asp Ile Thr Pro Cys Ser His His His His His His
 305 310 315

<210> 24

<211> 855

<212> DNA

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 24

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cctgttaaca ctaccactga agacgagact gctcaaattc cagctgaagc agttatcggc 120

tactctgacc ttgagggtga tttcgacgtc gctgttttgc ctttctctaa ctccactaac 180

aacggtttgt tgttcattaa caccactatc gcttccattg ctgctaagga agagggtgtc 240

tctctcgaga agagaaacat caccaacttg tgccccttcg gcgaggtgtt caacgctact 300

cgtttcgctt ccgtgtacgc ttggaaccgc aagcgcattc ctaactgcgt ggccgactac 360

tccgtcctgt acaactccgc ttccttcagc accttcaagt gctacgggtgt ctcccctacc 420

aagctgaacg acctgtgctt caccaacgtc tacgctgact ctttcgtgat ccgtggcgac 480

gaagtgcgtc agatcgctcc tgggtcaaacc ggcaagatcg ctgactacaa ctacaagctg 540

cccgacgact tcaccggttg cgtgatcgcc tggaactcca acaacctgga ctctaaagtc 600

ggcggcaact acaattacct gtaccgtctg ttccgcaagt ccaacctgaa gcctttcgag 660

cgtgacatct ctaccgagat ctaccaggct ggttctaccc cttgcaacgg tgctgagggc 720

ttcaactgct acttcccact gcagtcctac ggtttccagc ctaccaacgg cgtcgggttac 780

cagccttacc gtgtggtggt gctgtccttc gaactgctgc acgctcctgc tactgtgcac 840
caccatcacc accac 855

<210> 25
<211> 285
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 25

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Glu Lys Arg Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val
85 90 95

Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg
100 105 110

Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser
115 120 125

Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp
130 135 140

Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp

145 150 155 160

Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr
165 170 175

Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn
180 185 190

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr
195 200 205

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

Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly
225 230 235 240

Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn
245 250 255

Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu
260 265 270

Leu His Ala Pro Ala Thr Val His His His His His His
275 280 285

<210> 26
<211> 1273
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 26

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
210 215 220

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

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
325 330 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
340 345 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
355 360 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
370 375 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
385 390 395 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
405 410 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
420 425 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
435 440 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
450 455 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465 470 475 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
485 490 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
500 505 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
515 520 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
530 535 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545 550 555 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
565 570 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
580 585 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
595 600 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
610 615 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625 630 635 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
645 650 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
660 665 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
675 680 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
690 695 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705 710 715 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
725 730 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
740 745 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
755 760 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
770 775 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
785 790 795 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
805 810 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
820 825 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
835 840 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
850 855 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
865 870 875 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
900 905 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
915 920 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
930 935 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945 950 955 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
980 985 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
995 1000 1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn
1010 1015 1020

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1025 1030 1035

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1040 1045 1050

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1055 1060 1065

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1070 1075 1080

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1085 1090 1095

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1100 1105 1110

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1115 1120 1125

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1130 1135 1140

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1145 1150 1155

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1160 1165 1170

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
1175 1180 1185

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
1190 1195 1200

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu
1205 1210 1215

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
1220 1225 1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
1235 1240 1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
1250 1255 1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
1265 1270

<210> 27

<211> 1198

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 27

Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
1 5 10 15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
20 25 30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr
35 40 45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
50 55 60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
65 70 75 80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
85 90 95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
100 105 110

Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val
115 120 125

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
130 135 140

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

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
165 170 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
180 185 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu
195 200 205

Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
210 215 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
225 230 235 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
245 250 255

Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
260 265 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
275 280 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
290 295 300

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

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
325 330 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
340 345 350

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
355 360 365

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
370 375 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
385 390 395 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
405 410 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly

420

425

430

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
 435 440 445

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
 450 455 460

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
 465 470 475 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
 485 490 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
 500 505 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
 515 520 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
 530 535 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
 545 550 555 560

Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser
 565 570 575

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
 580 585 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
 595 600 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
 610 615 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His
 625 630 635 640

Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys
645 650 655

Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val
660 665 670

Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn
675 680 685

Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr
690 695 700

Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser
705 710 715 720

Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn
725 730 735

Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu
740 745 750

Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala
755 760 765

Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly
770 775 780

Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg
785 790 795 800

Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala
805 810 815

Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg
820 825 830

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

Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala

850

855

860

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

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

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

Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser
 915 920 925

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

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

Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val
 965 970 975

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

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

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
 1010 1015 1020

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
 1025 1030 1035

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
 1040 1045 1050

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
 1055 1060 1065

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
 1070 1075 1080

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
 1085 1090 1095

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
 1100 1105 1110

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
 1115 1120 1125

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
 1130 1135 1140

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
 1145 1150 1155

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
 1160 1165 1170

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
 1175 1180 1185

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro
 1190 1195

<210> 28
 <211> 1273
 <212> PRT
 <213> artificial sequence

<220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 28

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
 20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
210 215 220

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

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
325 330 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
340 345 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
355 360 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
370 375 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
385 390 395 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
405 410 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
420 425 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
435 440 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
450 455 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465 470 475 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
485 490 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
500 505 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
515 520 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
530 535 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545 550 555 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
565 570 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
580 585 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
595 600 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
610 615 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625 630 635 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
645 650 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
660 665 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Ala Ser Val Ala
675 680 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
690 695 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705 710 715 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
725 730 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
740 745 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
755 760 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
770 775 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
785 790 795 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Ala Ser
805 810 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
820 825 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
835 840 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
850 855 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
865 870 875 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
900 905 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
915 920 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
930 935 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945 950 955 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
980 985 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
995 1000 1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn
1010 1015 1020

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1025 1030 1035

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1040 1045 1050

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1055 1060 1065

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
1070 1075 1080

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
1085 1090 1095

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
1100 1105 1110

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
1115 1120 1125

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
1130 1135 1140

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
1145 1150 1155

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
1160 1165 1170

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
1175 1180 1185

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
1190 1195 1200

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu
1205 1210 1215

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
1220 1225 1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
1235 1240 1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
1250 1255 1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
1265 1270

<210> 29

<211> 1198

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 29

Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
1 5 10 15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
20 25 30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr
35 40 45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
50 55 60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
65 70 75 80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
85 90 95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
100 105 110

Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val
115 120 125

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
130 135 140

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

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
165 170 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
180 185 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu

195

200

205

Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
 210 215 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
 225 230 235 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
 245 250 255

Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
 260 265 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
 275 280 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
 290 295 300

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

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
 325 330 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
 340 345 350

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
 355 360 365

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
 370 375 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
 385 390 395 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
 405 410 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
420 425 430

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
435 440 445

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
450 455 460

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
465 470 475 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
485 490 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
500 505 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
515 520 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
530 535 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
545 550 555 560

Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser
565 570 575

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
580 585 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
595 600 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
610 615 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His

625		630		635		640									
Val	Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys
				645					650					655	
Ala	Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Ala	Ser	Val
			660					665					670		
Ala	Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn
		675					680					685			
Ser	Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr
	690					695					700				
Ile	Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser
705					710					715					720
Val	Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn
				725					730					735	
Leu	Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu
			740					745					750		
Thr	Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala
		755					760					765			
Gln	Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly
		770				775					780				
Phe	Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Ala
785					790					795					800
Ser	Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala
				805					810					815	
Gly	Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg
			820					825					830		
Asp	Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro
		835					840					845			

Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala
850 855 860

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

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

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

Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser
915 920 925

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

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

Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val
965 970 975

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

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

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
1010 1015 1020

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
1025 1030 1035

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
1040 1045 1050

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His

1055

1060

1065

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
 1070 1075 1080

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
 1085 1090 1095

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
 1100 1105 1110

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
 1115 1120 1125

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
 1130 1135 1140

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
 1145 1150 1155

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
 1160 1165 1170

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
 1175 1180 1185

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro
 1190 1195

<210> 30

<211> 344

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 30

Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr
 1 5 10 15

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
20 25 30

Gln Pro Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Cys Asn Gly Val
35 40 45

Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro
50 55 60

Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Ala Gly Ser
65 70 75 80

Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln
85 90 95

Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser
100 105 110

Gly Ser Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn
115 120 125

Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val
130 135 140

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

Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe
165 170 175

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Ala
180 185 190

Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro
195 200 205

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

Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly
225 230 235 240

Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn
245 250 255

Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro
260 265 270

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
275 280 285

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser
290 295 300

Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr
305 310 315 320

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
325 330 335

Gln Pro His His His His His
340

<210> 31

<211> 302

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 31

Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln
1 5 10 15

Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala
20 25 30

Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly
35 40 45

Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser

50

55

60

Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr
 65 70 75 80

Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro
 85 90 95

Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly
 100 105 110

Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn
 115 120 125

Gly Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly
 130 135 140

Val Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val
 145 150 155 160

Glu Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu
 165 170 175

Gly Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly
 180 185 190

Ser Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser
 195 200 205

Gly Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly
 210 215 220

Ser Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser
 225 230 235 240

Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln
 245 250 255

Ala Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala
 260 265 270

Gly Ser Thr Pro Gly Asn Gly Val Glu Gly Ser Gly Ser Gln Ala Gly
275 280 285

Ser Thr Pro Gly Asn Gly Val Glu His His His His His His
290 295 300

<210> 32

<211> 324

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 32

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro
1 5 10 15

Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn
20 25 30

Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val
35 40 45

Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr
50 55 60

Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro
65 70 75 80

Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser
85 90 95

Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser
100 105 110

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro
115 120 125

Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn
130 135 140

Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val
145 150 155 160

Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr
165 170 175

Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro
180 185 190

Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser
195 200 205

Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser
210 215 220

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro
225 230 235 240

Thr Asn Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn
245 250 255

Gly Val Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val
260 265 270

Gly Tyr Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr
275 280 285

Gln Pro Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro
290 295 300

Gly Ser Gly Ser Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro His His
305 310 315 320

His His His His

<210> 33
<211> 333
<212> PRT
<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or concatemer

<400> 33

Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly
1 5 10 15

Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe
20 25 30

Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn
35 40 45

Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly
50 55 60

Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr
65 70 75 80

Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe
85 90 95

Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro
100 105 110

Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu
115 120 125

Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln
130 135 140

Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser
145 150 155 160

Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr
165 170 175

Gly Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly
180 185 190

Ser Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser
195 200 205

Gly Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly
210 215 220

Ser Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser
225 230 235 240

Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly
245 250 255

Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe
260 265 270

Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn
275 280 285

Gly Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly
290 295 300

Tyr Phe Pro Leu Gln Ser Tyr Gly Ser Gly Ser Gly Phe Asn Gly Tyr
305 310 315 320

Phe Pro Leu Gln Ser Tyr Gly His His His His His His
325 330

<210> 34
<211> 322
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 34

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
1 5 10 15

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
20 25 30

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
35 40 45

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
50 55 60

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
65 70 75 80

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
85 90 95

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
100 105 110

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
115 120 125

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
130 135 140

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
145 150 155 160

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
165 170 175

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

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
195 200 205

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
210 215 220

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
225 230 235 240

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
245 250 255

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
260 265 270

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
275 280 285

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Gly Ser Gly Ser
290 295 300

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr His His His His
305 310 315 320

His His

<210> 35

<211> 302

<212> PRT

<213> artificial sequence

<220>

<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 35

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
1 5 10 15

Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
20 25 30

Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala
35 40 45

Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser
50 55 60

Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser
65 70 75 80

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
85 90 95

Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
100 105 110

Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala
115 120 125

Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser
130 135 140

Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser
145 150 155 160

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
165 170 175

Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
180 185 190

Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala
195 200 205

Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser
210 215 220

Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile Gly Ser Gly Ser
225 230 235 240

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
245 250 255

Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
260 265 270

Ser Gln Ser Ile Gly Ser Gly Ser Gln Thr Asn Ser Pro Arg Arg Ala
275 280 285

Arg Ser Val Ala Ser Gln Ser Ile His His His His His His

290

295

300

<210> 36
 <211> 34
 <212> PRT
 <213> artificial sequence

<220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 36

Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr
 1 5 10 15

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
 20 25 30

Gln Pro

<210> 37
 <211> 11
 <212> PRT
 <213> artificial sequence

<220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 37

Gln Ala Gly Ser Thr Pro Gly Asn Gly Val Glu
 1 5 10

<210> 38
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> Sars CoV 2 spike protein of fragment and/or mutant and/or
 concatemer

<400> 38

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro
 1 5 10

<210> 39
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 39

Gly Phe Asn Gly Tyr Phe Pro Leu Gln Ser Tyr Gly
1 5 10

<210> 40
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 40

Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr
1 5 10

<210> 41
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> Sars CoV 2 spike protein of fragment and/or mutant and/or
concatemer

<400> 41

Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser Gln Ser Ile
1 5 10 15