

# SEQUENCE LISTING

<110> EUROIMMUN Medizinische Labordiagnostika AG  
 <120> Methods and reagents for diagnosis of SARS-CoV-2 infection  
 <130> 20PP007W0  
 <160> 56  
 <170> PatentIn version 3.5  
 <210> 1  
 <211> 670  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SARS-CoV-2 S1 domain from S Protein

<400> 1

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  
660 665 670

<210> 2

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> SARS-CoV-2 S1 domain from S Protein, C-terminally his-tagged

<400> 2

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 Leu Glu His  
675 680 685

His His His His His His His  
690 695

<210> 3  
<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> SARS-CoV-2 S1 domain from S Protein, C-terminally his-tagged, as after cleavage of signal peptide

<400> 3

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 Leu Glu  
 660 665 670

His His His His His His His His  
 675 680

<210> 4  
 <211> 2088  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> SARS-CoV-2 S1 domain from S Protein, nucleotide sequence encoding  
 SEQ ID NO: 2

<400> 4  
 atgttcgtat tccttggttct gctgcctttg gtttagcagtc agtgtgtcaa cctgacaact 60  
 cgcacgcaac tgccgccagc ttacaccaac tctttcacaa gaggcgtcta ctacccggac 120  
 aaagtgtttc gctcatcagt gctgcactct acacaagatt tgtttctgcc attcttctct 180  
 aacgtaacct ggtttcacgc gattcatgtg tctgggacaa atgggaccaa gcgcttcgac 240  
 aaccccgatg tgccattcaa tgacgggggtg tattttgcct ccaccgagaa atccaatatc 300  
 atccgaggat ggattttcgg tactacgctg gactctaaaa cgcagtctct cttgatcggt 360  
 aataacgcca caaatgttgt cattaagggtg tgcgagtttc agttctgtaa tgatcccttt 420  
 ctgggtgtgt attaccacaa gaataacaag tcatggatgg aaagcgagtt tcgcgtgtac 480  
 tcaagtcca ataactgcac attcgagtat gtgtcccagc ctttctgat ggatctcgaa 540  
 ggcaaacagg ggaacttcaa gaatctgctg gagttcgtgt ttaagaacat cgacggttat 600  
 ttcaagatct acagcaaaca tacaccatt aacctggtca gggatctccc tcagggatcc 660  
 tccgccctgg aacccttggg ggacttgccc attgggatta acatcactag attccagacc 720  
 ctgctggccc ttaccgttc ctatcttact cctggcgaca gtagcagtggt atggaccgca 780

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ggagcagccg cttactatgt aggctatctg cagccacgga ccttcctcct caagtacaat | 840  |
| gaaaatggta ccataactga tgctgtggac tgcgctctgg atccactctc cgaaactaaa | 900  |
| tgcaccctta aaagcttcac ggtcgaaaag ggaatctacc agacaagtaa ctttcgggta | 960  |
| caaccactg agtccatcgt gcggtttcct aacatcacaa atctctgccc ctttggtgaa  | 1020 |
| gtgtttaacg ccactagggt cgcttctgtt tatgcgtgga atcggaagag gatttccaat | 1080 |
| tgcgtggcag actactctgt cctgtataat agcgctagct tcagcacctt caaatgttac | 1140 |
| ggggtaagcc caactaaact gaacgacctc tgttttacca acgtgtatgc cgatagcttt | 1200 |
| gtcatacgag gagatgaggt tcgtcagatt gtccttgcc aaacggggaa aatcgagac   | 1260 |
| tacaactaca agcttccga cgacttcaca ggatgcgtga tgcgtggaa ctcaaataat   | 1320 |
| ctggatagca aggttggtgg caattataac tacctgtatc gactgttcag gaaaagcaac | 1380 |
| ctcaaaccct ttgagcgcga catcagcacc gagatatacc aagccggttc aacaccttgc | 1440 |
| aatggggtgg aagggtttaa ctgctatttc ccacttcaga gctatgggtt tcagccaacc | 1500 |
| aatggagtcg gctaccagcc ctatcgggtg gtagtcctgt cctttgagct gttgcatgcg | 1560 |
| cctgccacag tctgtggccc taagaagagt acgaatctgg tgaagaacaa gtgcgtcaac | 1620 |
| ttcaatttta acggcttgac tggaacagga gttctgaccg agtccaacaa gaaattcctt | 1680 |
| ccttttcagc agtttggaag ggatatagcc gacactaccg atgccgttcg ggatccacag | 1740 |
| acactggaga ttctggacat tactccgtgc tcatttggcg gtgtatctgt catcacacct | 1800 |
| gggaccaata cctcaaatca ggtggctgtg ctctaccagg atgtgaattg taccgaagtt | 1860 |
| ccagtggcaa ttcatgccga tcaactgact cccacctgga gagtgtacag tactggcagt | 1920 |
| aacgtgtttc agacaagagc tggctgtctc ataggcgcag aacacgtcaa caacagctat | 1980 |
| gagtgtgaca ttccgatcgg cgcaggcatc tgtgcatcct accagacgca aaccaactct | 2040 |
| cccagaagag ccaggctcga gcaccacat caccatcacc atcactaa               | 2088 |

<210> 5

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> possible SARS-CoV-2 S1 epitope

<400> 5

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

<210> 6

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> S1 [MERS\_CoV]

<400> 6

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

Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile Asp  
20 25 30

Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr Ser  
35 40 45

Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp His  
50 55 60

Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr Pro  
65 70 75 80

Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe Ala  
85 90 95

Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly Thr  
100 105 110

Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr Pro  
115 120 125

Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys Met  
130 135 140

Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys Gly  
145 150 155 160

Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly Asn  
165 170 175

His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His Thr  
180 185 190

Pro Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser Leu  
195 200 205

Asn Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met Tyr  
210 215 220

Thr Tyr Asn Ile Thr Glu Asp Glu Ile Leu Glu Trp Phe Gly Ile Thr  
225 230 235 240

Gln Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp Leu  
245 250 255

Tyr Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp Thr  
260 265 270

Ile Lys Tyr Tyr Ser Ile Ile Pro His Ser Ile Arg Ser Ile Gln Ser  
275 280 285

Asp Arg Lys Ala Trp Ala Ala Phe Tyr Val Tyr Lys Leu Gln Pro Leu  
290 295 300

Thr Phe Leu Leu Asp Phe Ser Val Asp Gly Tyr Ile Arg Arg Ala Ile  
305 310 315 320

Asp Cys Gly Phe Asn Asp Leu Ser Gln Leu His Cys Ser Tyr Glu Ser  
325 330 335

Phe Asp Val Glu Ser Gly Val Tyr Ser Val Ser Ser Phe Glu Ala Lys  
340 345 350

Pro Ser Gly Ser Val Val Glu Gln Ala Glu Gly Val Glu Cys Asp Phe  
355 360 365

Ser Pro Leu Leu Ser Gly Thr Pro Pro Gln Val Tyr Asn Phe Lys Arg  
370 375 380

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

Phe Ser Val Asn Asp Phe Thr Cys Ser Gln Ile Ser Pro Ala Ala Ile  
405 410 415

Ala Ser Asn Cys Tyr Ser Ser Leu Ile Leu Asp Tyr Phe Ser Tyr Pro  
420 425 430

Leu Ser Met Lys Ser Asp Leu Ser Val Ser Ser Ala Gly Pro Ile Ser  
435 440 445

Gln Phe Asn Tyr Lys Gln Ser Phe Ser Asn Pro Thr Cys Leu Ile Leu  
450 455 460

Ala Thr Val Pro His Asn Leu Thr Thr Ile Thr Lys Pro Leu Lys Tyr  
465 470 475 480

Ser Tyr Ile Asn Lys Cys Ser Arg Leu Leu Ser Asp Asp Arg Thr Glu  
485 490 495

Val Pro Gln Leu Val Asn Ala Asn Gln Tyr Ser Pro Cys Val Ser Ile  
500 505 510

Val Pro Ser Thr Val Trp Glu Asp Gly Asp Tyr Tyr Arg Lys Gln Leu  
515 520 525

Ser Pro Leu Glu Gly Gly Gly Trp Leu Val Ala Ser Gly Ser Thr Val  
530 535 540

Ala Met Thr Glu Gln Leu Gln Met Gly Phe Gly Ile Thr Val Gln Tyr  
545 550 555 560

Gly Thr Asp Thr Asn Ser Val Cys Pro Lys Leu Glu Phe Ala Asn Asp  
565 570 575

Thr Lys Ile Ala Ser Gln Leu Gly Asn Cys Val Glu Tyr Ser Leu Tyr  
580 585 590

Gly Val Ser Gly Arg Gly Val Phe Gln Asn Cys Thr Ala Val Gly Val  
595 600 605

Arg Gln Gln Arg Phe Val Tyr Asp Ala Tyr Gln Asn Leu Val Gly Tyr  
610 615 620

Tyr Ser Asp Asp Gly Asn Tyr Tyr Cys Leu Arg Ala Cys Val Ser Val  
625 630 635 640

Pro Val Ser Val Ile Tyr Asp Lys Glu Thr Lys Thr His Ala Thr Leu  
645 650 655

Phe Gly Ser Val Ala Cys Glu His Ile Ser Ser Thr Met Ser Gln Tyr  
660 665 670

Ser Arg Ser Thr Arg Ser Met Leu Lys Arg Arg Asp Ser Thr Tyr Gly  
675 680 685

Pro Leu Gln Thr Pro Val Gly Cys Val Leu Gly Leu Val Asn Ser Ser  
690 695 700

Leu Phe Val Glu Asp Cys Lys Leu Pro Leu Gly Gln Ser Leu Cys Ala  
705 710 715 720

Leu Pro Asp Thr Pro Ser Thr Leu Thr Pro Arg Ser Val Arg  
725 730

<210> 7  
<211> 521  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> S1 [HCoV-229E]

<400> 7

Cys Gln Thr Thr Asn Gly Leu Asn Thr Ser Tyr Ser Val Cys Asn Gly  
1 5 10 15

Cys Val Gly Tyr Ser Glu Asn Val Phe Ala Val Glu Ser Gly Gly Tyr  
20 25 30

Ile Pro Ser Asp Phe Ala Phe Asn Asn Trp Phe Leu Leu Thr Asn Thr  
35 40 45

Ser Ser Val Val Asp Gly Val Val Arg Ser Phe Gln Pro Leu Leu Leu  
50 55 60

Asn Cys Leu Trp Ser Val Ser Gly Leu Arg Phe Thr Thr Gly Phe Val  
65 70 75 80

Tyr Phe Asn Gly Thr Gly Arg Gly Asp Cys Lys Gly Phe Ser Ser Asp  
85 90 95

Val Leu Ser Asp Val Ile Arg Tyr Asn Leu Asn Phe Glu Glu Asn Leu  
100 105 110

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

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

Gly Thr Val Leu Gly Asn Phe Tyr Cys Phe Val Asn Thr Thr Ile Gly  
145 150 155 160

Asn Glu Thr Thr Ser Ala Phe Val Gly Ala Leu Pro Lys Thr Val Arg  
165 170 175

Glu Phe Val Ile Ser Arg Thr Gly His Phe Tyr Ile Asn Gly Tyr Arg  
180 185 190

Tyr Phe Thr Leu Gly Asn Val Glu Ala Val Asn Phe Asn Val Thr Thr  
195 200 205

Ala Glu Thr Thr Asp Phe Cys Thr Val Ala Leu Ala Ser Tyr Ala Asp  
210 215 220

Val Leu Val Asn Val Ser Gln Thr Ser Ile Ala Asn Ile Ile Tyr Cys  
225 230 235 240

Asn Ser Val Ile Asn Arg Leu Arg Cys Asp Gln Leu Ser Phe Asp Val  
245 250 255

Pro Asp Gly Phe Tyr Ser Thr Ser Pro Ile Gln Ser Val Glu Leu Pro  
260 265 270

Val Ser Ile Val Ser Leu Pro Val Tyr His Lys His Thr Phe Ile Val  
275 280 285

Leu Tyr Val Asp Phe Lys Pro Gln Ser Gly Gly Gly Lys Cys Phe Asn  
290 295 300

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

Lys Gly Pro Leu Cys Val Asp Thr Ser His Phe Thr Thr Lys Tyr Val  
325 330 335

Ala Val Tyr Ala Asn Val Gly Arg Trp Ser Ala Ser Ile Asn Thr Gly  
340 345 350

Asn Cys Pro Phe Ser Phe Gly Lys Val Asn Asn Phe Val Lys Phe Gly  
355 360 365

Ser Val Cys Phe Ser Leu Lys Asp Ile Pro Gly Gly Cys Ala Met Pro  
370 375 380

Ile Val Ala Asn Trp Ala Tyr Ser Lys Tyr Tyr Thr Ile Gly Ser Leu  
385 390 395 400

Tyr Val Ser Trp Ser Asp Gly Asp Gly Ile Thr Gly Val Pro Gln Pro  
405 410 415

Val Glu Gly Val Ser Ser Phe Met Asn Val Thr Leu Asp Lys Cys Thr  
420 425 430

Lys Tyr Asn Ile Tyr Asp Val Ser Gly Val Gly Val Ile Arg Val Ser  
435 440 445

Asn Asp Thr Phe Leu Asn Gly Ile Thr Tyr Thr Ser Thr Ser Gly Asn  
450 455 460

Leu Leu Gly Phe Lys Asp Val Thr Lys Gly Thr Ile Tyr Ser Ile Thr  
465 470 475 480

Pro Cys Asn Pro Pro Asp Gln Leu Val Val Tyr Gln Gln Ala Val Val  
485 490 495

Gly Ala Met Leu Ser Glu Asn Phe Thr Ser Tyr Gly Phe Ser Asn Val  
500 505 510

Val Glu Leu Pro Lys Phe Phe Tyr Ala  
515 520

<210> 8  
<211> 745  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> S1 [HCoV-OC43]

<400> 8

Ala Val Ile Gly Asp Leu Lys Cys Thr Ser Asp Asn Ile Asn Asp Lys  
1 5 10 15

Asp Thr Gly Pro Pro Pro Ile Ser Thr Asp Thr Val Asp Val Thr Asn  
20 25 30

Gly Leu Gly Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr  
35 40 45

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

Met Ala Leu Lys Gly Ser Val Leu Leu Ser Arg Leu Trp Phe Lys Pro  
65 70 75 80

Pro Phe Leu Ser Asp Phe Ile Asn Gly Ile Phe Ala Lys Val Lys Asn  
85 90 95

Thr Lys Val Ile Lys Asp Arg Val Met Tyr Ser Glu Phe Pro Ala Ile  
100 105 110

Thr Ile Gly Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln  
115 120 125

Pro Arg Thr Ile Asn Ser Thr Gln Asp Gly Asp Asn Lys Leu Gln Gly  
130 135 140

Leu Leu Glu Val Ser Val Cys Gln Tyr Asn Met Cys Glu Tyr Pro Gln  
145 150 155 160

Thr Ile Cys His Pro Asn Leu Gly Asn His Arg Lys Glu Leu Trp His  
165 170 175

Leu Asp Thr Gly Val Val Ser Cys Leu Tyr Lys Arg Asn Phe Thr Tyr  
180 185 190

Asp Val Asn Ala Asp Tyr Leu Tyr Phe His Phe Tyr Gln Glu Gly Gly  
195 200 205

Thr Phe Tyr Ala Tyr Phe Thr Asp Thr Gly Val Val Thr Lys Phe Leu  
210 215 220

Phe Asn Val Tyr Leu Gly Met Ala Leu Ser His Tyr Tyr Val Met Pro  
225 230 235 240

Leu Thr Cys Asn Ser Lys Leu Thr Leu Glu Tyr Trp Val Thr Pro Leu  
245 250 255

Thr Ser Arg Gln Tyr Leu Leu Ala Phe Asn Gln Asp Gly Ile Ile Phe  
260 265 270

Asn Ala Glu Asp Cys Met Ser Asp Phe Met Ser Glu Ile Lys Cys Lys  
275 280 285

Thr Gln Ser Ile Ala Pro Pro Thr Gly Val Tyr Glu Leu Asn Gly Tyr  
290 295 300

Thr Val Gln Pro Ile Ala Asp Val Tyr Arg Arg Lys Pro Asn Leu Pro  
305 310 315 320

Asn Cys Asn Ile Glu Ala Trp Leu Asn Asp Lys Ser Val Pro Ser Pro  
325 330 335

Leu Asn Trp Glu Arg Lys Thr Phe Ser Asn Cys Asn Phe Asn Met Ser  
340 345 350

Ser Leu Met Ser Phe Ile Gln Ala Asp Ser Phe Thr Cys Asn Asn Ile  
355 360 365

Asp Ala Ala Lys Ile Tyr Gly Met Cys Phe Ser Ser Ile Thr Ile Asp  
370 375 380

Lys Phe Ala Ile Pro Asn Gly Arg Lys Val Asp Leu Gln Leu Gly Asn  
385 390 395 400

Leu Gly Tyr Leu Gln Ser Phe Asn Tyr Arg Ile Asp Thr Thr Ala Thr  
405 410 415

Ser Cys Gln Leu Tyr Tyr Asn Leu Pro Ala Ala Asn Val Ser Val Ser  
420 425 430

Arg Phe Asn Pro Ser Thr Trp Asn Lys Arg Phe Gly Phe Ile Glu Asp  
435 440 445

Ser Val Phe Lys Pro Arg Pro Ala Gly Val Leu Thr Asn His Asp Val  
450 455 460

Val Tyr Ala Gln His Cys Phe Lys Ala Pro Lys Asn Phe Cys Pro Cys  
465 470 475 480

Lys Leu Asn Gly Ser Cys Val Gly Ser Gly Pro Gly Lys Asn Asn Gly  
485 490 495

Ile Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys Asp Asn Leu  
500 505 510

Cys Thr Pro Asp Pro Ile Thr Phe Thr Gly Thr Tyr Lys Cys Pro Gln  
515 520 525

Thr Lys Ser Leu Val Gly Ile Gly Glu His Cys Ser Gly Leu Ala Val  
530 535 540

Lys Ser Asp Tyr Cys Gly Gly Asn Ser Cys Thr Cys Arg Pro Gln Ala  
545 550 555 560

Phe Leu Gly Trp Ser Ala Asp Ser Cys Leu Gln Gly Asp Lys Cys Asn  
565 570 575

Ile Phe Ala Asn Phe Ile Leu His Asp Val Asn Ser Gly Leu Thr Cys  
580 585 590

Ser Thr Asp Leu Gln Lys Ala Asn Thr Asp Ile Ile Leu Gly Val Cys  
595 600 605

Val Asn Tyr Asp Leu Tyr Gly Ile Leu Gly Gln Gly Ile Phe Val Glu  
610 615 620

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

Asn Gly Asn Leu Tyr Gly Phe Arg Asp Tyr Ile Ile Asn Arg Thr Phe  
645 650 655

Met Ile Arg Ser Cys Tyr Ser Gly Arg Val Ser Ala Ala Phe His Ala  
660 665 670

Asn Ser Ser Glu Pro Ala Leu Leu Phe Arg Asn Ile Lys Cys Asn Tyr  
675 680 685

Val Phe Asn Asn Ser Leu Thr Arg Gln Leu Gln Pro Ile Asn Tyr Phe  
690 695 700

Asp Ser Tyr Leu Gly Cys Val Val Asn Ala Tyr Asn Ser Thr Ala Ile  
705 710 715 720

Ser Val Gln Thr Cys Asp Leu Thr Val Gly Ser Gly Tyr Cys Val Asp  
725 730 735

Tyr Ser Lys Asn Arg Arg Ser Arg Gly  
740 745

<210> 9  
<211> 744  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> S1 [HCoV-HKU1]

<400> 9

Ala Val Ile Gly Asp Phe Asn Cys Thr Asn Ser Phe Ile Asn Asp Tyr  
1 5 10 15

Asn Lys Thr Ile Pro Arg Ile Ser Glu Asp Val Val Asp Val Ser Leu  
20 25 30

Gly Leu Gly Thr Tyr Tyr Val Leu Asn Arg Val Tyr Leu Asn Thr Thr  
35 40 45

Leu Leu Phe Thr Gly Tyr Phe Pro Lys Ser Gly Ala Asn Phe Arg Asp  
50 55 60

Leu Ala Leu Lys Gly Ser Ile Tyr Leu Ser Thr Leu Trp Tyr Lys Pro  
65 70 75 80

Pro Phe Leu Ser Asp Phe Asn Asn Gly Ile Phe Ser Lys Val Lys Asn  
85 90 95

Thr Lys Leu Tyr Val Asn Asn Thr Leu Tyr Ser Glu Phe Ser Thr Ile  
100 105 110

Val Ile Gly Ser Val Phe Val Asn Thr Ser Tyr Thr Ile Val Val Gln  
115 120 125

Pro His Asn Gly Ile Leu Glu Ile Thr Ala Cys Gln Tyr Thr Met Cys  
130 135 140

Glu Tyr Pro His Thr Val Cys Lys Ser Lys Gly Ser Ile Arg Asn Glu  
145 150 155 160

Ser Trp His Ile Asp Ser Ser Glu Pro Leu Cys Leu Phe Lys Lys Asn  
165 170 175

Phe Thr Tyr Asn Val Ser Ala Asp Trp Leu Tyr Phe His Phe Tyr Gln  
180 185 190

Glu Arg Gly Val Phe Tyr Ala Tyr Tyr Ala Asp Val Gly Met Pro Thr  
195 200 205

Thr Phe Leu Phe Ser Leu Tyr Leu Gly Thr Ile Leu Ser His Tyr Tyr  
210 215 220

Val Met Pro Leu Thr Cys Asn Ala Ile Ser Ser Asn Thr Asp Asn Glu  
225 230 235 240

Thr Leu Glu Tyr Trp Val Thr Pro Leu Ser Arg Arg Gln Tyr Leu Leu  
245 250 255

Asn Phe Asp Glu His Gly Val Ile Thr Asn Ala Val Asp Cys Ser Ser  
260 265 270

Ser Phe Leu Ser Glu Ile Gln Cys Lys Thr Gln Ser Phe Ala Pro Asn  
275 280 285

Thr Gly Val Tyr Asp Leu Ser Gly Phe Thr Val Lys Pro Val Ala Thr  
290 295 300

Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asp Ile Asp Asn Trp  
305 310 315 320

Leu Asn Asn Val Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Arg Ile  
325 330 335

Phe Ser Asn Cys Asn Phe Asn Leu Ser Thr Leu Leu Arg Leu Val His  
340 345 350

Val Asp Ser Phe Ser Cys Asn Asn Leu Asp Lys Ser Lys Ile Phe Gly  
355 360 365

Ser Cys Phe Asn Ser Ile Thr Val Asp Lys Phe Ala Ile Pro Asn Arg  
370 375 380

Arg Arg Asp Asp Leu Gln Leu Gly Ser Ser Gly Phe Leu Gln Ser Ser  
385 390 395 400

Asn Tyr Lys Ile Asp Ile Ser Ser Ser Ser Cys Gln Leu Tyr Tyr Ser  
405 410 415

Leu Pro Leu Val Asn Val Thr Ile Asn Asn Phe Asn Pro Ser Ser Trp  
420 425 430

Asn Arg Arg Tyr Gly Phe Gly Ser Phe Asn Leu Ser Ser Tyr Asp Val  
435 440 445

Val Tyr Ser Asp His Cys Phe Ser Val Asn Ser Asp Phe Cys Pro Cys  
450 455 460

Ala Asp Pro Ser Val Val Asn Ser Cys Ala Lys Ser Lys Pro Pro Ser  
465 470 475 480

Ala Ile Cys Pro Ala Gly Thr Lys Tyr Arg His Cys Asp Leu Asp Thr  
485 490 495

Thr Leu Tyr Val Lys Asn Trp Cys Arg Cys Ser Cys Leu Pro Asp Pro  
500 505 510

Ile Ser Thr Tyr Ser Pro Asn Thr Cys Pro Gln Lys Lys Val Val Val  
515 520 525

Gly Ile Gly Glu His Cys Pro Gly Leu Gly Ile Asn Glu Glu Lys Cys  
530 535 540

Gly Thr Gln Leu Asn His Ser Ser Cys Phe Cys Ser Pro Asp Ala Phe  
545 550 555 560

Leu Gly Trp Ser Phe Asp Ser Cys Ile Ser Asn Asn Arg Cys Asn Ile  
565 570 575

Phe Ser Asn Phe Ile Phe Asn Gly Ile Asn Ser Gly Thr Thr Cys Ser  
580 585 590

Asn Asp Leu Leu Tyr Ser Asn Thr Glu Ile Ser Thr Gly Val Cys Val  
595 600 605

Asn Tyr Asp Leu Tyr Gly Ile Thr Gly Gln Gly Ile Phe Lys Glu Val  
610 615 620

Ser Ala Ala Tyr Tyr Asn Asn Trp Gln Asn Leu Leu Tyr Asp Ser Asn  
625 630 635 640

Gly Asn Ile Ile Gly Phe Lys Asp Phe Leu Thr Asn Lys Thr Tyr Thr  
645 650 655

Ile Leu Pro Cys Tyr Ser Gly Arg Val Ser Ala Ala Phe Tyr Gln Asn  
660 665 670

Ser Ser Ser Pro Ala Leu Leu Tyr Arg Asn Leu Lys Cys Ser Tyr Val  
675 680 685

Leu Asn Asn Ile Ser Phe Ile Ser Gln Pro Phe Tyr Phe Asp Ser Tyr  
690 695 700

Leu Gly Cys Val Leu Asn Ala Val Asn Leu Thr Ser Tyr Ser Val Ser  
705 710 715 720

Ser Cys Asp Leu Arg Met Gly Ser Gly Phe Cys Ile Asp Tyr Ala Leu  
725 730 735

Pro Ser Ser Arg Arg Lys Arg Arg  
740

<210> 10  
<211> 702  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> S1 [HCoV-NL63]

<400> 10

Phe Phe Thr Cys Asn Ser Asn Ala Asn Leu Ser Met Leu Gln Leu Gly  
1 5 10 15

Val Pro Asp Asn Ser Ser Thr Ile Val Thr Gly Leu Leu Pro Thr His  
20 25 30

Trp Phe Cys Ala Asn Gln Ser Thr Ser Val Tyr Ser Ala Asn Gly Phe  
35 40 45

Phe Tyr Ile Asp Val Gly Asn His Arg Ser Ala Phe Ala Leu His Thr  
50 55 60

Gly Tyr Tyr Asp Ala Asn Gln Tyr Tyr Ile Tyr Val Thr Asn Glu Ile  
65 70 75 80

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

Thr Thr Phe Asp Phe Leu Ser Asn Ala Ser Ser Ser Phe Asp Cys Ile  
100 105 110

Val Asn Leu Leu Phe Thr Glu Gln Leu Gly Ala Pro Leu Gly Ile Thr  
115 120 125

Ile Ser Gly Glu Thr Val Arg Leu His Leu Tyr Asn Val Thr Arg Thr  
130 135 140

Phe Tyr Val Pro Ala Ala Tyr Lys Leu Thr Lys Leu Ser Val Lys Cys  
145 150 155 160

Tyr Phe Asn Tyr Ser Cys Val Phe Ser Val Val Asn Ala Thr Val Thr  
165 170 175

Val Asn Val Thr Thr His Asn Gly Arg Val Val Asn Tyr Thr Val Cys  
180 185 190

Asp Asp Cys Asn Gly Tyr Thr Asp Asn Ile Phe Ser Val Gln Gln Asp  
195 200 205

Gly Arg Ile Pro Asn Gly Phe Pro Phe Asn Asn Trp Phe Leu Leu Thr  
210 215 220

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

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

Phe Val Tyr Phe Asn Ala Thr Gly Ser Asp Val Asn Cys Asn Gly Tyr  
260 265 270

Gln His Asn Ser Val Val Asp Val Met Arg Tyr Asn Leu Asn Phe Ser  
275 280 285

Ala Asn Ser Leu Asp Asn Leu Lys Ser Gly Val Ile Val Phe Lys Thr  
290 295 300

Leu Gln Tyr Asp Val Leu Phe Tyr Cys Ser Asn Ser Ser Ser Gly Val  
305 310 315 320

Leu Asp Thr Thr Ile Pro Phe Gly Pro Ser Ser Gln Pro Tyr Tyr Cys  
325 330 335

Phe Ile Asn Ser Thr Ile Asn Thr Thr His Val Ser Thr Phe Val Gly  
340 345 350

Ile Leu Pro Pro Thr Val Arg Glu Ile Val Val Ala Arg Thr Gly Gln  
355 360 365

Phe Tyr Ile Asn Gly Phe Lys Tyr Phe Asp Leu Gly Phe Ile Glu Ala  
370 375 380

Val Asn Phe Asn Val Thr Thr Ala Ser Ala Thr Asp Phe Trp Thr Val  
385 390 395 400

Ala Phe Ala Thr Phe Val Asp Val Leu Val Asn Val Ser Ala Thr Asn  
405 410 415

Ile Gln Asn Leu Leu Tyr Cys Asp Ser Pro Phe Glu Lys Leu Gln Cys  
420 425 430

Glu His Leu Gln Phe Gly Leu Gln Asp Gly Phe Tyr Ser Ala Asn Phe  
435 440 445

Leu Asp Asp Asn Val Leu Pro Glu Thr Tyr Val Ala Leu Pro Ile Tyr  
450 455 460

Tyr Gln His Thr Asp Ile Asn Phe Thr Ala Thr Ala Ser Phe Gly Gly  
465 470 475 480

Ser Cys Tyr Val Cys Lys Pro His Gln Val Asn Ile Ser Leu Asn Gly  
485 490 495

Asn Thr Ser Val Cys Val Arg Thr Ser His Phe Ser Ile Arg Tyr Ile  
500 505 510

Tyr Asn Arg Val Lys Ser Gly Ser Pro Gly Asp Ser Ser Trp His Ile  
515 520 525

Tyr Leu Lys Ser Gly Thr Cys Pro Phe Ser Phe Ser Lys Leu Asn Asn  
530 535 540

Phe Gln Lys Phe Lys Thr Ile Cys Phe Ser Thr Val Glu Val Pro Gly  
545 550 555 560

Ser Cys Asn Phe Pro Leu Glu Ala Thr Trp His Tyr Thr Ser Tyr Thr  
565 570 575

Ile Val Gly Ala Leu Tyr Val Thr Trp Ser Glu Gly Asn Ser Ile Thr  
580 585 590

Gly Val Pro Tyr Pro Val Ser Gly Ile Arg Glu Phe Ser Asn Leu Val  
595 600 605

Leu Asn Asn Cys Thr Lys Tyr Asn Ile Tyr Asp Tyr Val Gly Thr Gly  
610 615 620

Ile Ile Arg Ser Ser Asn Gln Ser Leu Ala Gly Gly Ile Thr Tyr Val  
625 630 635 640

Ser Asn Ser Gly Asn Leu Leu Gly Phe Lys Asn Val Ser Thr Gly Asn  
645 650 655

Ile Phe Ile Val Thr Pro Cys Asn Gln Pro Asp Gln Val Ala Val Tyr  
660 665 670

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

Gly Leu Gln Asn Leu Leu Gln Leu Pro Asn Phe Tyr Tyr Val  
690 695 700

<210> 11  
<211> 657  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> S1 [SARS\_CoV]

<400> 11

Ser Gly Ser Asp Leu Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala  
1 5 10 15

Pro Asn Tyr Thr Gln His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro  
20 25 30

Asp Glu Ile Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe  
35 40 45

Leu Pro Phe Tyr Ser Asn Val Thr Gly Phe His Thr Ile Asn His Thr  
50 55 60

Phe Gly Asn Pro Val Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala  
65 70 75 80

Thr Glu Lys Ser Asn Val Val Arg Gly Trp Val Phe Gly Ser Thr Met  
85 90 95

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

Val Ile Arg Ala Cys Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala  
115 120 125

Val Ser Lys Pro Met Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn  
130 135 140

Ala Phe Asn Cys Thr Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp  
145 150 155 160

Val Ser Glu Lys Ser Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe  
165 170 175

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

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

Phe Lys Leu Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu  
210 215 220

Thr Ala Phe Ser Pro Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala  
225 230 235 240

Tyr Phe Val Gly Tyr Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp  
245 250 255

Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu  
260 265 270

Ala Glu Leu Lys Cys Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile  
275 280 285

Tyr Gln Thr Ser Asn Phe Arg Val Val Pro Ser Gly Asp Val Val Arg  
290 295 300

Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala  
305 310 315 320

Thr Lys Phe Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn  
325 330 335

Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr  
340 345 350

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

Ser Asn Val Tyr Ala Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg  
370 375 380

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

Leu Pro Asp Asp Phe Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn  
405 410 415

Ile Asp Ala Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu  
420 425 430

Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro  
435 440 445

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

Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr  
465 470 475 480

Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro  
485 490 495

Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln  
500 505 510

Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr  
515 520 525

Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val  
530 535 540

Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu  
545 550 555 560

Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly  
565 570 575

Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys  
580 585 590

Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp  
595 600 605

Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys  
610 615 620

Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro  
625 630 635 640

Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg  
645 650 655

Leu

<210> 12  
<211> 649  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fragment of SEQ ID NO1

<400> 12

Asn Ser Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser  
1 5 10 15

Ser Val Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn  
20 25 30

Val Thr Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys  
35 40 45

Arg Phe Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala  
50 55 60

Ser Thr Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr  
65 70 75 80

Leu Asp Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn  
85 90 95

Val Val Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu  
100 105 110

Gly Val Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe  
115 120 125

Arg Val Tyr Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln  
130 135 140

Pro Phe Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu  
145 150 155 160

Arg Glu Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser  
165 170 175

Lys His Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser  
180 185 190

Ala Leu Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg  
195 200 205

Phe Gln Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp  
210 215 220

Ser Ser Ser Gly Trp Thr Ala Gly Ala Ala Tyr Tyr Val Gly Tyr  
225 230 235 240

Leu Gln Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile  
245 250 255

Thr Asp Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys  
260 265 270

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

Phe Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr  
290 295 300

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser  
305 310 315 320

Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr  
325 330 335

Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly  
340 345 350

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

Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly  
370 375 380

Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe  
385 390 395 400

Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val  
405 410 415

Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu  
420 425 430

Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser  
435 440 445

Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln  
450 455 460

Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg  
465 470 475 480

Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys  
485 490 495

Gly Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe  
500 505 510

Asn Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys  
515 520 525

Lys Phe Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr  
 530 535 540

Asp Ala Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro  
 545 550 555 560

Cys Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser  
 565 570 575

Asn Gln Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro  
 580 585 590

Val Ala Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser  
 595 600 605

Thr Gly Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala  
 610 615 620

Glu His Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly  
 625 630 635 640

Ile Cys Ala Ser Tyr Gln Thr Gln Thr  
 645

<210> 13  
 <211> 29903  
 <212> DNA  
 <213> SARS-CoV-2

<400> 13  
 attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct 60  
 gttctctaaa cgaacttta aatctgtgtg gctgtcactc ggctgcatgc ttagtgcact 120  
 cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc 180  
 ttctgcaggc tgcttacggg ttcgtccgtg ttgcagccga tcatcagcac atctaggttt 240  
 cgtccgggtg tgaccgaaag gtaagatgga gagccttgct cctggtttca acgagaaaac 300  
 acacgtccaa ctcagtttgc ctgttttaca ggttcgcgac gtgctcgtac gtggctttgg 360  
 agactccgtg gaggaggtct tatcagaggc acgtcaacat cttaaagatg gcacttgtgg 420

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cttagtagaa gttgaaaaag gcgttttgcc tcaacttgaa cagccctatg tgttcatcaa  | 480  |
| acgttcggat gctcgaactg cacctcatgg tcatgttatg gttgagctgg tagcagaact  | 540  |
| cgaaggcatt cagtacggtc gtagtggtga gacacttggt gtccttgtcc ctcatgtggg  | 600  |
| cgaaatacca gtggcttacc gcaaggttct tcttcgtaag aacggtaata aaggagctgg  | 660  |
| tggccatagt tacggcgccg atctaaagtc atttgactta ggcgacgagc ttggcactga  | 720  |
| tccttatgaa gattttcaag aaaactggaa cactaaacat agcagtgggtg ttacccgtga | 780  |
| actcatgcgt gagcttaacg gaggggcata cactcgctat gtcgataaca acttctgtgg  | 840  |
| ccctgatggc taccctcttg agtgcattaa agaccttcta gcacgtgctg gtaaagcttc  | 900  |
| atgcactttg tccgaacaac tggactttat tgacactaag aggggtgtat actgctgccg  | 960  |
| tgaacatgag catgaaattg cttggtacac ggaacgttct gaaaagagct atgaattgca  | 1020 |
| gacacctttt gaaattaaat tggcaaagaa atttgacacc ttcaatgggg aatgtccaaa  | 1080 |
| ttttgtattt cccttaaatt ccataatcaa gactattcaa ccaagggttg aaaagaaaaa  | 1140 |
| gcttgatggc tttatgggta gaattcgatc tgtctatcca gttgcgtcac caaatgaatg  | 1200 |
| caaccaaatg tgcctttcaa ctctcatgaa gtgtgatcat tgtggtgaaa cttcatggca  | 1260 |
| gacgggcgat tttgttaaag ccacttgcca attttgtggc actgagaatt tgactaaaga  | 1320 |
| aggtgccact acttgtggtt acttacccca aaatgctgtt gttaaaattt attgtccagc  | 1380 |
| atgtcacaat tcagaagtag gacctgagca tagtcttgcc gaataccata atgaatctgg  | 1440 |
| cttgaaaacc attcttcgta agggtggtcg cactattgcc tttggaggct gtgtgttctc  | 1500 |
| ttatgttggt tgccataaca agtgtgccta ttgggttcca cgtgctagcg ctaacatagg  | 1560 |
| ttgtaaccat acaggtgttg ttggagaagg ttccgaaggt cttaatgaca accttcttga  | 1620 |
| aatactcaa aaagagaaag tcaacatcaa tattgttgggt gactttaaac ttaatgaaga  | 1680 |
| gatcgccatt attttggcat ctttttctgc ttccacaagt gcttttgtgg aaactgtgaa  | 1740 |
| aggtttgat tataaagcat tcaaacaaat tgttgaatcc tgtggttaatt ttaaagttac  | 1800 |
| aaaaggaaaa gctaaaaaag gtgcctggaa tattggtgaa cagaaatcaa tactgagtcc  | 1860 |
| tctttatgca tttgcatcag aggctgctcg tgttgtacga tcaattttct cccgcactct  | 1920 |
| tgaaactgct caaaattctg tgcgtgtttt acagaaggcc gctataacaa tactagatgg  | 1980 |
| aatttcacag tattcactga gactcattga tgctatgatg ttcacatctg atttggctac  | 2040 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| taacaatcta gttgtaatgg cctacattac aggtggtggt gttcagttga cttcgcagtg  | 2100 |
| gctaactaac atctttggca ctgtttatga aaaactcaaa cccgtccttg attggccttg  | 2160 |
| agagaagttt aaggaagggt tagagtttct tagagacggt tgggaaattg ttaaatttat  | 2220 |
| ctcaacctgt gcttgtagaa ttgtcggtgg acaaattgtc acctgtgcaa aggaaattaa  | 2280 |
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| agtataaact ttgtaagaat aataatgagg ctttggcttt gctggaaatg ccgttcacaa  | 25800 |
| aaccattac tttatgatgc caactatttt ctttgctggc atactaattg ttacgactat   | 25860 |
| tgtatacctt acaatagtgt aacttcttca attgtcatta cttcaggtga tggcacaaca  | 25920 |
| agtcctatTT ctgaacatga ctaccagatt ggtgggttata ctgaaaaatg ggaatctgga | 25980 |
| gtaaaagact gtgttgattt acacagttac ttcacttcag actattacca gctgtactca  | 26040 |
| actcaattga gtacagacac tgggtgtgaa catgttacct tcttcatcta caataaaatt  | 26100 |
| gttgatgagc ctgaagaaca tgtccaaatt cacacaatcg acggttcac cggagttgtt   | 26160 |
| aatccagtaa tggaaccaat ttatgatgaa ccgacgacga ctactagcgt gcctttgtaa  | 26220 |
| gcacaagctg atgagtacga acttatgtac tcattcgttt cggaagagac aggtacgtta  | 26280 |
| atagttaata gcgtacttct ttttcttgct ttcgtggtat tcttgctagt tacactagcc  | 26340 |

|                                                                    |       |
|--------------------------------------------------------------------|-------|
| atccttactg cgcttcgatt gtgtgcgtac tgctgcaata ttgttaacgt gagtcttgta  | 26400 |
| aaaccttctt tttacgttta ctctcgtgtt aaaaatctga attcttctag agttcctgat  | 26460 |
| cttctgggtct aaacgaacta aatattatat tagtttttct gtttggaact ttaattttag | 26520 |
| ccatggcaga ttccaacggt actattaccg ttgaagagct taaaaagctc cttgaacaat  | 26580 |
| ggaacctagt aataggtttc ctattcctta catggatttg tcttctacaa tttgcctatg  | 26640 |
| ccaacaggaa taggtttttg tatataatta agttaatttt cctctggctg ttatggccag  | 26700 |
| taacttttagc ttgttttggt cttgctgctg tttacagaat aaattggatc accggtggaa | 26760 |
| ttgctatcgc aatggcttgt cttgtaggct tgatgtggct cagctacttc attgcttctt  | 26820 |
| tcagactgtt tgcgcgtacg cgttccatgt ggtcattcaa tccagaaact aacattcttc  | 26880 |
| tcaacgtgcc actccatggc actattctga ccagaccgct tctagaaagt gaactcgtaa  | 26940 |
| tcggagctgt gatccttcgt ggacatcttc gtattgctgg acaccatcta ggacgctgtg  | 27000 |
| acatcaagga cctgcctaaa gaaatcactg ttgctacatc acgaacgctt tcttattaca  | 27060 |
| aattgggagc ttcgcagcgt gtagcaggtg actcaggttt tgctgcatac agtcgctaca  | 27120 |
| ggattggcaa ctataaatta aacacagacc attccagtag cagtgacaat attgctttgc  | 27180 |
| ttgtacagta agtgacaaca gatgtttcat ctcgttgact ttcaggttac tatagcagag  | 27240 |
| atattactaa ttattatgag gactttttaa gtttccattt ggaatcttga ttacatcata  | 27300 |
| aacctcataa ttaaaaattt atctaagtca ctaactgaga ataaatattc tcaattagat  | 27360 |
| gaagagcaac caatggagat tgattaaacg aacatgaaaa ttattctttt cttggcactg  | 27420 |
| ataacactcg ctacttgtag gctttatcac taccaagagt gtgttagagg tacaacagta  | 27480 |
| cttttaaaag aaccttgctc ttctggaaca tacgagggca attcaccatt tcatcctcta  | 27540 |
| gctgataaca aatttgact gacttgcttt agcactcaat ttgcttttgc ttgtcctgac   | 27600 |
| ggcgtaaaac acgtctatca gttacgtgcc agatcagttt cacctaaact gttcatcaga  | 27660 |
| caagaggaag ttcaagaact ttactctcca atttttctta ttgttgcggc aatagtgttt  | 27720 |
| ataacacttt gcttcacact caaaagaaag acagaatgat tgaactttca ttaattgact  | 27780 |
| tctatttgtg ctttttagcc tttctgctat tccttgtttt aattatgctt attatctttt  | 27840 |
| ggttctcact tgaactgcaa gatcataatg aaacttgta cgcttaaagc aacatgaaat   | 27900 |
| ttcttgtttt cttaggaatc atcacaactg tagctgcatt tcaccaagaa tgtagtttac  | 27960 |

|                                                                    |       |
|--------------------------------------------------------------------|-------|
| agtcatgtac tcaacatcaa ccatatgtag ttgatgaccc gtgtcctatt cacttctatt  | 28020 |
| ctaaatggta tattagagta ggagctagaa aatcagcacc ttttaattgaa ttgtgcgtgg | 28080 |
| atgaggctgg ttctaaatca cccattcagt acatcgatat cggtaattat acagtttctt  | 28140 |
| gtttaccttt tacaattaat tgccaggaac ctaaattggg tagtcttgta gtgcgttggt  | 28200 |
| cgttctatga agacttttta gagtatcatg acgttcgtgt tgttttagat ttcattctaaa | 28260 |
| cgaacaaact aaaatgtctg ataatggacc caaaaatcag cgaaatgcac cccgcattac  | 28320 |
| gtttggtgga ccctcagatt caactggcag taaccagaat ggagaacgca gtggggcgcg  | 28380 |
| atcaaaaaca cgtcggcccc aaggtttacc caataatact gcgtcttggt tcaccgctct  | 28440 |
| cactcaacat ggcaaggaag accttaaatt ccctcgagga caaggcggtc caattaacac  | 28500 |
| caatagcagt ccagatgacc aaattggcta ctaccgaaga gctaccagac gaattcgtgg  | 28560 |
| tggtgacggg aaaatgaaag atctcagtcc aagatggtat ttctactacc taggaactgg  | 28620 |
| gccagaagct ggacttcctt atggtgctaa caaagacggc atcatatggg ttgcaactga  | 28680 |
| gggagccttg aatacaccaa aagatcacat tggcacccgc aatcctgcta acaatgctgc  | 28740 |
| aatcgtgcta caacttcctc aaggaacaac attgccaaaa ggcttctacg cagaaggag   | 28800 |
| cagaggcggc agtcaagcct cttctcggtc ctcatcacgt agtcgcaaca gttcaagaaa  | 28860 |
| ttcaactcca ggcagcagta ggggaacttc tcctgctaga atggctggca atggcggtga  | 28920 |
| tgctgctctt gctttgctgc tgcttgacag attgaaccag cttgagagca aaatgtctgg  | 28980 |
| taaaggccaa caacaacaag gccaaactgt cactaagaaa tctgctgctg aggcttctaa  | 29040 |
| gaagcctcgg caaaaacgta ctgccactaa agcatacaat gtaacacaag ctttcggcag  | 29100 |
| acgtggtcca gaacaaacc aaggaaattt tggggaccag gaactaatca gacaaggaac   | 29160 |
| tgattacaaa cattggccgc aaattgcaca atttgcccc agcgcttcag cgttcttcgg   | 29220 |
| aatgtcgcgc attggcatgg aagtcacacc ttcgggaacg tggttgacct acacaggtgc  | 29280 |
| catcaaattg gatgacaaag atccaaattt caaagatcaa gtcattttgc tgaataagca  | 29340 |
| tattgacgca taaaaacat tcccaccaac agagcctaaa aaggacaaaa agaagaaggc   | 29400 |
| tgatgaaact caagccttac cgcagagaca gaagaaacag caaactgtga ctcttcttcc  | 29460 |
| tgctgcagat ttggatgatt tctccaaaca attgcaacaa tccatgagca gtgctgactc  | 29520 |
| aactcaggcc taaactcatg cagaccacac aaggcagatg ggctatataa acgttttcgc  | 29580 |

|                                                                   |       |
|-------------------------------------------------------------------|-------|
| ttttccggtt acgatata gtctactctt gtgcagaatg aattctcgta actacatagc   | 29640 |
| acaagtagat gtagttaact ttaatctcac atagcaatct ttaatcagtg tgtaacatta | 29700 |
| gggaggactt gaaagagcca ccacattttc accgaggcca cgcggagtac gatcgagtgt | 29760 |
| acagtgaaca atgctagga gagctgccta tatggaagag ccctaattgtg taaaattaat | 29820 |
| tttagtagtg ctatcccat gtgattttta tagcttctta ggagaatgac aaaaaaaaaa  | 29880 |
| aaaaaaaaa aaaaaaaaaa aaa                                          | 29903 |

<210> 14  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 30-44 of SEQ ID NO1

<400> 14

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Leu | His | Ser | Thr | Gln | Asp | Leu | Phe | Leu | Pro | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

<210> 15  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 48-68 of SEQ ID NO1

<400> 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Trp | Phe | His | Ala | Ile | His | Val | Ser | Gly | Thr | Asn | Gly | Thr | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Phe | Asp | Asn | Pro | Val |
|     |     |     |     | 20  |

<210> 16  
 <211> 57  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 110-166 of SEQ ID NO1

<400> 16

Asn Val Val Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe  
1 5 10 15

Leu Gly Val Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu  
20 25 30

Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser  
35 40 45

Gln Pro Phe Leu Met Asp Leu Glu Gly  
50 55

<210> 17  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> 200-214 of SEQ ID NO1

<400> 17

Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu Pro Leu Val Asp Leu  
1 5 10 15

<210> 18  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> 226-250 of SEQ ID NO1

<400> 18

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser  
1 5 10 15

Gly Trp Thr Ala Gly Ala Ala Ala Tyr  
20 25

<210> 19  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>

<223> 256-277 of SEQ ID NO1

<400> 19

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Arg | Thr | Phe | Leu | Leu | Lys | Tyr | Asn | Glu | Asn | Gly | Thr | Ile | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ala | Val | Asp | Cys | Ala | Leu | Asp | Pro |
|     |     |     | 20  |     |     |     | 25  |     |

<210> 20

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 328-342 of SEQ ID NO1

<400> 20

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Thr | Arg | Phe | Ala | Ser | Val | Tyr | Ala | Trp | Asn | Arg | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 21

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 399-414 of SEQ ID NO1

<400> 21

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Lys | Ile | Ala | Asp | Tyr | Asn | Tyr | Lys | Leu | Pro | Asp | Asp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 434-448 of SEQ ID NO1

<400> 22

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asn | Tyr | Leu | Tyr | Arg | Leu | Phe | Arg | Lys | Ser | Asn | Leu | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 23  
<211> 23  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> 550-572 of SEQ ID NO1  
  
<400> 23

Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg Asp Pro Gln  
1 5 10 15

Thr Leu Glu Ile Leu Asp Ile  
20

<210> 24  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> 590-604 of SEQ ID NO1  
  
<400> 24

Ser Asn Gln Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu  
1 5 10 15

<210> 25  
<211> 19  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> 632-650 of SEQ ID NO1  
  
<400> 25

Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn Asn Ser Tyr Glu Cys  
1 5 10 15

Asp Ile Pro

<210> 26  
<211> 15  
<212> PRT

<213> Artificial Sequence

<220>

<223> 354-368 of SEQ ID NO1

<400> 26

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asn | Ser | Ala | Ser | Phe | Ser | Thr | Phe | Lys | Cys | Tyr | Gly | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 27

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 622-636 of SEQ ID NO1

<400> 27

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Gly | Ser | Asn | Val | Phe | Gln | Thr | Arg | Ala | Gly | Cys | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 28

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 30-44 of SEQ ID NO1

<400> 28

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Leu | His | Ser | Thr | Gln | Asp | Leu | Phe | Leu | Pro | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 29

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 226-250 of SEQ ID NO1

<400> 29

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ala | Leu | His | Arg | Ser | Tyr | Leu | Thr | Pro | Gly | Asp | Ser | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly Trp Thr Ala Gly Ala Ala Ala Tyr

20

25

<210> 30  
 <211> 419  
 <212> PRT  
 <213> SARS-CoV-2

<400> 30

Met Ser Asp Asn Gly Pro Gln Asn Gln Arg Asn Ala Pro Arg Ile Thr  
 1 5 10 15

Phe Gly Gly Pro Ser Asp Ser Thr Gly Ser Asn Gln Asn Gly Glu Arg  
 20 25 30

Ser Gly Ala Arg Ser Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn Asn  
 35 40 45

Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Asp Leu  
 50 55 60

Lys Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Ser Pro  
 65 70 75 80

Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Ile Arg Gly  
 85 90 95

Gly Asp Gly Lys Met Lys Asp Leu Ser Pro Arg Trp Tyr Phe Tyr Tyr  
 100 105 110

Leu Gly Thr Gly Pro Glu Ala Gly Leu Pro Tyr Gly Ala Asn Lys Asp  
 115 120 125

Gly Ile Ile Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys Asp  
 130 135 140

His Ile Gly Thr Arg Asn Pro Ala Asn Asn Ala Ala Ile Val Leu Gln  
 145 150 155 160

Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly Ser  
 165 170 175

Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg Asn  
180 185 190

Ser Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Thr Ser Pro Ala  
195 200 205

Arg Met Ala Gly Asn Gly Gly Asp Ala Ala Leu Ala Leu Leu Leu Leu  
210 215 220

Asp Arg Leu Asn Gln Leu Glu Ser Lys Met Ser Gly Lys Gly Gln Gln  
225 230 235 240

Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys  
245 250 255

Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Ala Tyr Asn Val Thr Gln  
260 265 270

Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly Asp  
275 280 285

Gln Glu Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln Ile  
290 295 300

Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg Ile  
305 310 315 320

Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr Thr Gly Ala  
325 330 335

Ile Lys Leu Asp Asp Lys Asp Pro Asn Phe Lys Asp Gln Val Ile Leu  
340 345 350

Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu Pro  
355 360 365

Lys Lys Asp Lys Lys Lys Lys Ala Asp Glu Thr Gln Ala Leu Pro Gln  
370 375 380

Arg Gln Lys Lys Gln Gln Thr Val Thr Leu Leu Pro Ala Ala Asp Leu  
385 390 395 400

Asp Asp Phe Ser Lys Gln Leu Gln Gln Ser Met Ser Ser Ala Asp Ser  
405 410 415

Thr Gln Ala

<210> 31  
<211> 223  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> RBD, a fragment from S1 domain from SARS-CoV-2 S protein

<400> 31

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  
210 215 220

<210> 32

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> RBD, a fragment from S1 domain from SARS-CoV-2 S protein, with  
C-terminal His tag

<400> 32

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 Leu  
 210 215 220

Glu His His His His His His His  
 225 230

<210> 33

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> S2 domain from SARS-CoV-2 S protein

<400> 33

Ser Val Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala  
 1 5 10 15

Glu Asn Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn

20

25

30

Phe Thr Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys  
 35 40 45

Thr Ser Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys  
 50 55 60

Ser Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg  
 65 70 75 80

Ala Leu Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val  
 85 90 95

Phe Ala Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe  
 100 105 110

Gly Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser  
 115 120 125

Lys Arg Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala  
 130 135 140

Asp Ala Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala  
 145 150 155 160

Ala Arg Asp Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu  
 165 170 175

Pro Pro Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu  
 180 185 190

Leu Ala Gly Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala  
 195 200 205

Leu Gln Ile Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile  
 210 215 220

Gly Val Thr Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn  
 225 230 235 240

Gln Phe Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr  
245 250 255

Ala Ser Ala Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln  
260 265 270

Ala Leu Asn Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile  
275 280 285

Ser Ser Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala  
290 295 300

Glu Val Gln Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln  
305 310 315 320

Thr Tyr Val Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser  
325 330 335

Ala Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser  
340 345 350

Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro  
355 360 365

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro  
370 375 380

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly  
385 390 395 400

Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His  
405 410 415

Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr  
420 425 430

Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val  
435 440 445

Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys

450

455

460

Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp  
 465 470 475 480

Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys  
 485 490 495

Glu Ile Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu  
 500 505 510

Ile Asp Leu Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro  
 515 520 525

Trp Tyr Ile Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met  
 530 535 540

Val Thr Ile Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys  
 545 550 555 560

Gly Cys Cys Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser  
 565 570 575

Glu Pro Val Leu Lys Gly Val Lys Leu His Tyr Thr  
 580 585

&lt;210&gt; 34

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RBD as used in the examples

&lt;400&gt; 34

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Gly Pro Met Arg Val Gln Pro Thr Glu Ser Ile Val Arg  
 20 25 30

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

35

40

45

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

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

Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe  
 85 90 95

Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg  
 100 105 110

Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys  
 115 120 125

Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn  
 130 135 140

Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe  
 145 150 155 160

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

Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys  
 180 185 190

Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly  
 195 200 205

Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala  
 210 215 220

Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val Lys Asn  
 225 230 235 240

Lys Cys Val Asn Phe Leu Glu His His His His His His His  
 245 250 255

<210> 35  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
  
<400> 35

Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly  
1 5 10

<210> 36  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
  
<400> 36

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

<210> 37  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
  
<400> 37

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

<210> 38  
<211> 255  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> His-tagged RBD  
  
<400> 38

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

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

Pro Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val Lys Asn  
225 230 235 240

Lys Cys Val Asn Phe Leu Glu His His His His His His His  
245 250 255

<210> 39  
<211> 805  
<212> PRT  
<213> Homo sapiens

<400> 39

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala  
1 5 10 15

Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe  
20 25 30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp  
35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn  
50 55 60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala  
65 70 75 80

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln  
85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys  
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser  
115 120 125

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

Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu  
145 150 155 160

Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu  
165 170 175

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
180 185 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
195 200 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
210 215 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
225 230 235 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
245 250 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
260 265 270

Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys  
275 280 285

Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
290 295 300

Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
305 310 315 320

Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
325 330 335

Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
340 345 350

Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
355 360 365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
370 375 380

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
385 390 395 400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
405 410 415

His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
420 425 430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
435 440 445

Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
450 455 460

Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met  
465 470 475 480

Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr  
485 490 495

Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
500 505 510

Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala  
515 520 525

Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile  
530 535 540

Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu  
545 550 555 560

Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala  
565 570 575

Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe  
580 585 590

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr  
595 600 605

Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
610 615 620

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met  
625 630 635 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu  
645 650 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val  
660 665 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro  
675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val  
740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg  
755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp  
785 790 795 800

Val Gln Thr Ser Phe  
805

<210> 40  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

<400> 40

Arg Thr Trp Leu Pro Pro Ala Tyr Thr Asn Ser  
1 5 10

<210> 41  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

<400> 41

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

<210> 42  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

<400> 42

Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn  
1 5 10

<210> 43  
<211> 143  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

<400> 43

Met Ser His His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Arg Thr Gln Leu Pro Pro Ala  
115 120 125

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

<210> 44

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion

<400> 44

Met Ser His His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu

20

25

30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
 35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
 50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
 65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
 85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
 100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Met Ser His His His His His  
 115 120 125

His His His Ser Pro Met Tyr Ser Ile Ile Thr Pro Asn Ile Leu Arg  
 130 135 140

Leu Glu Ser Glu Glu Thr Met Val Leu Glu Ala His Asp Ala Gln Gly  
 145 150 155 160

Asp Val Pro Val Thr Val Thr Val His Asp Phe Pro Gly Lys Lys Leu  
 165 170 175

Val Leu Ser Ser Glu Lys Thr Val Leu Thr Pro Ala Thr Asn His Met  
 180 185 190

Gly Asn Val Thr Phe Thr Ile Pro Ala Asn Arg Glu Phe Lys Ser Glu  
 195 200 205

Lys Gly Arg Asn Lys Phe Val Thr Val Gln Ala Thr Phe Gly Thr Gln  
 210 215 220

Val Val Glu Lys Val Val Leu Val Ser Leu Gln Ser Gly Ile Glu Gly  
 225 230 235 240

Arg Met Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn Ser Gly Thr  
245 250 255

Asn Gly Thr Lys Arg Phe Asp Asn  
260

<210> 45

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion

<400> 45

Met Ser His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Leu Thr Pro Gly Asp Ser Ser  
115 120 125

Ser Gly Trp Thr Ala Gly Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp  
130 135 140

Thr Ala Gly  
145

<210> 46  
<211> 139  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion

<400> 46

Met Ser His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Asn Asn Leu Asp Ser Lys Val  
115 120 125

Gly Gly Asn Asn Leu Asp Ser Lys Val Gly Gly  
130 135

<210> 47

<211> 143  
<212> PRT  
<213> Artificial Sequence

<220>

<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion

<400> 47

Met Ser His His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Tyr Gln Ala Gly Ser Thr Pro  
115 120 125

Cys Asn Gly Val Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val  
130 135 140

<210> 48  
<211> 145  
<212> PRT  
<213> Artificial Sequence

<220>

<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion

<400> 48

Met Ser His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Tyr Gly Phe Gln Pro Thr Asn  
115 120 125

Gly Val Gly Tyr Gln Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr  
130 135 140

Gln  
145

<210> 49

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies  
with GST fusion, P1-P6

<400> 49

Met Ser His His His His His His His His Ser Pro Met Tyr Ser Ile  
1 5 10 15

Ile Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu  
20 25 30

Glu Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His  
35 40 45

Asp Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu  
50 55 60

Thr Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala  
65 70 75 80

Asn Arg Glu Phe Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val  
85 90 95

Gln Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser  
100 105 110

Leu Gln Ser Gly Ile Glu Gly Arg Met Arg Thr Gln Leu Pro Pro Ala  
115 120 125

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

Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly Asn Asn Leu Asp  
145 150 155 160

Ser Lys Val Gly Gly Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val  
165 170 175

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

<210> 50

<211> 773

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminally His-tagged extracellular domain of human ACE2

<400> 50

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala  
1 5 10 15

Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe  
20 25 30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp  
35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn  
50 55 60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala  
65 70 75 80

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln  
85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys  
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser  
115 120 125

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

Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu  
145 150 155 160

Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu  
165 170 175

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
180 185 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
195 200 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
210 215 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
225 230 235 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
245 250 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
260 265 270

Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys  
275 280 285

Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
290 295 300

Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
305 310 315 320

Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
325 330 335

Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
340 345 350

Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
355 360 365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
370 375 380

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
385 390 395 400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
405 410 415

His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
420 425 430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
435 440 445

Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
450 455 460

Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met  
465 470 475 480

Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr  
485 490 495

Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
500 505 510

Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala  
515 520 525

Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile  
530 535 540

Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu  
545 550 555 560

Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala  
565 570 575

Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe  
580 585 590

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr  
595 600 605

Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
610 615 620

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met  
625 630 635 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu  
645 650 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val  
660 665 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro  
675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
725 730 735

Pro Pro Val Ser Leu Glu Gly Ser Gly Ser Gly Ser His His His His  
740 745 750

His His His His Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys  
755 760 765

Ile Glu Trp His Glu  
770

<210> 51  
<211> 648  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO1 with mutations of SARS-CoV-2 U.K. variant B.1.1.7

<400> 51

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 Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn  
50 55 60

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

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

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

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

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

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

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

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

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

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

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

Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg  
245 250 255

Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val  
260 265 270

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Pro Thr Tyr Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu  
485 490 495

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

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

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

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

Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly  
565 570 575

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

Val Leu Tyr Gln Gly Val Asn Cys Thr Glu Val Pro Val Ala Ile His  
595 600 605

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

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

Asn Ser Tyr Glu Cys Asp Ile His  
645

<210> 52  
<211> 650  
<212> PRT  
<213> Artificial Sequence

<220>

<223> SEQ ID NO1 with mutations of SARS-CoV-2 South African variant  
B.1.351

<400> 52

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

Gly Phe Gln Pro Thr Tyr 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 Gly 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  
645 650

<210> 53  
<211> 650  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO1 with mutations of SARS-CoV-2 Brazilian variant P.1

<400> 53

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

Gly Phe Gln Pro Thr Tyr 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  
645 650

<210> 54  
<211> 648  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO1 with mutations of SARS-CoV-2 Mink Variant from Denmark

<400> 54

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 Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn  
50 55 60

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

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

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

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

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

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

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

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

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

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

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

Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg  
245 250 255

Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val  
260 265 270

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

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

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

|                 |                                 |                     |             |     |  |     |
|-----------------|---------------------------------|---------------------|-------------|-----|--|-----|
| 305             |                                 | 310                 |             | 315 |  | 320 |
| Phe Gly Glu Val | Phe Asn Ala Thr Arg             | Phe Ala Ser Val Tyr | Ala Trp     |     |  |     |
|                 | 325                             | 330                 | 335         |     |  |     |
| Asn Arg Lys Arg | Ile Ser Asn Cys Val             | Ala Asp Tyr Ser     | Val Leu Tyr |     |  |     |
|                 | 340                             | 345                 | 350         |     |  |     |
| Asn Ser Ala Ser | Phe Ser Thr Phe Lys Cys Tyr     | Gly Val Ser Pro     | Thr         |     |  |     |
|                 | 355                             | 360                 | 365         |     |  |     |
| Lys Leu Asn Asp | Leu Cys Phe Thr Asn Val Tyr     | Ala Asp Ser Phe     | Val         |     |  |     |
|                 | 370                             | 375                 | 380         |     |  |     |
| Ile Arg Gly Asp | Glu Val Arg Gln Ile Ala Pro Gly | Gln Thr Gly         | Lys         |     |  |     |
|                 | 385                             | 390                 | 395         | 400 |  |     |
| Ile Ala Asp Tyr | Asn Tyr Lys Leu Pro Asp Asp     | Phe Thr Gly Cys     | Val         |     |  |     |
|                 | 405                             | 410                 | 415         |     |  |     |
| Ile Ala Trp Asn | Ser Asn Asn Leu Asp Ser Lys     | Val Gly Gly         | Asn Tyr     |     |  |     |
|                 | 420                             | 425                 | 430         |     |  |     |
| Asn Tyr Leu Phe | Arg Leu Phe Arg Lys Ser Asn     | Leu Lys Pro Phe     | Glu         |     |  |     |
|                 | 435                             | 440                 | 445         |     |  |     |
| Arg Asp Ile Ser | Thr Glu Ile Tyr Gln Ala Gly     | Ser Thr Pro Cys     | Asn         |     |  |     |
|                 | 450                             | 455                 | 460         |     |  |     |
| Gly Val Glu Gly | Phe Asn Cys Tyr Phe Pro         | Leu Gln Ser Tyr     | Gly Phe     |     |  |     |
|                 | 465                             | 470                 | 475         | 480 |  |     |
| Gln Pro Thr Asn | Gly Val Gly Tyr Gln Pro Tyr     | Arg Val Val         | Val Leu     |     |  |     |
|                 | 485                             | 490                 | 495         |     |  |     |
| Ser Phe Glu Leu | Leu His Ala Pro Ala Thr         | Val Cys Gly Pro     | Lys Lys     |     |  |     |
|                 | 500                             | 505                 | 510         |     |  |     |
| Ser Thr Asn Leu | Val Lys Asn Lys Cys Val         | Asn Phe Asn Phe     | Asn Gly     |     |  |     |
|                 | 515                             | 520                 | 525         |     |  |     |

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

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

Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly  
565 570 575

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

Val Leu Tyr Gln Gly Val Asn Cys Thr Glu Val Pro Val Ala Ile His  
595 600 605

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

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

Asn Ser Tyr Glu Cys Asp Ile Pro  
645

<210> 55  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

<400> 55

Asn Asn Leu Asp Ser Lys Val Gly Gly  
1 5

<210> 56  
<211> 67  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SEQ ID NO: 1-derived peptide reactive with SARS-CoV-2 antibodies

with GST fusion, P1-P6

<400> 56

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

Thr Lys Arg Phe Asp Asn Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp  
20 25 30

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

Ser Thr Pro Cys Asn Gly Val Tyr Gly Phe Gln Pro Thr Asn Gly Val  
50 55 60

Gly Tyr Gln  
65