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<120> SARS-COV-2 IMMUNOGENIC COMPOSITIONS, VACCINES, AND METHODS

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<150> US 63/052,264

<151> 2020-07-15

<150> US 63/130,202

<151> 2020-12-23

<150> PCT/IB2021/000293

<151> 2021-02-02

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<170> PatentIn version 3.5

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Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
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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
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Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
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Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
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Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
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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
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Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
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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
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Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
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Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
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Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
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Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
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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
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Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
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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
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Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
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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
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Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
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Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
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Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
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Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
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Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
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Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
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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
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Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
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Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
690 695 700

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

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

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770 775 780

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885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
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Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
915 920 925

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

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

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

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

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

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Val	Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu
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Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
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Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
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<220>
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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
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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
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Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
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Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val

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Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro
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Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe
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Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly
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Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys
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Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
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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

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His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
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645 650 655

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675 680 685

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

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
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Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
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Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu

740

745

750

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Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
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Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
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Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
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Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
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His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn

1160

1165

1170

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<220>

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Thr	Arg	Gly	Val	Tyr	Tyr	Pro	Asp	Lys	Val	Phe	Arg	Ser	Ser	Val	Leu
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Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
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Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
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Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
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Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
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Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
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Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
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Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
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Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
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Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
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Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
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Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
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Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
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Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
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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

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420 425 430

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tgactgggca caacagacaa tcggctgctc tgatgccgcc gtgttcggc tgtcagcgca	9660
ggggcgccc gttctttttg tcaagaccga cctgtccggt gccctgaatg aactgcaaga	9720
cgaggcagcg cggctatcgt ggctggccac gacgggcgtt ccttgccgag ctgtgctcga	9780

cgttgctact gaagcgggaa gggactggct gctattgggc gaagtgccgg ggcaggatct	9840
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gctgcatacg cttgatccgg ctacctgccc attcgaccac caagcgaaac atcgcatcga	9960
gcgagcacgt actcggatgg aagccggctt tgtcgatcag gatgatctgg acgaagagca	10020
tcaggggctc gcgccagccg aactgttcgc caggctcaag gcgagcatgc ccgacggcga	10080
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gtgcggtatt tcacaccgca tacagggtggc acttttcggg gaaatgtgcg cggaaccctt	10440
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taaatgcctt aataatagca cgtgctaaaa cttcatTTTT aatttaaaag gatctaggtg	10560
aagatccttt ttgataatct catgaccaa atcccttaac gtgagttttc gttccactga	10620
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atctgctgct tgcaaacaaa aaaaccaccg ctaccagcgg tggtttgttt gccggatcaa	10740
gagctaccaa ctctttttcc gaaggtaact ggcttcagca gagcgcagat accaaatact	10800
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ggttcgtgca cacagcccag cttggagcga acgacctaca ccgaactgag atacctacag	11040
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tcaggggggc ggagcctatg gaaaaacgcc agcaacgcgg cctttttacg gttcctgggc	11280
ttttgctggc cttttgctca catgttcttg actcttcgcg atgtacgggc cagatatacg	11340
cg	11342

<210> 26
<211> 3249
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 26
atccagtggg ggaatataaa ggtgaaagca ggagagaccc ctctgactgg aacctcttac 60
ctcccagaag ccttgatgc aaaaccagtg ggcattcatt tgtatgttat tttgcatccc 120
gtttgcctcc cagccttcag caggccccga ccctcccctg gccagcttcc accctgactg 180
ccccctggct ggctcccatt gagcactgtg ggctctcccc accattaggt gacagatcag 240
gaacaatcca ggctcaggct ctttatctgt gctctgcctc ccacctggca ggtccactgg 300
ccaggctttt ccagggtccc ttctctcca ggtctgcctt actatttgtc ctccccttcc 360
ccctcagctg gtagctcgat aagaatcaat aggtccactc cagagcaaag aacacagcca 420
aatgtgtcat accaggccct gccagaaaaa cgagctgctg gagctgacaa acttgaaggc 480
caaacaccta aggttcccc caacacttca ttcagcaggg atggtcattc agcttcaggg 540
ggcaggcagc atgaaagcct ccctacctcc atccttctca cacagaggct ggggagagca 600
tcttgaggga tgcagtcccc tggggccagg cttctaattc agacagccct tacaaggggg 660
gacaggggaa ggactggctt ggagaaaagt cctagaaaag aggggagggg cactggccac 720
cagggtggg tcgctgctat gatggtccta ggagtgcctg cctgtcctct caggcccat 780
gcgatgtagg acacattact tttatttatt tatttattta ttttgagtca gaggttcgt 840
ctggttgccc aggctggagc gcgacggcac gatcttggct cactgcaacc tctgcctcct 900
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tgctggttaa tttttgtatt tttagtagag aaggggtgtc accatgttgg tcaggctggt 1020
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gctggagtgc agtggcatcg aactcttgac ctcaagtgat ccaccgcct cggcctccca 1140
aagtgcttgg attacaggca tgagccactg tgcccggcga tgtgggacac attatcatct 1200
ctgtgagaga tttttggtct cttttgtcac cgcccttctc tcccagctcc tagaactggg 1260

cctggctcac agtaggtgct gaatgcatac tggttgaatt gtaaagtctc aggatttgtt	1320
taattaagga tgcaggaaag gtgatatacc ggtgtgcaga agtcaggatg cattccctgt	1380
ccaaatcaca gtgttccact gaggcaaggc ccttgggagt gaggtcggga gaggggaggg	1440
tgggtggaggg ggctcagaga ctgggtttgt tttggggagt ctgcacctat ttgctgagtg	1500
aatgtatgtg tgtgtgcatt tgagagcaca cctctgtatg attcgggtgt gagtgtgtgt	1560
gaggaaacgt gggcaggcga ggagtgtttg ggagccaggt gcagctgggg tgtgagtgtg	1620
taagcaagca gctatgaggc tgggcattgc ttctcctcct cttctccagc tcccagcctt	1680
tcttccccgg gactcctggg gctccaggat gcccccaaga tcccctccac aagtggataa	1740
tttgggctgc aggttaagga cagctagagg gactcacagg ccattccacc cgcacaccac	1800
cagaccccca aatttctttt ttcttttttt tttgagacag agtctcactc tgtcgccagg	1860
ctgcagtggc gcgatctcgg ctcaactgcaa cctccgcctc ccaggttcaa gcgattcccc	1920
ttcctcagcc tcccaagtag ctgagactac aggcgtgcac catcacgtcc ggctaatttt	1980
ttgtatttta gtagagaggg gtttcacat gttggctagg atggtctcga tctcctgacc	2040
tcgtgatccg cccacctagg cctcccaaag tgctgagatt acaggcgtga gccactgcgc	2100
ccggtcaaga ctcccaaatt tcaaactcgc cagcacctcc tccacctggg ggagaagagc	2160
ataataacgt catttctgc cctgaaagca gcctcgaggg ccaacaacac ctgctgtccg	2220
tgtccatgcc cggttggcca ccccgtttct ggggggtgag cggggcttgg cagggctgcg	2280
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ctgcgatata actcgggtcg cgcggctcgc gcaggccgcc accgtcgtcc gcaaagcctg	2460
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ggacctcaac tcccagcctt gtctgaccct ccaattatac actcctttgc ctctttccgt	2580
cattccataa ccaccccaac ccctactcca ccgggagggg gttgggcata cctggatttc	2640
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atggagggag gtaaggaaag gcctgtaaag aggaggagac actggctctg gcggaatggg	2820
gactattgga gggttaagcg gatgtggcta aggctgagtc atctaggagt aaacaagagg	2880

ccttcctttg ggaggagcca atccagggtg tagggggccc agagtgacca ggtgcactag	2940
ggaaaaaatg ccaggagagg gccaggaaga ggacttgтта gtagcgactc acttctgggc	3000
aggcaggcca gccagctagc cagcctgctg aggcttcca agaggggcag agtgctggga	3060
tctgggaatc caggaaagga gggaatgggg tggggctaga tgaaaaggga taggtgtcca	3120
gggagagcct ctggctattc ctgggaccag gaagttttca ctaggataca taacactttt	3180
tacacactca cccacccat ccctggcttt ctattcatgg aacaacctct ctcctttttc	3240
cttccaggt	3249

<210> 27
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 27	
aagtggtag	9

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 28	
ctttttcctt ccaggt	16

<210> 29
 <211> 2418
 <212> DNA
 <213> Homo sapiens

<400> 29	
atgtcaagct cttcctggct cttctcagc cttgttgctg taactgctgc tcagtccacc	60
attgaggaac aggccaagac atttttggac aagtttaacc acgaagccga agacctgttc	120
tatcaaagtt cacttgcttc ttggaattat aacaccaata ttactgaaga gaatgtccaa	180

aacatgaata atgctgggga caaatgggtct gccttttttaa aggaacagtc cacacttgcc	240
caaatgtatc cactacaaga aattcagaat ctcacagtca agcttcagct gcaggctctt	300
cagcaaaatg ggtcttcagt gctctcagaa gacaagagca aacggttgaa cacaattcta	360
aatacaatga gcaccatcta cagtactgga aaagtttgta acccagataa tccacaagaa	420
tgcttattac ttgaaccagg tttgaatgaa ataatggcaa acagtttaga ctacaatgag	480
aggctctggg cttgggaaag ctggagatct gaggtcggca agcagctgag gccattatat	540
gaagagtatg tggctctgaa aaatgagatg gcaagagcaa atcattatga ggactatggg	600
gattattgga gaggagacta tgaagtaa at ggggtagatg gctatgacta cagccgcggc	660
cagttgattg aagatgtgga acataccttt gaagagatta aaccattata tgaacatctt	720
catgcctatg tgagggcaaa gttgatgaat gcctatcctt cctatatcag tccaattgga	780
tgctccctg ctcatctgct tggatgatg tgggtagat tttggacaaa tctgtactct	840
ttgacagttc cttttggaca gaaaccaa atagatgtta ctgatgcaat ggtggaccag	900
gcctgggatg cacagagaat attcaaggag gccgagaagt tctttgtatc tgttggctct	960
cctaatatga ctcaaggatt ctgggaaa at tccatgctaa cggaccag aaatgttcag	1020
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aaacaagcac tcacgattgt tgggactctg ccatttactt acatgttaga gaagtggagg	1380
tggatggtct ttaaagggga aattcccaa gaccagtgga tgaaaaagtg gtgggagatg	1440
aagcgagaga tagttggggt ggtggaacct gtgccccatg atgaaacata ctgtgacccc	1500
gcatctctgt tccatgtttc taatgattac tcattcattc gatattacac aaggaccctt	1560
taccaattcc agtttcaaga agcactttgt caagcagcta aacatgaagg ccctctgcac	1620
aatgtgaca tctcaaaact tacagaagct ggacagaaac tgttcaatat gctgaggctt	1680
ggaaaatcag aaccctggac ctagcattg gaaaatgttg taggagcaaa gaacatgaat	1740
gtaaggccac tgctcaacta ctttgagccc ttatttacct ggctgaaaga ccagaacaag	1800

aattcttttg tgggatggag taccgactgg agtccatatg cagaccaaag catcaaagtg	1860
aggataagcc taaaatcagc tcttgagat aaagcatatg aatggaacga caatgaaatg	1920
tacctgttcc gatcatctgt tgcatatgct atgaggcagt acttttttaa agtaaaaaat	1980
cagatgattc tttttgggga ggaggatgtg cgagtggcta atttgaaacc aagaatctcc	2040
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gaaaaggcca tcaggatgtc ccggagccgt atcaatgatg ctttccgtct gaatgacaac	2160
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atcttcactg ggatcagaga tcggaagaag aaaaataaag caagaagtgg agaaaatcct	2340
tatgcctcca tcgatattag caaaggagaa aataatccag gattccaaaa cactgatgat	2400
gttcagacct ccttttaa	2418

<210> 30
 <211> 859
 <212> PRT
 <213> Homo sapiens

<400> 30

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

Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn
100 105 110

Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys
115 120 125

Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn
130 135 140

Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser
145 150 155 160

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

Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro Asp Asn Pro
180 185 190

Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile Met Ala Asn
195 200 205

Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser
210 215 220

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

Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr
245 250 255

Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser
260 265 270

Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu Glu Ile Lys
275 280 285

Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys Leu Met Asn
290 295 300

Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro Ala His Leu
305 310 315 320

Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr
325 330 335

Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp Ala Met Val
340 345 350

Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe
355 360 365

Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe Trp Glu Asn
370 375 380

Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val Cys His Pro
385 390 395 400

Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu Met Cys Thr
405 410 415

Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu Met Gly His
420 425 430

Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn
435 440 445

Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile Met Ser Leu
450 455 460

Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu Leu Ser Pro
465 470 475 480

Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln
485 490 495

Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys
500 505 510

Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp Gln Trp Met
515 520 525

Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val Val Glu Pro
530 535 540

Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu Phe His Val
545 550 555 560

Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln
565 570 575

Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His Glu Gly Pro
580 585 590

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

Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu
610 615 620

Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro Leu Leu Asn
625 630 635 640

Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser
645 650 655

Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile
660 665 670

Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu
675 680 685

Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala
690 695 700

Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile Leu Phe Gly
705 710 715 720

Glu Glu Asp Val Arg Val Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn
725 730 735

Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile Pro Arg Thr
740 745 750

Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile Asn Asp Ala
755 760 765

Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr
770 775 780

Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu Ile Val Phe
785 790 795 800

Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile Leu Ile Phe
805 810 815

Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu
820 825 830

Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly
835 840 845

Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
850 855

<210> 31
<211> 605
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 31
aatccccgat aatcaacctc tggattacaa aatttgtgaa agattgactg gtattcttaa 60
ctatgttgct ccttttacgc tatgtggata cgctgcttta atgcctttgt atcatgctat 120
tgcttcccgt atggctttca ttttctcctc cttgtataaa tcctggttgc tgtctcttta 180
tgaggagttg tggcccgttg tcaggcaacg tggcgtggtg tgcactgtgt ttgctgacgc 240
aacccccact ggttggggca ttgccaccac ctgtcagctc ctttccggga ctttcgcttt 300
ccccctccct attgccacgg cggaactcat cgccgcctgc cttgcccgt gctggacagg 360
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atggctgctc gcctgtgttg ccacctggat tctgcgcggg acgtccttct gctacgtccc 480
 ttcggccctc aatccagcgg accttccttc ccgcggcctg ctgccggctc tgcggcctct 540
 tccgcgtctt cgccttcgcc ctacagacgag tcggatctcc ctttgggccg cctccccgca 600
 tcggg 605

<210> 32
 <211> 20
 <212> PRT
 <213> Severe acute respiratory syndrome coronavirus 2

<400> 32
 Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
 1 5 10 15

Pro Arg Thr Phe
 20

<210> 33
 <211> 263
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 33
 Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu
 1 5 10 15

Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp
 20 25 30

Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val
 35 40 45

Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala
 50 55 60

Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu
 65 70 75 80

Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val
85 90 95

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

Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala
115 120 125

Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg
130 135 140

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

His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Ser
165 170 175

Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu
180 185 190

Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys
195 200 205

Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr
210 215 220

Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu
225 230 235 240

Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr
245 250 255

Arg Leu Leu Asp Glu Phe Phe
260

<210> 34

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 34
 acaggtacgt taatagttaa tagcgt 26

 <210> 35
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 35
 atattgcagc agtacgcaca ca 22

 <210> 36
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic probe"

 <400> 36
 aactagcca tccttactgc gcttcg 26

 <210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 37
 atgggaagcc gaacatactg 20

 <210> 38
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 38

cagtctcagt gggggtgaat

20

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 39

ttcaccacca tggagaaggc

20

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 40

ggcatggact gtggatcatga

20

<210> 41

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 41

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<210> 42

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 <400> 42
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<210> 43
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 <400> 43
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<210> 44
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<210> 45
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<210> 46
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cgaggtcaca ggagaaggga 20

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<400> 54
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<210> 55
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primer"

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<210> 56
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primer"

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<210> 59

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 <400> 62
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<223> /note="Description of Artificial Sequence: Synthetic primer"

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23

<210> 66

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<212> DNA

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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 66

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<210> 67

<211> 23

<212> DNA

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<400> 67

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23

<210> 68

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<212> DNA

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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 68

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<210> 69

<211> 20
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<210> 73
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<400> 73
gtgcccacgt caaggagtat 20

<210> 74
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<400> 74
gggaagcgta tacagggtca 20

<210> 75
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 75
gcatttctgt tgctgttcac gctg 24

<210> 76
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<220>
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primer"

<400> 76

cctccttctg gtttttcagt ttagc 25

<210> 77

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 77

aaaatttcac cacgcccttg 20

<210> 78

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 78

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<210> 79

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

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<210> 80

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic primer"

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<400> 81
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<210> 82
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<210> 83
<211> 11
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 84
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<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 84
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<210> 85
<211> 19
<212> DNA
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<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 85
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<210> 86
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 86
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<210> 87
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 <212> DNA
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 87
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<210> 88
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 <212> DNA
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 88
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<210> 89
 <211> 20
 <212> DNA
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 89
 gccagaaca tcattccctgc 20

 <210> 90
 <211> 21
 <212> DNA
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 <220>
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 <400> 90
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 <210> 91
 <211> 26
 <212> DNA
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 <220>
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 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 91
 acaggtacgt taatagttaa tagcgt 26

 <210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 92
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 <210> 93
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<212> DNA
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 <400> 93
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<210> 94
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 <400> 94
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<210> 95
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <223> /note="Description of Artificial Sequence: Synthetic
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<210> 96
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 <212> DNA
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 <220>
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 <223> /note="Description of Artificial Sequence: Synthetic
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 <400> 96
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<210> 97
<211> 6
<212> DNA
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<220>
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oligonucleotide"

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6

<210> 98
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<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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tgcttcccgt atggctttca ttttctctc cttgtataaa tcctggttgc tgtctcttta 180
tgaggagttg tggcccgttg tcaggcaacg tggcgtggtg tgcactgtgt ttgctgacgc 240
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ccccctcct attgccacgg cggaactcat cgccgcctgc cttgcccgt gctggacagg 360
ggctcggctg ttgggcactg acaattccgt ggtgttgtcg gggaagctga cgtcctttcc 420
gcggctgctc gcctgtgttg ccacctggat tctgcgcggg acgtccttct gctacgtccc 480
ttcggccctc aatccagcgg accttccttc ccgcggcctg ctgccggctc tgcggcctct 540
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tcggg 605

<210> 99
<211> 4
<212> PRT
<213> Severe acute respiratory syndrome coronavirus 2

<400> 99

Arg Arg Ala Arg
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<210> 100
<211> 20
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 100
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<210> 101
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 101
ctgctgcact ataccagaca 20

<210> 102
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 102
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<210> 103
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primer"

<400> 103
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<210> 104
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<400> 104
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1 5

<210> 105
<211> 18
<212> DNA
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<220>
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primer"

<400> 105
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<210> 106
<211> 10077
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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tggggcgagg aatgggcgga actgggcgga gttaggggcg ggatgggcgg agttaggggc 180
gggactatgg ttgctgacta attgagatgc ccgacattga ttattgacta gttggaaggg 240

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<211> 1270

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 108

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

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

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

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

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

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

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

Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val Phe Lys
180 185 190

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

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

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

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

Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe
260 265 270

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

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

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

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

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

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

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

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

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

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

Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr
435 440 445

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

Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val
465 470 475 480

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

Thr Tyr Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe
500 505 510

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

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

Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro Phe Gln
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Gln Phe Gly Arg Asp Ile Asp Asp Thr Thr Asp Ala Val Arg Asp Pro
565 570 575

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

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

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

Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn Val Phe
625 630 635 640

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

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

Thr Gln Thr Asn Ser His Arg Arg Ala Arg Ser Val Ala Ser Gln Ser
675 680 685

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

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

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

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

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

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

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785 790 795 800

Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser Phe Ile Glu
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Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Ile Lys
820 825 830

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

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

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

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

Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn Val
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915 920 925

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

Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu Val
945 950 955 960

Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn Asp
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Ile Leu Ala Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp Arg
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995 1000 1005

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Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
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Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Ala
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Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
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Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
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Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
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Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
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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
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Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
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Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
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Pro Ile Asn Leu Val Arg Gly Leu Pro Gln Gly Phe Ser Ala Leu Glu
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Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
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Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr
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Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser Phe Thr
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Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly
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Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg
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Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser
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Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu
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Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg
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Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Asn Ile Ala

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410

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Lys Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro
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755 760 765

Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln Val Lys Gln
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835

840

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Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
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Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His
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Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
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<210> 113

<211> 3813

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<211> 1270
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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

Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe
260 265 270

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

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

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

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

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

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

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

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

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

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

Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr
435 440 445

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

Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val
465 470 475 480

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

Thr Tyr Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe
500 505 510

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

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

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

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

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

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

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

Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn Val Phe
625 630 635 640

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu Val
945 950 955 960

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

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

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

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

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

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala
1040 1045 1050

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

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

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

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

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

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

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

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
1160 1165 1170

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

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
1190 1195 1200

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

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

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

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
1250 1255 1260

Gly Val Lys Leu His Tyr Thr
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<211> 10064
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<210> 116

<211> 3825

<212> DNA

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 116

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<210> 117

<211> 1273

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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<400> 117

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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
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His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
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Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
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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
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Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
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Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
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Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
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Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
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Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys

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295

300

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Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
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Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
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Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
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 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
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Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
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Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
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ggtgccgccc ctactacgt tggatatctg cagccacgca cttttctgct gaagtacaac	840
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cagcccaccg agagcatcgt gcgcttcccc aatatcacca atctgtgccc cttcggcgag	1020
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tgcagctgcc tgaagggatg ctgcagtgc ggaagctgct gcaagttcga cgaggatgat	3780
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<210> 120

<211> 1273

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 120

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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 Tyr 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 Ser 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

Thr 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 Lys Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
485 490 495

Phe Gln Pro Thr Tyr 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 Gly 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 Tyr Val
645 650 655

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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<211> 9

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 121
Leu Thr Asp Glu Met Ile Ala Gln Tyr
1 5

<210> 122
<211> 9
<212> PRT
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<400> 122
Phe Leu His Val Thr Tyr Val Pro Ala
1 5

<210> 123
<211> 9
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<213> Severe acute respiratory syndrome coronavirus 2

<400> 123
Lys Ile Tyr Ser Lys His Thr Pro Ile
1 5

<210> 124
<211> 10
<212> PRT
<213> Severe acute respiratory syndrome coronavirus 2

<400> 124
Lys Leu Pro Asp Asp Phe Thr Gly Cys Val
1 5 10

<210> 125
<211> 9
<212> PRT
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<400> 125
Leu Leu Phe Asn Lys Val Thr Leu Ala
1 5

<210> 126
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<400> 126
Arg Leu Asp Lys Val Glu Ala Glu Val
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<210> 127
<211> 10
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<400> 127
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu
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<210> 128
<211> 9
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Arg Leu Gln Ser Leu Gln Thr Tyr Val
1 5

<210> 129
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<400> 129
Thr Leu Asp Ser Lys Thr Gln Ser Leu
1 5

<210> 130
<211> 9
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<400> 130
Val Leu Asn Asp Ile Leu Ser Arg Leu
1 5

<210> 131
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<212> PRT
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<400> 131
Tyr Leu Gln Pro Arg Thr Phe Leu Leu
1 5

<210> 132
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<212> PRT
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<400> 132
Arg Leu Asn Glu Val Ala Lys Asn Leu
1 5

<210> 133
<211> 9
<212> PRT
<213> Severe acute respiratory syndrome coronavirus 2

<400> 133
Val Val Phe Leu His Val Thr Tyr Val
1 5

<210> 134
<211> 9
<212> PRT
<213> Severe acute respiratory syndrome coronavirus 2

<400> 134
Asn Leu Asn Glu Ser Leu Ile Asp Leu
1 5

<210> 135
<211> 9
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<213> Severe acute respiratory syndrome coronavirus 2

<400> 135
Phe Ile Ala Gly Leu Ile Ala Ile Val
1 5

<210> 136
<211> 9
<212> PRT
<213> Severe acute respiratory syndrome coronavirus 2

<400> 136
Lys Cys Tyr Gly Val Ser Pro Thr Lys
1 5

<210> 137
<211> 9
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<400> 137

Gly Val Tyr Phe Ala Ser Thr Glu Lys
1 5

<210> 138
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<213> Severe acute respiratory syndrome coronavirus 2

<400> 138
Arg Leu Phe Arg Lys Ser Asn Leu Lys
1 5

<210> 139
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Gly Thr His Trp Phe Val Thr Gln Arg
1 5

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<211> 10
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<213> Severe acute respiratory syndrome coronavirus 2

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1 5 10

<210> 141
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Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
1 5

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Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe
1 5

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Arg Phe Asp Asn Pro Val Leu Pro Phe
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<210> 144
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Ser Pro Arg Arg Ala Arg Ser Val Ala
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<400> 145
Ala Pro His Gly Val Val Phe Leu
1 5

<210> 146
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Gln Pro Thr Glu Ser Ile Val Arg Phe
1 5

<210> 147
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<400> 147
Leu Pro Phe Asn Asp Gly Val Tyr Phe
1 5

<210> 148
<211> 9
<212> PRT
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<400> 148

Ile Pro Phe Ala Met Gln Met Ala Tyr
1 5

<210> 149

<211> 9

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 149

Tyr Glu Gln Tyr Ile Lys Trp Pro Trp
1 5

<210> 150

<211> 15

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 150

Ile Thr Arg Phe Gln Thr Leu Leu Ala Leu His Arg Ser Tyr Leu
1 5 10 15

<210> 151

<211> 15

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 151

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

<210> 152

<211> 18

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 152

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Thr Lys