SEQUENCE LISTING

<110> Technische Universität Dresden

<120> Fusion of site-specific recombinases for efficient and specific genome editing

<130> TUD131WO

<150> EP 19 214 152.1
<151> 2019-12-06

<160> 106

<170> PatentIn version 3.5

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Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
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Gly Ser Gly Gly Ser Gly Gly Ser
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Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
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<400> 6

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Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20   25   30

Ser Gly Gly Ser
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<400> 7

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Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20   25   30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
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Ala Glu Ala Thr Ser Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
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Gly Ser Asn Gly Ala Arg Arg Thr
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<210> 9
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<213> Artificial Sequence

<220>
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Gly Ser Gly Arg Arg Gly Ala Lys
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<220>
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<400> 10

Lys Asn Gly Arg Gly Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
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<210> 11
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<400> 11

Gly Gly Ser Gly Gly Ser Thr Ala Ala Lys Glu Gly Ala Ala Ser Ser
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Ala Ser Gly Gly Ser Gly Gly Ser
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Gly Gly Ser Gly Gly Ser Asn Ser Arg Ser Asn Thr Glu Asn Ser Asp
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Lys Gly Gly Gly Ser Gly Gly Ser
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<223> Synthetic peptide

<400> 13

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Ala Thr Gly Gly Ser Gly Gly Ser
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Arg Gly Gly Gly Ser Gly Gly Ser
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Glu Lys Thr Gly Thr Asn Ser Ala
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<400> 16

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<400> 29
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<210> 30
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<212> PRT
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<220>
<223> Recombinant peptide

<400> 30

Met Ser Asp Leu Gln Thr Leu His Gln Asn Leu Ser Ala Leu Leu Val

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Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Val Phe Arg
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Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Asn Thr Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Ser Asn Asn Arg Glu Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Val
65                  70                  75                  80

Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu Ala Leu Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Gly Ser Ser Asp Arg Arg Asn Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Val His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu Val Glu Arg Trp
    210                 215                 220
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Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240


Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Ser Ser Gln Leu
                245                 250                 255


Thr Thr Asp Val Leu Arg Gly Ile Phe Val Ala Ala His Arg Leu Val
            260                 265                 270


His Gly Ala Arg Asp Asp Ser Gly Gln Arg Tyr Leu Thr Trp Ser Gly
        275                 280                 285


His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300


Ser Ile Ala Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Glu Ser
305                 310                 315                 320


Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335


Arg Leu Leu Glu Asp Gly Asp
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<210>  31
<211>  343
<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  31

Met Ser Asn Leu Gln Ala Leu His Gln Asn Pro Ser Thr Leu Leu Ala
1               5                   10                  15


Asp Ala Thr Cys Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30


Asp Ser Gln Ala Phe Ser Glu His Thr Trp Lys Ala Leu Gln Ser Val
        35                  40                  45
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Cys Arg Ser Trp Val Ala Trp Cys Lys Leu Asn Ser Arg Arg Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Thr
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
                85                  90                  95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Ala Asp Leu Asp Gln
    130                 135                 140

Val Arg Ala Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu Arg Ile Gly Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asp Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
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260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Leu Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Asp Asp
340

<210> 32
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 32

Met Ser Asn Leu Gln Thr Leu His Gln Asn Leu Ser Ala Leu Leu Ala
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Asn Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Val Phe Arg
20 25 30

Asp Arg Arg Ala Phe Ser Glu Ala Thr Trp Lys Thr Leu Leu Ser Val
35 40 45

Cys Arg Thr Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Val
65 70 75 80

Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu Ala Leu Leu Asn

```
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Ser Ala
            100                 105                 110

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

Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Lys
    130                 135                 140

Val Arg Ser Leu Met Gly Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu Val Gly Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

Ser Thr Asp Val Leu Arg Gly Val Phe Ala Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Thr Lys Asp Asp Ser Gly Gln Gly Tyr Leu Thr Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300
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Ser Ile Ala Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Glu Ser
305                 310                 315                 320


Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335


Arg Leu Leu Glu Asp Gly Asp
            340


<210>  33
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<212>  PRT
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<220>
<223>  Recombinant protein

<400>  33

Met Ser Asn Ile Gln Thr Pro His Gln Ser Leu Ser Ala Leu Leu Thr
1               5                   10                  15


Asp Ala Thr Ser Asp Val Thr Arg Lys Asn Leu Ala Asp Met Phe Arg
            20                  25                  30


Asp Ser Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45


Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Lys Trp Leu
    50                  55                  60


Pro Val Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Thr
65                  70                  75                  80


Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
                85                  90                  95


Met Leu His Arg Arg Ala Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110


Val Ser Leu Val Met Arg Arg Ile Arg Arg Glu Asn Val Asp Ala Gly
        115                 120                 125
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Glu Arg Ala Gln Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Val Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Ala Lys Gly Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Pro Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Ser Asp
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340

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<212> DNA
<213> Artificial Sequence

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<223> Recombinant DNA

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acctggaata cgctcctgtc cgtttgccgg tcgtgggcag catggtgcaa gtcgaataac 180

cgggaatggt ttcccgcaga acctgaagat gttcgcgatt atcttctaca cctccaggta 240

cgcggtctgg cagtaaacac tatccagcga catttggcgc tgctgaacat gcttcaccgt 300

cggtccgggc tgccacgacc aggcgacagc aatgctgttt cactggttat gcggcgtatc 360

cggaaagaaa acgttgatgc cggtgagcgt gtaagacagg ctctggcgtt cgaacgcacc 420

gatttcgacc aggttcgttc actcatgggg agtagcgatc ggcgcaatga tatacgtaat 480

ctggcatttc ttggggttgc atataacacc ctgttacgta tatccgaaat cgccaggatt 540

cggataaaag atatctcgcg tactgacggt gggaggatgc tagtccatat tggcagaacg 600

aaaacgctgg tcagcaccgc aggcgtagag aaagcactta gcctgggggt aaccagactg 660

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cgggtcagaa aaaacggtgt tgccgcgcca tctgcctcca gccagctgac aaccgacgtc 780

ctgcgaggga tttttgtagc cgcccaccgc ctggtccacg gtgccaggga tgactctggg 840

cagagatacc tgacctggtc tggacacagt gcccgcgtcg gagccgcgcg ggacatggcc 900

cgcgctggag tctcaatagc ggagattatg caggctggtg gctggaccac cgtagagagc 960

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cggaggtggt ttcccgcaga gcccgaagat gttcgcgatt atcttctgca tcttcagacg 240

cgcggtctgg cagtaaaaac catccagcac catctgggct cactaaacat gcttcatcgt 300

cagtccgggc tgccacgacc aggtgacagc aatgccgttt cactggttat gcggcgaatc 360

cgaagagaaa acgttgatgc cggtgaacgt gcaaaacagg ctctggcgtt cgagcgcgct 420

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aaaacactgg tcagcaccgc aggtgtggag aaggcactta gcctgggggt aactaaactg 660

gtcgagcgat ggatttccgt ctccggtgta gctgatgacc cagataacta cctgttttgc 720

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cgcggtctgg cggtgaacac aatccagcga cacttggccc tgctaaacat gcttcaccgt 300

cggtccgggc tgccgcgacc aggtgacagc agcgctgttt cactggttat gcggcgtatc 360

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ctggcatttc tgggtgttgc atataacacc ctgctacgca tatccgaaat tgccaggatt 540

cggataaaag atatctcacg taccgacggt gggaggatgc taatccatat cggcagaacg 600

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gtcgggcggt ggatttctgt ctctggtgta gctggcgacc cgaataacta cctgttctgc 720

cgggtcagaa aaaatggtgt tgccgcgcca tctgccacca gccagctatc gaccgacgtc 780

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caggggtacc tgacctggtc tggacacagt gcccgcgtcg gagccgcgcg ggatatggcc 900

cgcgctgggg tttcaatagc ggagattatg caggctggtg gctggaccac cgtagagagc 960

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cggaaatggc ttcccgtaga acctgaggat gttcgcgatt acctcctgca ccttcagacg 240

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cgggctgggc tgccacgacc gggtgacagc aatgctgttt cactggttat gcggcgtatc 360

cgaagagaaa acgttgatgc cggtgaacgc gcacaacagg ccctggcgtt cgaacgcacc 420

gatttcgacc aggttcggtc actcgtggaa aacagcgacc gctgccagga tatacgtaat 480

ctggcatttc tgggggtcgc ttataacacc ctgttgcgta tatccgaaat tgccaggatt 540

cgggttaagg atatctcacg tactgacggt gggaggatgt taatccatat tggcagaacg 600

aaaacgctgg ttagtaccgc aggtgtagag aaggcactca gcctgggggt gaccaaactg 660

gtcgagcgat ggatttccgt ctccggtgta gccgatgacc caaataacta cctgttttgc 720

cgggtcagaa gatatggcgt tgccaagccg tctgccacca gccagctgtc aacttacgcc 780

ctgcaaggga ttttcggagc cgcccaccgc ctggtctacg gtgccaaggg tgactctggc 840

cagaagtacc tggcctggtc gggacacagt gcccgtgtcg gagccgcacg agacatggcc 900

cgcgctggag ttccaatacc ggagattatg caggctggtg gctggaccac cgtgaatagt 960

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<223> Synthetic oligonucleotide

<400> 44

tcgagggcgg tagcggtggc tctggcggca gcggtggtag cggtggctct ggcggtagtg 60

gtggtagtgg cggca 75

<210> 45
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 45
gtacatgctg ccgccactac caccactacc gccagagcca ccgctaccac cgctgccgcc 60

agagcc 66

<210> 46
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 46
tcgagggcgg tagcggtggc tctggcggca gcggtggtag cggtggctct ggcggtagtg 60

gtggtagtgg cggcagcggt ggctctggcg gtagtat 97

<210> 47
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 47
gtacatacta ccgccagagc caccgctgcc gccactacca ccactaccgc cagagccacc 60

gctaccaccg ctgccgccag agccaccgct accgccc 97

<210> 48
<211> 115
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 48
tcgagggcgg tagcggtggc tctggcggca gcggtggtag cggtggctct ggcggtagtg 60

gtggtagtgg cggcagcggt ggctctggcg gtagtggtgg tagcggtggc tctat 115

<210> 49
<211> 115
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 49
gtacatagag ccaccgctac caccactacc gccagagcca ccgctgccgc cactaccacc 60

actaccgcca gagccaccgc taccaccgct gccgccagag ccaccgctac cgccc 115

<210> 50
<211> 133
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tcgagggcgg tagcggtggc tctggcggca gcggtggtag cggtggctct ggcggtagtg 60

gtggtagtgg cggcagcggt ggctctggcg gtagtggtgg tagcggtggc tctggaggta 120

gtggcggatc aat 133

<210> 51
<211> 133
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
gtacattgat ccgccactac ctccagagcc accgctacca ccactaccgc cagagccacc 60

gctgccgcca ctaccaccac taccgccaga gccaccgcta ccaccgctgc cgccagagcc 120

accgctaccg ccc 133

<210> 52

<211> 128
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> variation
<222> (29)..(46)
<223> r is a or g

v is a or c or g

m is a or c

<220>
<221> variation
<222> (83)..(100)
<223> r is a or g

v is a or c or g

m is a or c

<400> 52
gaagtgccat tccgcctgac ctctcgagrv mrvmrvmrvm rvmrvmggcg gcagcggtgg 60

tagcggtggc tctggcggta gtrvmrvmrv mrvmrvmrvm atgtacaagg ctaggtggag 120

gctcagtg 128

<210> 53
<211> 128
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> variation
<222> (47)..(82)
<223> r is a or g

v is a or c or g

m is a or c

<400> 53
gaagtgccat tccgcctgac ctctcgaggg cggtagcggt ggctctrvmr vmrvmrvmrv 60

mrvmrvmrvm rvmrvmrvmr vmggtggtag tggcggcagc atgtacaagg ctaggtggag 120

gctcagtg 128

<210> 54
<211> 128
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<220>
<221> variation
<222> (29)..(100)
<223> r is a or g

v is a or c or g

m is a or c

<400> 54
gaagtgccat tccgcctgac ctctcgagrv mrvmrvmrvm rvmrvmrvmr vmrvmrvmrv 60

mrvmrvmrvm rvmrvmrvmr vmrvmrvmrv mrvmrvmrvm atgtacaagg ctaggtggag 120

gctcagtg 128

<210> 55
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 55
gccgaagcaa caagcgaagg cggcagcggt ggtagcggtg gctctggcgg tagtaacggc 60

gcaagaagaa cc 72

<210> 56
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 56
gcaggaacaa ccgcaagagg cggcagcggt ggtagcggtg gctctggcgg tagtggaaga 60

agaggagcaa aa 72

<210> 57
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 57
aaaaacggaa gaggaagagg cggcagcggt ggtagcggtg gctctggcgg tagtagaaca 60

aaaagagaaa ca 72

<210> 58
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> recombinant oligonucleotide

<400> 58
ggcggtagcg gtggctctac cgccgccaaa gaaggagcag caagcagcgc cagcggtggt 60

agtggcggca gc 72

<210> 59
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 59
ggcggtagcg gtggctctaa cagcagaagc aacacagaaa acagcgacaa aggcggtggt 60

agtggcggca gc 72

<210> 60
<211> 72
<212> DNA
<213> Artificial Sequence

<220>

<223> Recombinant oligonucleotide

<400> 60
ggcggtagcg gtggctctaa cggcgaagaa ggaaccgaaa gaggcaaagc aacaggtggt 60

agtggcggca gc 72

<210> 61
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 61
ggcggtagcg gtggctctac caccaaagca aacagagcaa aaggcggcag aggaggtggt 60

agtggcggca gc 72

<210> 62
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 62
ggcgcaaacg aagacacaaa cacagaagca gccggaagcg aaggcaacga aaaaaccgga 60

acaaacagcg ct 72

<210> 63
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant oligonucleotide

<400> 63
ggcgaaagca gagcagaaga cggcgcaaaa ggaaacggca gaggcaaagg agaagcaaca 60

gcaggcgcag ca 72

<210> 64
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant DNA

<400> 64
atgtccaatt tacaggcctt acaccaaaat ccgtccacat tactggctga cgcgacgtgt 60

gacgaggttc gcaagaacct gatggacatg ttcagggata gccaggcgtt ttcagagcat 120

acctggaaag cgcttcaatc cgtttgccgg tcgtgggtgg catggtgcaa actgaacagc 180

cggaggtggt ttcccgcaga gcccgaagat gttcgcgatt atcttctgca tcttcagacg 240

cgcggtctgg cagtaaaaac catccagcac catctgggct cactaaacat gcttcatcgt 300

cagtccgggc tgccacgacc aggtgacagc aatgccgttt cactggttat gcggcgaatc 360

cgaagagaaa acgttgatgc cggtgaacgt gcaaaacagg ctctggcgtt cgagcgcgct 420

gacctcgacc aggtccgtgc actcatggaa aacagcgatc gctgccagga tatacgtaat 480

ctggcatttc tgggcgttgc ttacaacacc ctgttacgaa taggcgaaat tgccagaatc 540

cgggttagag atatctcacg tactgacggt gggagaatgt taatccacat tggcagaacg 600

aaaacactgg tcagcaccgc aggtgtggag aaggcactta gcctgggggt aactaaactg 660

gtcgagcgat ggatttccgt ctccggtgta gctgatgacc cagataacta cctgttttgc 720

cgggtcagaa gatatggcgt tgccaagcca tctgccacca gccagctgtc aacctacgcc 780

ctgcaaggga tttttggagc cgctcaccgc ctggtctacg gtgctaagga tgactctggt 840

cagaaatacc tggcctggtc tggacacagt gcccgtgtcg gagccgcgcg ggatatggcc 900

cgcgctggag tttcgttacc ggagattatg caggctggtg gctggaccac cgtaaatagt 960

gtcatgaact atatccgtaa cctggatagt gagacagggg ccatggtgcg cctgctggaa 1020

gatgacgact cgctcgaggg cggtagcggt ggctctacca ccaaagcaaa cagagcaaaa 1080

ggcggcagag gaggtggtag tggcggcagc atgtacatgt ccgatttaca gaccttacac 1140

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gacgtgttca gggaccgcca ggcgttttct gaggcaacct ggaatacgct cctgtccgtt 1260

tgccggtcgt gggcagcatg gtgcaagtcg aataaccggg aatggtttcc cgcagaacct 1320

gaagatgttc gcgattatct tctacacctc caggtacgcg gtctggcagt aaacactatc 1380

cagcgacatt tggcgctgct gaacatgctt caccgtcggt ccgggctgcc acgaccaggc 1440

gacagcaatg ctgtttcact ggttatgcgg cgtatccgga aagaaaacgt tgatgccggt 1500

gagcgtgtaa gacaggctct ggcgttcgaa cgcaccgatt tcgaccaggt tcgttcactc 1560

atggggagta gcgatcggcg caatgatata cgtaatctgg catttcttgg ggttgcatat 1620

aacaccctgt tacgtatatc cgaaatcgcc aggattcgga taaaagatat ctcgcgtact 1680

gacggtggga ggatgctagt ccatattggc agaacgaaaa cgctggtcag caccgcaggc 1740

gtagagaaag cacttagcct gggggtaacc agactggtcg agcgatggat ttccgtctct 1800

ggcgtagctg gtgatccgaa taactacctg ttttgccggg tcagaaaaaa cggtgttgcc 1860

gcgccatctg cctccagcca gctgacaacc gacgtcctgc gagggatttt tgtagccgcc 1920

caccgcctgg tccacggtgc cagggatgac tctgggcaga gatacctgac ctggtctgga 1980

cacagtgccc gcgtcggagc cgcgcgggac atggcccgcg ctggagtctc aatagcggag 2040

attatgcagg ctggtggctg gaccaccgta gagagcgtca tgagctatct ccgtaacctg 2100

gatagtgaaa cgggggcaat ggtgcgcctg ctggaagacg gcgattag 2148

<210> 65
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant DNA

<400> 65
atgtccaata tacagacccc acaccaaagt ttgtctgcat tactgactga tgcaacgagt 60

gatgtgactc gcaagaacct ggcggacatg ttcagggata gccaggcgtt ttcagagcat 120

acctggaaaa tgctcctgtc cgtttgccgg tcgtgggcgg catggtgcga gctgaataac 180

cggaaatggc ttcccgtaga acctgaggat gttcgcgatt acctcctgca ccttcagacg 240

cgtggtctgg cggtaaaaac tatccagcat catctgggct cgctaaacat gcttcaccgt 300

cgggctgggc tgccacgacc gggtgacagc aatgctgttt cactggttat gcggcgtatc 360

cgaagagaaa acgttgatgc cggtgaacgc gcacaacagg ccctggcgtt cgaacgcacc 420

gatttcgacc aggttcggtc actcgtggaa aacagcgacc gctgccagga tatacgtaat 480

ctggcatttc tgggggtcgc ttataacacc ctgttgcgta tatccgaaat tgccaggatt 540

cgggttaagg atatctcacg tactgacggt gggaggatgt taatccatat tggcagaacg 600

aaaacgctgg ttagtaccgc aggtgtagag aaggcactca gcctgggggt gaccaaactg 660

gtcgagcgat ggatttccgt ctccggtgta gccgatgacc caaataacta cctgttttgc 720

cgggtcagaa gatatggcgt tgccaagccg tctgccacca gccagctgtc aacttacgcc 780

ctgcaaggga ttttcggagc cgcccaccgc ctggtctacg gtgccaaggg tgactctggc 840

cagaagtacc tggcctggtc gggacacagt gcccgtgtcg gagccgcacg agacatggcc 900

cgcgctggag ttccaatacc ggagattatg caggctggtg gctggaccac cgtgaatagt 960

gtcatgaact atatccgtaa cctggatagc gagacaggag caatggtgcg cctgctggaa 1020

gacagcgatt cgctcgaggg cggtagcggt ggctctacca ccaaagcaaa cagagcaaaa 1080

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cagaatttgt ccgcactact ggccaatgca acaagtgatg aggctcgcaa gaacctgatg 1200

gacgtcttca gggaccgccg ggcgttttct gaagctacct ggaaaacgct tctgtccgtt 1260

tgccggacgt gggcggcatg gtgcaagctg aataaccgga aatggtttcc cgcagaacct 1320

gaagatgtac gcgattatct tctacatctc caggtacgcg gtctggcggt gaacacaatc 1380

cagcgacact tggccctgct aaacatgctt caccgtcggt ccgggctgcc gcgaccaggt 1440

gacagcagcg ctgtttcact ggttatgcgg cgtatccgaa aggaaaacgt tgatgccggt 1500

gaacgcgtaa ggcaggccct ggcgttcgag cgcactgatt tcgacaaggt tcgttcactc 1560

atgggaaaca gcgatcgctg ccaggatata cgtaatctgg catttctggg tgttgcatat 1620

aacaccctgc tacgcatatc cgaaattgcc aggattcgga taaaagatat ctcacgtacc 1680

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ggtgtagctg gcgacccgaa taactacctg ttctgccggg tcagaaaaaa tggtgttgcc 1860

gcgccatctg ccaccagcca gctatcgacc gacgtcctga gaggggtttt tgcagccgcc 1920

caccgtctgg tctacggtac caaggatgac tctggtcagg ggtacctgac ctggtctgga 1980

cacagtgccc gcgtcggagc cgcgcgggat atggcccgcg ctggggtttc aatagcggag 2040

attatgcagg ctggtggctg gaccaccgta gagagcgtta tgagctatct ccgtaacctg 2100

gatagtgaga caggtgcaat ggtgcgcctg ctggaggatg gcgattag 2148

<210> 66
<211> 343

<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 66

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Met Ser Asn Leu Gln Thr Leu His Gln Asn Leu Ser Ala Leu Leu Ala
1               5                  10                  15


Asp Ala Thr Ser Asp Glu Thr Arg Lys Asn Leu Met Asp Val Leu Arg
            20                  25                  30


Asp Ser Gln Ala Phe Ser Glu Gln Thr Trp Lys Ser Leu Leu Phe Val
        35                  40                  45


Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Glu Trp Phe
    50                  55                  60


Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65                  70                  75                  80


Arg Gly Leu Ala Val Lys Thr Ile Gln Asn His Leu Gly Ser Leu Asn
                85                  90                  95


Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110


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


Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Ala Asp Phe Ser Arg
    130                 135                 140


Val Arg Ala Leu Met Glu Asn Ser Asp Arg Pro Gln Asp Ile Arg Asn
145                 150                 155                 160


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


Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190
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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Val Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Arg Gly Gly Val Ala Lys Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

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

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Pro Ile Val Gln Ile Met Gln Ala Gly Gly Trp Thr Thr Val Glu Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210> 67
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant DNA

<400> 67
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acctggaaat cactcctgtt cgtttgccgg tcgtgggcgg catggtgcga gctgaataac 180

cgggaatggt tccctgcgga acctgaagat gtccgcgatt atcttctgca ccttcaggcg 240

cgcggtctgg cagtaaaaac tatccagaac catttgggct cgctaaacat gctccaccgt 300

cggtccgggc tgccacggcc aggcgacagc aatgccgttt cactggttat gcgacgaatc 360

cgaaaagaaa acgttgatgc cggtgaacgt gcaaagcagg ccctggcgtt cgaacgcgcc 420

gacttcagcc gagttcgtgc gctcatggaa aatagcgatc gcccccagga tatacgtaat 480

ctggcctttc tgggggttgc ttataacacc ctgttacgca tatccgagat tgccaggatt 540

cgggttaagg acatctcacg tactgacggt gggagaatgt taatccacat cggcaggacg 600

aaaacgctgg tcagcaccgc aggcgtagag aaggcgctta gcctgggggt aaccaagctg 660

gtcgagcggt ggatctccgt ctctggtgta gtcgatgacc cgaataacta cctgttctgc 720

agggtcagac gaggtggtgt tgccaagcca tctgccacca gccagctatc aacttgcgcc 780

ctgcaaggga tttttgcagc cgcccaccgt ctgctctacg gtgccaagga tgactctggt 840

cagagatacc tggcctggtc tggacacagc gcccgcgtcg gggccgcgcg ggacatggcc 900

cgcgccgggg ttccaatagt gcagattatg caggctggtg gctggaccac cgtagagagt 960

gtcatgaact atatccgtaa cctggatagt gaaacaggag caatggtacg tctgctggag 1020

gacggcgatt ag 1032

<210> 68
<211> 343
<212> PRT
<213> Homo sapiens

<400> 68

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe

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    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270
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Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210> 69
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 69

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Met Ser Asn Leu Leu Thr Leu His His Ser Leu Pro Ala Leu Pro Ala
1               5                   10                  15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Val Phe Arg
            20                  25                  30

Asp Arg Pro Ala Phe Ser Glu His Thr Trp Glu Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Cys Arg Leu Asn
                85                  90                  95
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Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Thr Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Arg Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
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305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 70
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 70

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

Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Val Leu Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu Arg Thr Trp Lys Val Leu Leu Ser Val
35 40 45

Cys Arg Thr Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Asn Thr Ile Leu Gln His Leu Ala Gln Leu Asn
85 90 95

Met Leu His Arg Arg Phe Gly Leu Pro Arg Pro Gly Asp Ser Asp Ala
100 105 110

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

Glu Arg Thr Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln

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    130                 135                 140

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

Leu Ala Leu Leu Gly Val Ala Tyr Asn Thr Leu Leu Arg Val Ser Glu
                165                 170                 175

Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Ser Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Ser Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Gln Val Arg Ile Asn Gly Val Ala Val Pro Ser Ala Thr Ser Arg Leu
                245                 250                 255

Ser Thr Asp Val Leu Arg Lys Ile Phe Glu Ala Ala His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Gly Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Ala Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Glu Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210> 71
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Rcombinant protein

<400> 71

Met Ser Asn Leu Gln Ala Leu His Gln Asn Pro Ser Thr Leu Leu Ala
1 5 10 15

Asp Ala Thr Cys Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Ser Gln Ala Phe Ser Glu His Thr Trp Lys Ala Leu Gln Ser Val
35 40 45

Cys Arg Ser Trp Val Ala Trp Cys Lys Leu Asn Ser Arg Arg Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Thr
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
85 90 95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
100 105 110

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

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Ala Asp Leu Asp Gln
130 135 140

Val Arg Ala Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu Arg Ile Gly Glu
165 170 175

```
Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asp Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Leu Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Asp Asp Ser Leu Glu Gly Gly Ser Gly Gly Ser
            340                 345                 350

Thr Thr Lys Ala Asn Arg Ala Lys Gly Gly Arg Gly Gly Gly Ser Gly
        355                 360                 365

Gly Ser Met Tyr Met Ser Asp Leu Gln Thr Leu His Gln Asn Leu Ser
    370                 375                 380

Ala Leu Leu Val Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met
```

```
385                 390                 395                 400

Asp Val Phe Arg Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Asn Thr
                405                 410                 415

Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys Ser Asn Asn
            420                 425                 430

Arg Glu Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu
        435                 440                 445

His Leu Gln Val Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu
    450                 455                 460

Ala Leu Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly
465                 470                 475                 480

Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn
                485                 490                 495

Val Asp Ala Gly Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr
            500                 505                 510

Asp Phe Asp Gln Val Arg Ser Leu Met Gly Ser Ser Asp Arg Arg Asn
        515                 520                 525

Asp Ile Arg Asn Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu
    530                 535                 540

Arg Ile Ser Glu Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr
545                 550                 555                 560

Asp Gly Gly Arg Met Leu Val His Ile Gly Arg Thr Lys Thr Leu Val
                565                 570                 575

Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu
            580                 585                 590

Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn
        595                 600                 605
```

```
Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala
    610                 615                 620

Ser Ser Gln Leu Thr Thr Asp Val Leu Arg Gly Ile Phe Val Ala Ala
625                 630                 635                 640

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

Thr Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala
            660                 665                 670

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

Thr Val Glu Ser Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr
    690                 695                 700

Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
705                 710                 715
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<210> 72
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 72

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Met Ser Asn Ile Gln Thr Pro His Gln Ser Leu Ser Ala Leu Leu Thr
1               5                   10                  15

Asp Ala Thr Ser Asp Val Thr Arg Lys Asn Leu Ala Asp Met Phe Arg
            20                  25                  30

Asp Ser Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Lys Trp Leu
    50                  55                  60
```

```
Pro Val Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Thr
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ala Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Ala Gln Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Val Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Ala Lys Gly Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
```

```
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Pro Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Ser Asp Ser Leu Glu Gly Gly Ser Gly Gly Ser
            340                 345                 350

Thr Thr Lys Ala Asn Arg Ala Lys Gly Gly Arg Gly Gly Gly Ser Gly
        355                 360                 365

Gly Ser Met Tyr Met Ser Asn Leu Gln Thr Leu His Gln Asn Leu Ser
    370                 375                 380

Ala Leu Leu Ala Asn Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met
385                 390                 395                 400

Asp Val Phe Arg Asp Arg Arg Ala Phe Ser Glu Ala Thr Trp Lys Thr
                405                 410                 415

Leu Leu Ser Val Cys Arg Thr Trp Ala Ala Trp Cys Lys Leu Asn Asn
            420                 425                 430

Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu
        435                 440                 445

His Leu Gln Val Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu
    450                 455                 460

Ala Leu Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly
465                 470                 475                 480

Asp Ser Ser Ala Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn
                485                 490                 495
```

```
Val Asp Ala Gly Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr
            500                 505                 510

Asp Phe Asp Lys Val Arg Ser Leu Met Gly Asn Ser Asp Arg Cys Gln
        515                 520                 525

Asp Ile Arg Asn Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu
    530                 535                 540

Arg Ile Ser Glu Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr
545                 550                 555                 560

Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val
                565                 570                 575

Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu
            580                 585                 590

Val Gly Arg Trp Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn
        595                 600                 605

Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala
    610                 615                 620

Thr Ser Gln Leu Ser Thr Asp Val Leu Arg Gly Val Phe Ala Ala Ala
625                 630                 635                 640

His Arg Leu Val Tyr Gly Thr Lys Asp Asp Ser Gly Gln Gly Tyr Leu
                645                 650                 655

Thr Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala
            660                 665                 670

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

Thr Val Glu Ser Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr
    690                 695                 700

Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
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705 710 715

<210> 73
<211> 34
<212> DNA
<213> Homo sapiens

<400> 73
ataacttcgt ataatgtatg ctatacgaag ttat 34

<210> 74
<211> 32
<212> DNA
<213> Homo sapiens

<400> 74
taactttaaa taatgccaat tatttaaagt ta 32

<210> 75
<211> 34
<212> DNA
<213> Homo sapiens

<400> 75
tcaatttctg agaatgacag ttctcggaaa ttga 34

<210> 76
<211> 34
<212> DNA
<213> Homo sapiens

<400> 76
ctcgtgtccg ataactgtaa ttatcggaca tgat 34

<210> 77
<211> 34
<212> DNA
<213> Homo sapiens

<400> 77
aataggtctg agaatgggcg ttctcagacg tatt 34

<210> 78
<211> 21
<212> DNA
<213> Homo sapiens

<400> 78

cagctttttt atactaagtt g 21

<210> 79
<211> 34
<212> DNA
<213> Homo sapiens

<400> 79
gaagttccta tactttctag agaataggaa cttc 34

<210> 80
<211> 31
<212> DNA
<213> Homo sapiens

<400> 80
ttgatgaaag aataacgtat tctttcatca a 31

<210> 81
<211> 43
<212> DNA
<213> Homo sapiens

<400> 81
acgaaaaatg gtaaggaata gaccattcct taccattttt cgt 43

<210> 82
<211> 61
<212> DNA
<213> Homo sapiens

<400> 82
aaacgatatc agacatttgt ctgataatgc ttcattatca gacaaatgtc tgatatcgtt 60

t 61

<210> 83
<211> 39
<212> DNA
<213> Homo sapiens

<400> 83
gagtttcatt aaggaataac taattcccta atgaaactc 39

<210> 84
<211> 33
<212> DNA
<213> Homo sapiens

<400> 84
ggttgcttaa gaataagtaa ttcttaagca acc 33

<210> 85
<211> 34
<212> DNA
<213> Homo sapiens

<400> 85
tgaatgtcct ataattacac ttataggaca ttca 34

<210> 86
<211> 34
<212> DNA
<213> Homo sapiens

<400> 86
gaaactttaa ataataagtc ttatttaaag tttc 34

<210> 87
<211> 34
<212> DNA
<213> Homo sapiens

<400> 87
ataaatatgt gtgtatatat acacacaaac atat 34

<210> 88
<211> 34
<212> DNA
<213> Homo sapiens

<400> 88
atatatctgt gtatatatat acacacacac atat 34

<210> 89
<211> 34
<212> DNA
<213> Homo sapiens

<400> 89
atatatatgt gtatatatat acacacatac atat 34

<210> 90
<211> 34
<212> DNA
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<400> 90
atatatgtgt gtatatatat acacacacac atac 34

<210> 91
<211> 34
<212> DNA
<213> Homo sapiens

<400> 91
ataaatatgt gtaaactaaa caacacactc ttaa 34

<210> 92
<211> 34
<212> DNA
<213> Homo sapiens

<400> 92
acaaatatgt ggaaactaaa caacacattc ttga 34

<210> 93
<211> 343
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant protein

<400> 93

Met Ser Ser Leu Gln Thr Leu His Gln Asn Leu Ser Ala Leu Leu Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Ala Arg Glu Asn Leu Ile Gly Gly Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Lys Thr Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Ser Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Val
65 70 75 80

Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu Ala Leu Leu Asn

```
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Val Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Arg
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Glu Ala Leu Ser Leu Gly Val Thr Arg Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

Thr Thr Asp Val Leu Arg Gly Ile Phe Val Ala Ala His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Arg Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300
```

```
Ser Ile Ala Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Glu Ser
305                 310                 315                 320


Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335


Arg Leu Leu Glu Asp Gly Asp
            340


<210>  94
<211>  343
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant protein

<400>  94

Met Ser Ser Leu Pro Thr Leu His Gln Ser Leu Ser Ala Leu Leu Val
1               5                   10                  15


Asp Ala Ala Ser Gly Glu Val Arg Thr Asn Leu Met Val Met Phe Arg
            20                  25                  30


Asp Ser Gln Ala Phe Ser Val His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45


Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60


Pro Ala Asp Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65                  70                  75                  80


Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asp
                85                  90                  95


Met Leu His Arg Arg Ala Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110


Val Ser Leu Val Met Arg Arg Ile Arg Arg Ala Asn Val Asp Ala Gly
        115                 120                 125
```

```
Glu Arg Ala Gly Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Val Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Ala
    290                 295                 300

Ser Leu Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Ser Asp
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340

<210> 95
<211> 1032
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant polynucleotide

<400> 95
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acctggaaga cgcttctgtc cgtttgccgg tcgtgggcag catggtgcaa gttgaatagc 180

cggaaatggt ttcccgcaga gcctgaagat gttcgcgatt atcttctaca tctccaggtt 240

cgcggtctgg ctgtaaacac tatccagcga catctggccc tgctaaacat gctacaccgt 300

cggtccgggc tgccacgacc aggtgacagc aacgctgttt cactggttat gcggcgtatc 360

cgaaaagaaa acgttgatgc cggtgagcgt gtaaaacagg ctctggcgtt cgaacgcact 420

gatttcgacc gggttcgttc actcatggaa aatagcgacc gctgccagga tatacgtaat 480

ctggcattcc tgggggttgc ttataacacc ctgttacgtg tatccgaaat cgccaggatt 540

cgggtaaaag atatctctcg tactgacggt gggagaatgt taatccatat tggcagaacg 600

aaaacgctgg ttagcaccgc aggcgtggag gaggcactta gcctgggggt aaccagactg 660

gtcgagcggt ggatttccgt ctctggtgtg gctggtgacc cgaataacta cctgttttgc 720

cgggtcagaa agaacggtgt cgccgcgcca tctgccacca gccagctaac aaccgatgtc 780

ctgcgaggga tttttgtagc cgcccaccgt ctgatctacg gtgccaggga tgactctggt 840

cagagatacc tggcctggtc tggacacagt gcccgcgtcg gagccgcgcg ggatatggcc 900

cgcgctggag tctcaatagc ggagattatg caggctggtg gctggaccac cgtagagagt 960

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gatggtgact ag 1032

<210> 96
<211> 1032
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant polynucleotide

<400> 96
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ggcgaggttc gcacgaacct gatggtcatg ttcagggata gccaggcgtt ttctgtgcat 120

acctggaaaa tgcttctgtc cgtttgccgg tcgtgggcgg catggtgcga gctgaacaac 180

cggaaatggt ttcccgcaga ccctgaagat gttcgcgatt atctcctaca ccttcaggcg 240

cgcggtctgg cagtaaaaac tatccagcat catttaggct cgctggacat gcttcatcgc 300

cgggccgggc tgccacgacc aggtgacagc aacgctgtct cactggttat gcggcgcatc 360

cgaagagcaa acgttgatgc cggcgaacgt gcagggcagg ccctggcgtt cgaacgcact 420

gacttcgacc aggttcgttc actcatggaa aatagcgatc gctgccagga tatacgtaac 480

ctggcattcc tgggggtcgc ttacaacacc ctgttacgta tatccgaaat tgccaggatc 540

cgggttagag atatctcacg tactgacggt gggaggatgt taatccacat cggcagaacg 600

aaaacgctgg tcagcaccgc aggtgtagag aaggcactta gcctgggagt aactaaactg 660

gtcgagcggt ggatctccgt ctctggtgta gctgatgatc caaataacta cctgttttgc 720

cgggtcagaa gatatggtgt tgccaagcca tctgccacca gccagctatc aacttacgcc 780

ctgcaaggga tttttggagc cgcccaccgc ctggtctacg gtgtcaagga tgactctggt 840

cagaagtacc tggcctggtc cggacacagt gcccgcgtcg gagccgcgcg agatatggcc 900

cgcgctggag cttcactacc ggagattatg caggctggtg gctggaccac tgtaaacagt 960

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gatagcgatt ag 1032

<210> 97
<211> 715
<212> PRT
<213> Artificial seqeunce

<220>
<223> Recombinant protein

<400> 97

Met Ser Ser Leu Pro Thr Leu His Gln Ser Leu Ser Ala Leu Leu Val
1   5   10   15

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Asp Ala Ala Ser Gly Glu Val Arg Thr Asn Leu Met Val Met Phe Arg
            20                  25                  30

Asp Ser Gln Ala Phe Ser Val His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Asp Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asp
                85                  90                  95

Met Leu His Arg Arg Ala Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Arg Ala Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Gly Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
```

```
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Val Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Ala
    290                 295                 300

Ser Leu Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Ser Asp Ser Leu Glu Gly Gly Ser Gly Gly Ser
            340                 345                 350

Thr Thr Lys Ala Asn Arg Ala Lys Gly Gly Arg Gly Gly Gly Ser Gly
        355                 360                 365

Gly Ser Met Tyr Met Ser Ser Leu Gln Thr Leu His Gln Asn Leu Ser
    370                 375                 380

Ala Leu Leu Val Asp Ala Thr Ser Asp Glu Ala Arg Glu Asn Leu Ile
385                 390                 395                 400

Gly Gly Phe Arg Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Lys Thr
                405                 410                 415

Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Ser
            420                 425                 430

Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu
        435                 440                 445
```

```
His Leu Gln Val Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu
    450                 455                 460

Ala Leu Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly
465                 470                 475                 480

Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn
                485                 490                 495

Val Asp Ala Gly Glu Arg Val Lys Gln Ala Leu Ala Phe Glu Arg Thr
            500                 505                 510

Asp Phe Asp Arg Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln
        515                 520                 525

Asp Ile Arg Asn Leu Ala Phe Leu Gly Val Ala Tyr Asn Thr Leu Leu
    530                 535                 540

Arg Val Ser Glu Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr
545                 550                 555                 560

Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val
                565                 570                 575

Ser Thr Ala Gly Val Glu Glu Ala Leu Ser Leu Gly Val Thr Arg Leu
            580                 585                 590

Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Gly Asp Pro Asn Asn
        595                 600                 605

Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala
    610                 615                 620

Thr Ser Gln Leu Thr Thr Asp Val Leu Arg Gly Ile Phe Val Ala Ala
625                 630                 635                 640

His Arg Leu Ile Tyr Gly Ala Arg Asp Asp Ser Gly Gln Arg Tyr Leu
                645                 650                 655

Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala
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660 665 670

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

Thr Val Glu Ser Val Met Ser Tyr Leu Arg Asn Leu Asp Ser Glu Thr
690 695 700

Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
705 710 715

<210> 98
<211> 2148
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant polynucleotide

<400> 98
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acctggaaaa tgcttctgtc cgtttgccgg tcgtgggcgg catggtgcga gctgaacaac 180

cggaaatggt ttcccgcaga ccctgaagat gttcgcgatt atctcctaca ccttcaggcg 240

cgcggtctgg cagtaaaaac tatccagcat catttaggct cgctggacat gcttcatcgc 300

cgggccgggc tgccacgacc aggtgacagc aacgctgtct cactggttat gcggcgcatc 360

cgaagagcaa acgttgatgc cggcgaacgt gcagggcagg ccctggcgtt cgaacgcact 420

gacttcgacc aggttcgttc actcatggaa aatagcgatc gctgccagga tatacgtaac 480

ctggcattcc tgggggtcgc ttacaacacc ctgttacgta tatccgaaat tgccaggatc 540

cgggttagag atatctcacg tactgacggt gggaggatgt taatccacat cggcagaacg 600

aaaacgctgg tcagcaccgc aggtgtagag aaggcactta gcctgggagt aactaaactg 660

gtcgagcggt ggatctccgt ctctggtgta gctgatgatc caaataacta cctgttttgc 720

cgggtcagaa gatatggtgt tgccaagcca tctgccacca gccagctatc aacttacgcc 780

ctgcaaggga tttttggagc cgcccaccgc ctggtctacg gtgtcaagga tgactctggt 840

cagaagtacc tggcctggtc cggacacagt gcccgcgtcg gagccgcgcg agatatggcc 900

cgcgctggag cttcactacc ggagattatg caggctggtg gctggaccac tgtaaacagt 960

gtcatgaact atatccgtaa cctggatagc gaaacaggag caatggtacg cttgctggaa 1020

gatagcgatt cgctcgaggg cggtagcggt ggctctacca ccaaagcaaa cagagcaaaa 1080

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ggtgggttca gggaccgcca ggcgttttct gaggctacct ggaagacgct tctgtccgtt 1260

tgccggtcgt gggcagcatg gtgcaagttg aatagccgga aatggtttcc cgcagagcct 1320

gaagatgttc gcgattatct tctacatctc caggttcgcg gtctggctgt aaacactatc 1380

cagcgacatc tggccctgct aaacatgcta caccgtcggt ccgggctgcc acgaccaggt 1440

gacagcaacg ctgtttcact ggttatgcgg cgtatccgaa aagaaaacgt tgatgccggt 1500

gagcgtgtaa aacaggctct ggcgttcgaa cgcactgatt tcgaccgggt tcgttcactc 1560

atggaaaata gcgaccgctg ccaggatata cgtaatctgg cattcctggg ggttgcttat 1620

aacaccctgt tacgtgtatc cgaaatcgcc aggattcggg taaaagatat ctctcgtact 1680

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caccgtctga tctacggtgc cagggatgac tctggtcaga gatacctggc ctggtctgga 1980

cacagtgccc gcgtcggagc cgcgcgggat atggcccgcg ctggagtctc aatagcggag 2040

attatgcagg ctggtggctg gaccaccgta gagagtgtca tgagctacct ccgtaacctg 2100

gatagtgaga cgggggcaat ggtgcgcctg ctggaggatg gtgactag 2148

<210> 99
<211> 343
<212> PRT
<213> Artificial squence

<220>
<223> Recombinant protein

<400> 99

Met Ser Asn Leu Gln Thr Ile His Gln Asn Leu Thr Ala Ser Leu Ala

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Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Val Leu Arg
            20                  25                  30

Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Lys Thr Leu Leu Ser Val
        35                  40                  45

Cys Arg Thr Trp Ala Ala Trp Cys Lys Ser Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Val
65                  70                  75                  80

Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu Ala Leu Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr Asp Leu Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Gly Asp Ser Asp Arg Cys Lys Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu Val Glu Arg Trp
    210                 215                 220
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Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Val Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Asp Val Leu Arg Gly Ile Phe Ala Thr Ala His Arg Leu Val
260 265 270

Tyr Gly Ala Arg Asp Gly Ser Gly Gln Arg Phe Leu Thr Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Ala Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Gly Ser
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 100
<211> 343
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant protein

<400> 100

Met Ser Asp Leu Gln Thr Leu His Gln Lys Leu Ser Ala Leu Leu Ala
1 5 10 15

Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Met Leu Arg
20 25 30

Asp Trp Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

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Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Ser Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
            100                 105                 110

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

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Leu Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Glu Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asp Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
```

260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Pro Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Gly Ser
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 101
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant polynucleotide

<400> 101
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acctggaaga cgctcctgtc cgtttgccgg acgtgggcag catggtgcaa gtcgaataac 180

cggaaatggt ttcccgcaga acctgaagat gttcgcgatt atcttctgca tctccaggta 240

cgcggtctgg cagtaaacac tatccagcga catctggccc tgctaaacat gcttcaccgt 300

cggtccgggc tgccacgacc aggtgacagc aatgctgttt cactggttat gcggcgaatc 360

cgaaaagaaa acgttgatgc cggtgaacgc gtaagacagg ccctggcgtt cgaacgcact 420

gatctcgacc aggttcgttc actcatggga gatagcgatc ggtgcaagga tatacgtaat 480

ctggcatttc cgggggttgc ttataacacc ctgttacgta tatccgaaat cgccaggatt 540

cggataaaag atatctcacg tactgacggt gggaggatgc ttatccatat tggcagaacg 600

aaaacgctgg ttagcaccgc aggcgtggag aaggcactaa gcctgggggt gaccagactg 660

gtcgagcgat ggatttccgt ctctggcgta gctgacgatc cgaataacta cctgttttgc 720

cgggtcagaa aaaatggtgt tgccgtgcca tctgccacca gccagctgtc gaccgacgtc 780

ctgcgaggga tttttgcgac cgcccaccgt ctggtctacg gtgccaggga tggctctggt 840

cagagattcc tgacctggtc tggacacagt gcccgcgtcg gagccgcgcg ggatatggcc 900

cgcgctgggg tttcaatagc ggagattatg caggctggtg gctggaccac cgtaggtagt 960

gtcatgaact atatccgtaa cctggacagc gaaacgggag cgatggtgcg cctgctggaa 1020

gatggcgatt ag 1032

<210> 102
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant polynucleotide

<400> 102
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acctggaaaa tgctcctgtc cgtttgccgg tcgtgggcgg catggtgcga gttgaatagc 180

cggaaatggt ttcccgcgga acctgaagat gttcgcgatt atcttctgta tcttcaggcg 240

cgaggcctgg cagtaaagac tatccagcac catctgggct cgctgaacat gcttcaccgc 300

cggtctgggc tgccacgacc aggtgacagc aatgccgttt cactggttat gcggcgaatc 360

cgaaaagaaa acgttgatgc cggtgaacgt gcgaaacagg ctctggcgtt cgagcgcact 420

gatttcgacc aggttcgctt actcatggaa aacagcgatc gctgccagga tatacgtaac 480

ctggcgtttc tggggattgc ttataacacc ctgttacgta tatccgaaat tgccaggatc 540

cgggtcagag atatctcacg tactgacggt gggagaatgt tgatccatat tggcaggacg 600

aaaacgctgg ttagcaccgc aggtgtagag gaggcgctta gcctgggggt gaccaaactg 660

gtcgagcggt ggatttctgt ctccggtgta gccgatgacc cggataacta cctgttttgc 720

cgggtcagaa gatacggtgt tgccaagcca tctgccacca gccagctatc aacctacgct 780

ctgcaaggga tttttggggc tgcccaccgt ctggtctacg gtgccaagga tgactctgga 840

cagaaatacc tggcctggtc tggacacagt gcccgtgtcg gggccgcgcg ggatatggcc 900

cgcgctggag ttccaatacc ggagattatg caggctggtg gctggaccac cgtaggtagt 960

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gatggcgatt ag 1032

<210> 103
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 103

Met Ser Asp Leu Gln Thr Leu His Gln Lys Leu Ser Ala Leu Leu Ala
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Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Met Leu Arg
20 25 30

Asp Trp Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Ser Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln His His Leu Gly Ser Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
100 105 110

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

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Leu Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn

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145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Arg Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Glu Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asp Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr Tyr Ala Leu Gln Gly Ile Phe Gly Ala Ala His Arg Leu Val
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Lys Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Pro Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Thr Val Gly Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp Ser Leu Glu Gly Gly Ser Gly Gly Ser
            340                 345                 350

Thr Thr Lys Ala Asn Arg Ala Lys Gly Gly Arg Gly Gly Gly Ser Gly
        355                 360                 365
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Gly Ser Met Tyr Met Ser Asn Leu Gln Thr Ile His Gln Asn Leu Thr
    370                 375                 380

Ala Ser Leu Ala Asp Ala Thr Ser Asp Glu Ala Arg Lys Asn Leu Met
385                 390                 395                 400

Asp Val Leu Arg Asp Arg Gln Ala Phe Ser Glu Ala Thr Trp Lys Thr
                405                 410                 415

Leu Leu Ser Val Cys Arg Thr Trp Ala Ala Trp Cys Lys Ser Asn Asn
            420                 425                 430

Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu
        435                 440                 445

His Leu Gln Val Arg Gly Leu Ala Val Asn Thr Ile Gln Arg His Leu
    450                 455                 460

Ala Leu Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly
465                 470                 475                 480

Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn
                485                 490                 495

Val Asp Ala Gly Glu Arg Val Arg Gln Ala Leu Ala Phe Glu Arg Thr
            500                 505                 510

Asp Leu Asp Gln Val Arg Ser Leu Met Gly Asp Ser Asp Arg Cys Lys
        515                 520                 525

Asp Ile Arg Asn Leu Ala Phe Pro Gly Val Ala Tyr Asn Thr Leu Leu
    530                 535                 540

Arg Ile Ser Glu Ile Ala Arg Ile Arg Ile Lys Asp Ile Ser Arg Thr
545                 550                 555                 560

Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val
                565                 570                 575

Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val Thr Arg Leu
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            580                 585                 590

Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn
        595                 600                 605

Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Val Pro Ser Ala
    610                 615                 620

Thr Ser Gln Leu Ser Thr Asp Val Leu Arg Gly Ile Phe Ala Thr Ala
625                 630                 635                 640

His Arg Leu Val Tyr Gly Ala Arg Asp Gly Ser Gly Gln Arg Phe Leu
                645                 650                 655

Thr Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala
            660                 665                 670

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

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

Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
705                 710                 715
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<210> 104
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant polynucleotide

<400> 104
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cggaaatggt ttcccgcgga acctgaagat gttcgcgatt atcttctgta tcttcaggcg 240

cgaggcctgg cagtaaagac tatccagcac catctgggct cgctgaacat gcttcaccgc 300

cggtctgggc tgccacgacc aggtgacagc aatgccgttt cactggttat gcggcgaatc 360

cgaaaagaaa acgttgatgc cggtgaacgt gcgaaacagg ctctggcgtt cgagcgcact 420

gatttcgacc aggttcgctt actcatggaa aacagcgatc gctgccagga tatacgtaac 480

ctggcgtttc tggggattgc ttataacacc ctgttacgta tatccgaaat tgccaggatc 540

cgggtcagag atatctcacg tactgacggt gggagaatgt tgatccatat tggcaggacg 600

aaaacgctgg ttagcaccgc aggtgtagag gaggcgctta gcctgggggt gaccaaactg 660

gtcgagcggt ggatttctgt ctccggtgta gccgatgacc cggataacta cctgttttgc 720

cgggtcagaa gatacggtgt tgccaagcca tctgccacca gccagctatc aacctacgct 780

ctgcaaggga tttttggggc tgcccaccgt ctggtctacg gtgccaagga tgactctgga 840

cagaaatacc tggcctggtc tggacacagt gcccgtgtcg gggccgcgcg ggatatggcc 900

cgcgctggag ttccaatacc ggagattatg caggctggtg gctggaccac cgtaggtagt 960

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ggcggcagag gaggtggtag tggcggcagc atgtacatgt ccaatttaca gaccatacac 1140

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gacgtgctca gggaccgcca ggcgttctct gaggctacct ggaagacgct cctgtccgtt 1260

tgccggacgt gggcagcatg gtgcaagtcg aataaccgga aatggtttcc cgcagaacct 1320

gaagatgttc gcgattatct tctgcatctc caggtacgcg gtctggcagt aaacactatc 1380

cagcgacatc tggccctgct aaacatgctt caccgtcggt ccgggctgcc acgaccaggt 1440

gacagcaatg ctgtttcact ggttatgcgg cgaatccgaa aagaaaacgt tgatgccggt 1500

gaacgcgtaa gacaggccct ggcgttcgaa cgcactgatc tcgaccaggt tcgttcactc 1560

atgggagata gcgatcggtg caaggatata cgtaatctgg catttccggg ggttgcttat 1620

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caccgtctgg tctacggtgc cagggatggc tctggtcaga gattcctgac ctggtctgga 1980

cacagtgccc gcgtcggagc cgcgcgggat atggcccgcg ctggggtttc aatagcggag 2040

attatgcagg ctggtggctg gaccaccgta ggtagtgtca tgaactatat ccgtaacctg 2100

gacagcgaaa cgggagcgat ggtgcgcctg ctggaagatg gcgattag 2148

<210> 105
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant protein

<400> 105

Met Ser Asn Leu Leu Thr Leu His His Ser Leu Ser Ala Leu Leu Ala
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Asp Ala Ala Ser Asp Glu Ala Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Phe Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65 70 75 80

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

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
100 105 110

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

Glu Arg Val Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

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Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

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

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Cys Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

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

Ser Thr His Ala Leu Gln Arg Ile Phe Glu Ala Ala His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Pro Glu Val Met Gln Ala Gly Gly Trp Thr Thr Val Asn Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210> 106

<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant Protein

<400> 106

Met Ser Asn Leu Leu Thr Leu His Gln Asn Leu Thr Ala Leu Leu Val
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Asp Ala Thr Ser Asp Glu Val Arg Lys Asp Leu Met Asp Val Leu Arg
20 25 30

Asp Ser Gln Ala Phe Ser Glu His Thr Trp Arg Val Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Glu Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu His Leu Gln Ala
65 70 75 80

Arg Gly Leu Thr Val Asn Thr Ile Gln Gln His Leu Ala Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Gly Asp Ser Asn Ala
100 105 110

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

Glu Arg Val Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asp Ser Asp Arg Cys Gln Asp Val Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Val Ala Tyr Ser Thr Leu Leu Arg Val Ser Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg

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            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Arg Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asp Asn Tyr Leu Phe Cys
225                 230                 235                 240

Gln Val Arg Arg Ser Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

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

Tyr Gly Ala Lys Asp Gly Ser Gly Gln Arg Tyr Leu Thr Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Val Ala Glu Ile Met Gln Ala Gly Gly Trp Ile Thr Val Glu Ser
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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