Sequence Listing

<110> Chengdu Kanghong Biotechnologies Co., Ltd.
<120> HUMANIZED ANTI-TNF-α ANTIBODY AND ANTIGEN-BINDING FRAGMENT (Fab) THEREOF AND USE OF THE SAME
<130> PCGNARI11034
<160> 39
<170> PatentIn version 3.5
<210> 1
<211> 120
<212> PRT
<213> Artificial sequence
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Glu or Gln
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Xaa Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Leu Thr Val Ser Ser
115 120
<210> 2
<211> 360
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 2
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct 120
ccagggaagg gactggagtg ggtagccgaa attcgttcta aaagcattaa tagcgccacc 180
cattatgccg aaagcgtgaa aggccggttc accatctcaa gagatgattc aaaaaacacg 240
gtgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtacta ctgcagccgt 300
aattactacg gcagcaccta cgattactgg ggccagggca ccaccctgac cgtgagctcc 360

<210> 3
<211> 120
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 3
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr
65 70 75 80
Leu Tyr Leu Glu Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 4
<211> 360
<212> DNA
<213> Artificial sequence
<220>

<223>
<400> 4
caggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct 120
ccagggaagg gcctggaatg ggtagccgaa attcgttcta aaagcattaa tagcgccacc 180
cattatgccg aaagcgtgaa gggccgattc accatctcca gagacaattc caagaaaacg 240
ttgtatctgg aaatgaacag cctgagagtt gaggacacag ctgtgtacta ctgcagccgt 300
aattactacg gcagcaccta cgattactgg ggccagggca ccaccctgac cgtgagctcc 360

<210> 5
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 5
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Ser Pro Lys
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Val His Met Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asn Gln Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Gly Ser Gln Ser Phe Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr
100 105

<210> 6
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 6
gaaattgtgc tgactcagtc tccagatttt cagtctgtgt ctccaaagga gacagtcacc 60
atcacctgcc gggccagtca gaccgttcat atgagtttac actggtacca gcagaaacca 120
aatcagtctc caaggctcct catcaagtat ggttcccagt ccttctcggg ggtcccctcg 180
aggttcagtg gcagtgggtc tgggacagat ttcaccctca ccatcaatag cctggaacct 240
gaagatgctg caacatacta ctgccagcag agccatagct ggccgttcac cttcggcagc 300
ggcaccaatg tggacatcaa acgtacg 327

<210> 7
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 7
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Ser Pro Lys
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Val His Met Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asn Gln Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Gly Ser Gln Ser Phe Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Phe Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr
100 105

<210> 8
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 8
gaaattgtgc tgactcagtc tccagatttt cagtctgtgt ctccaaagga gacagtcacc 60
atcacctgcc gggccagtca gaccgttcat atgagtttac actggtacca gcagaaacca 120

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aatcagtctc caaggctcct catcaagtat ggttcccagt ccttctcggg ggtcccctcg    180
aggttcagtg gcagtgggtc tgggacagat ttcaccctca ccatcaatag cctggaacct    240
gaagatgctg caacatacta ctgccagcag agccatttct ggccgttcac cttcggcagc    300
ggcaccaatg tggacatcaa acgtacg                                        327
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<210> 9
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 9

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

<210> 10
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 10

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gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc     60
atcacctgcc gggccagtca gagcatttat agtagcttac actggtacca gcagaaacca    120
gatcagtctc caaagctcct catcaagttt gcttcccagt ccgtctcagg ggtcccctcg    180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240
gaagatgctg caacgtacta ctgccagcag agccatagct ggccgttcac cttcggcagc    300
ggcaccaatg tggacatcaa acgtacg                                        327
```

<210> 11
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 11

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Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                  10                  15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Tyr Ser Ser
            20                  25                  30
Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45
Lys Phe Ala Ser Gln Ser Val Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Phe Trp Pro Phe
                85                  90                  95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr
            100                 105
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<210> 12
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 12

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gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc     60
atcacctgcc gggccagtca gagcatttat agtagcttac actggtacca gcagaaacca    120
gatcagtctc caaagctcct catcaagttt gcttcccagt ccgtctcagg ggtcccctcg    180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240
gaagatgctg caacgtacta ctgccagcag agccatttct ggccgttcac cttcggcagc    300
ggcaccaatg tggacatcaa acgtacg                                        327
```

<210> 13
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 13
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Ser Pro Lys
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Val His Met Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asn Gln Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Gly Ser Gln Ser Phe Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Trp Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr
100 105

<210> 14
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 14
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atcacctgcc gggccagtca gaccgttcat atgagtttac actggtacca gcagaaacca 120
aatcagtctc caaggctcct catcaagtat ggttcccagt ccttctcggg ggtcccctcg 180
aggttcagtg gcagtgggtc tgggacagat ttcaccctca ccatcaatag cctggaacct 240
gaagatgctg caacatacta ctgccagcag agccattggt ggccgttcac cttcggcagc 300
ggcaccaatg tggacatcaa acgtacg 327

<210> 15
<211> 109
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 15
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Tyr Ser Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Phe Ala Ser Gln Ser Val Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Trp Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr
100 105

<210> 16
<211> 327
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 16
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atcacctgcc gggccagtca gagcatttat agtagcttac actggtacca gcagaaacca 120
gatcagtctc caaagctcct catcaagttt gcttcccagt ccgtctcagg ggtcccctcg 180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240
gaagatgctg caacgtacta ctgtcagcag agccattggt ggccgttcac cttcggcagc 300
ggcaccaatg tggacatcaa acgtacg 327

<210> 17
<211> 330

<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 17
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 18
<211> 990
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 18
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ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 420
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960
cagaagagcc tctccctgtc tccgggtaaa 990

<210> 19
<211> 105
<212> PRT

<213> Artificial sequence
<220>
<223>
<400> 19
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
1 5 10 15
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
20 25 30
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
35 40 45
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
50 55 60
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
65 70 75 80
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
85 90 95
Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 20
<211> 315
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 20
gtcgctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 60
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 120
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 180
gacagcacct acagcctcag cagcaccctg acgctgagca aagcagacta cgagaaacac 240
aaagtctacg cctgcgaagt cacccatcag ggcctgagtt caccggtgac aaagagcttc 300
aacaggggag agtgt 315

<210> 21
<211> 450
<212> PRT
<213> Artificial sequence
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Glu or Gln
<400> 21
Xaa Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

```
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
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<210> 22
<211> 1350
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 22

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gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc     60
tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct    120
ccagggaagg gactggagtg ggtagccgaa attcgttcta aaagcattaa tagcgccacc    180
cattatgccg aaagcgtgaa aggccggttc accatctcaa gagatgattc aaaaaacacg    240
gtgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtacta ctgcagccgt    300
aattactacg gcagcaccta cgattactgg ggccagggca ccaccctgac cgtgagctcc    360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg    420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca    540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc    600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc    660
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga    720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct     780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg    840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac    900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag    960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag    1080
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc   1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg   1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   1320
cagaagagcc tctccctgtc tccgggtaaa                                    1350
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<210> 23
<211> 214
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 23

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Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Tyr Ser Ser
            20                  25                  30
Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45
Lys Phe Ala Ser Gln Ser Val Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Trp Trp Pro Phe
                85                  90                  95
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Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
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<210> 24
<211> 642
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 24

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gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc     60
atcacctgcc gggccagtca gagcatttat agtagcttac actggtacca gcagaaacca    120
gatcagtctc caaagctcct catcaagttt gcttcccagt ccgtctcagg ggtcccctcg    180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240
gaagatgctg caacgtacta ctgtcagcag agccattggt ggccgttcac cttcggcagc    300
ggcaccaatg tggacatcaa acgtacggtc gctgcaccat ctgtcttcat cttcccgcca    360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat    420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag    480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg    540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc    600
ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt                       642
```

<210> 25
<211> 223
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 25

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

<210> 26
<211> 669
<212> DNA

<213> Artificial sequence
<220>
<223>
<400> 26
caggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct 120
ccagggaagg gcctggaatg ggtagccgaa attcgttcta aaagcattaa tagcgccacc 180
cattatgccg aaagcgtgaa gggccgattc accatctcca gagacaattc caagaaaacg 240
ttgtatctgg aaatgaacag cctgagagtt gaggacacag ctgtgtacta ctgcagccgt 300
aattactacg gcagcaccta ccagtactgg ggccagggca ccaccctgac cgtgagctcc 360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 660
aaatcttgt 669

<210> 27
<211> 223
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 27
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Val Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Gln Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

<210> 28
<211> 669
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 28
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct 120
ccagggaagg gactggagtg ggtagccgaa attcgttcta aaagcattaa tagcgccacc 180
cattatgccg aaagcgtgaa aggccggttc accatctcaa gagatgattc aaaaaacacg 240
gtgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtacta ctgcagccgt 300
aattactacg gcagcaccta ccagtactgg ggccagggca ccaccctgac cgtgagctcc 360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 660
aaatcttgt 669

<210> 29
<211> 214

<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 29
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Ser Pro Lys
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Val His Met Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asn Gln Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Gly Ser Gln Ser Phe Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Lys Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 30
<211> 642
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 30
gaaattgtgc tgactcagtc tccagatttt cagtctgtgt ctccaaagga gacagtcacc 60
atcacctgcc gggccagtca gaccgttcat atgagtttac actggtacca gcagaaacca 120
aatcagtctc caaggctcct catcaagtat ggttcccagt ccttctcggg ggtcccctcg 180
aggttcagtg gcagtgggtc tgggacagat ttcaccctca ccatcaatag cctggaacct 240
gaagatgctg caacatacta ctgccagcag agccataaat ggccgttcac cttcggcagc 300
ggcaccaatg tggacatcaa acgtacggtc gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt 642

<210> 31
<211> 214
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 31
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Tyr Ser Ser
20 25 30
Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45
Lys Phe Ala Ser Gln Ser Val Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Lys Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
```

<210> 32
<211> 642
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 32

```
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc     60
atcacctgcc gggccagtca gagcatttat agtagcttac actggtacca gcagaaacca    120
gatcagtctc caaagctcct catcaagttt gcttcccagt ccgtctcagg ggtcccctcg    180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240
gaagatgctg caacgtacta ctgccagcag agccataaat ggccgttcac cttcggcagc    300
ggcaccaatg tggacatcaa acgtacggtc gctgcaccat ctgtcttcat cttcccgcca    360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat    420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag    480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg    540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc    600
ctgagttcac cggtgacaaa gagcttcaac aggggagagt gt                       642
```

<210> 33
<211> 98
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 33

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

<210> 34
<211> 294
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 34

```
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg     60
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca    180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc    240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agtt          294
```

<210> 35
<211> 94
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 35

```
gtcgactaat acgactcact atagggaat tgtgagcgga taacaattcc cctctagaaa     60
taattttgtt taactttaag aaggaggcgg ccgc                                94
```

<210> 36
<211> 232
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 36
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15
Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Gly Ser Ser Ser
65 70 75 80
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
85 90 95
Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
100 105 110
Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
115 120 125
Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
130 135 140
Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
145 150 155 160
Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
165 170 175
Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
180 185 190
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
195 200 205
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
210 215 220
Val Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 37
<211> 696
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 37
atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct ccccaagaag 60
acagggggc cccagggctc caggcggtgc ttgttcctca gcctcttctc cttcctgatc 120
gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg cccccagagg 180
gaagagttcc ccagggacct ctctctaatc agccctctgg cccaggcagg atcatcttct 240
cgaaccccga gtgacaagcc tgtagcccat gttgtagcaa accctcaagc tgaggggcag 300
ctccagtggc tgaaccgccg ggccaatgcc ctcctggcca atggcgtgga gctgagagat 360
aaccagctgg tggtgccatc agagggcctg tacctcatct actcccaggt cctcttcaag 420
ggccaaggct gcccctccac ccatgtgctc ctcacccaca ccatcagccg catcgccgtc 480
tcctaccaga ccaaggtcaa cctcctctct gccatcaaga gcccctgcca gagggagacc 540
ccagaggggg ctgaggccaa gccctggtat gagcccatct atctgggagg ggtcttccag 600
ctggagaagg gtgaccgact cagcgctgag atcaatcggc ccgactatct cgactttgcc 660
gagtctggac aggtctactt tgggatcatt gccctg 696

<210> 38
<211> 233
<212> PRT
<213> Artificial sequence
<220>
<223>
<400> 38
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15
Leu Pro Arg Lys Thr Ala Gly Pro Gln Gly Ser Arg Arg Cys Trp Phe
20 25 30
Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60
Lys Asp Pro Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65 70 75 80

```
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                85                  90                  95
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
            100                 105                 110
Leu Ala Asn Gly Val Glu Leu Thr Asp Asn Gln Leu Val Val Pro Ser
        115                 120                 125
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
    130                 135                 140
Cys Pro Ser Asn His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145                 150                 155                 160
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                165                 170                 175
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
            180                 185                 190
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
        195                 200                 205
Ser Ala Glu Ile Asn Leu Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
    210                 215                 220
Gln Val Tyr Phe Gly Ile Ile Ala Leu
225                 230
```

<210> 39
<211> 699
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 39

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atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct cccaaggaag      60
acagcggggc cccagggctc caggcggtgc tggttcctca gcctcttctc cttcctgctc      120
gtggcaggcg ccaccacgct cttctgtctg ctgcactttg gagtgatcgg ccccccagagg      180
gaagagttcc ccaaggaccc ctctctaatc agccctctgg ctcaggcagt cagatcatct      240
tctcgaaccc caagtgacaa gcctgtagcc catgttgtag caaaccctca agctgagggg      300
cagctccagt ggctgaaccg ccgggccaat gccctcctgg ccaatggcgt ggagctgaca      360
gataaccagc tggtggtgcc atcagaaggc ctgtacctca tctactccca ggtcctcttc      420
aagggccaag gctgcccctc caaccatgtg ctcctcaccc acaccatcag ccgcatcgcc      480
gtctcctacc agaccaaggt caacctcctc tctgccatca agagcccctg ccagagggag      540
actccagagg gggctgaggc caagccctgg tatgagccca tctacctagg aggggtcttt      600
cagctggaga agggtgatcg actcagcgct gagatcaatc tgcccgacta tctcgacttt      660
gccgagtctg ggcaggtcta ctttgggatc attgccctg                             699
```