SEQUENCE LISTING

<110> CHONGQING PRECISION BIOTECH COMPANY LIMITED.
CHONGQING PRECISION BIOLOGICAL INDUSTRIAL TECHNOLOGY RESEARCH INSTITUTE CO., LTD.

<120> FUSION PROTEIN FOR REVERSING TUMOR MICROENVIRONMENT AND USE THEREOF

<130> TFF00685

<160> 38

<170> PatentIn version 3.5

<210> 1
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 1

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Met Pro Val Pro Ala Ser Trp Pro His Pro Pro Gly Pro Phe Leu Leu
1               5                  10                  15

Leu Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu Leu
            20                  25                  30

Gln Met Ile Gln Pro Glu Lys Leu Leu Leu Val Thr Val Gly Lys Thr
        35                  40                  45

Ala Thr Leu His Cys Thr Val Thr Ser Leu Leu Pro Val Gly Pro Val
    50                  55                  60

Leu Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln
65                  70                  75                  80

Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu Thr Lys
                85                  90                  95

Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro Ala
            100                 105                 110

Asp Val Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Glu
        115                 120                 125
```

```
Asn Val Glu Phe Lys Ser Gly Pro Gly Thr Glu Met Ala Leu Gly Ala
    130                 135                 140

Lys Pro Ser Ala Pro Val Val Leu Gly Pro Ala Ala Arg Thr Thr Pro
145                 150                 155                 160

Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg
                165                 170                 175

Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe
            180                 185                 190

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

Ser Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln Val
    210                 215                 220

Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg Gly
225                 230                 235                 240

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

Thr Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys Gln
            260                 265                 270

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

Gly Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn Lys
    290                 295                 300

Asp Gly Thr Tyr Asn Trp Thr Ser Trp Phe Leu Val Asn Ile Ser Asp
305                 310                 315                 320

Gln Arg Asp Asp Val Val Leu Thr Cys Gln Val Lys His Asp Gly Gln
                325                 330                 335

Leu Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln Lys
            340                 345                 350
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Asp Gln Ser Ser Asp Ala Thr Pro Leu Glu
355 360

<210> 2
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 2

Met Pro Val Pro Ala Ser Trp Pro His Pro Pro Gly Pro Phe Leu Leu
1 5 10 15

Leu Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu Leu
20 25 30

Gln Met Ile Gln Pro Glu Lys Leu Leu Leu Val Thr Val Gly Lys Thr
35 40 45

Ala Thr Leu His Cys Thr Val Thr Ser Leu Leu Pro Val Gly Pro Val
50 55 60

Leu Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln
65 70 75 80

Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu Thr Lys
85 90 95

Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro Ala
100 105 110

Asp Val Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Glu
115 120 125

Asn Val Glu Phe Lys Ser Gly Pro Gly Thr Glu Met Ala Leu Gly Ala
130 135 140

Lys Pro Ser Ala Pro Val Val Leu Gly Pro Ala Ala Arg Thr Thr Pro
145 150 155 160

Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg

```
                165                 170                 175

Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe
            180                 185                 190

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

Ser Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln Val
    210                 215                 220

Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg Gly
225                 230                 235                 240

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

Thr Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys Gln
            260                 265                 270

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

Gly Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn Lys
    290                 295                 300

Asp Gly Thr Tyr Asn Trp Thr Ser Trp Phe Leu Val Asn Ile Ser Asp
305                 310                 315                 320

Gln Arg Asp Asp Val Val Leu Thr Cys Gln Val Lys His Asp Gly Gln
                325                 330                 335

Leu Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln Lys
            340                 345                 350

Asp Gln Ser Ser Asp Ala Thr Pro Leu Glu Phe Trp Val Leu Val Val
        355                 360                 365

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

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
```

385 390 395 400

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
405 410 415

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
420 425 430

<210> 3
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 3

Met Pro Val Pro Ala Ser Trp Pro His Pro Pro Gly Pro Phe Leu Leu
1 5 10 15

Leu Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu Leu
20 25 30

Gln Met Ile Gln Pro Glu Lys Leu Leu Leu Val Thr Val Gly Lys Thr
35 40 45

Ala Thr Leu His Cys Thr Val Thr Ser Leu Leu Pro Val Gly Pro Val
50 55 60

Leu Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln
65 70 75 80

Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu Thr Lys
85 90 95

Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro Ala
100 105 110

Asp Val Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Glu
115 120 125

Asn Val Glu Phe Lys Ser Gly Pro Gly Thr Glu Met Ala Leu Gly Ala
130 135 140

```
Lys Pro Ser Ala Pro Val Val Leu Gly Pro Ala Ala Arg Thr Thr Pro
145                 150                 155                 160

Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg
                165                 170                 175

Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe
            180                 185                 190

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

Ser Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln Val
    210                 215                 220

Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg Gly
225                 230                 235                 240

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

Thr Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys Gln
            260                 265                 270

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

Gly Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn Lys
    290                 295                 300

Asp Gly Thr Tyr Asn Trp Thr Ser Trp Phe Leu Val Asn Ile Ser Asp
305                 310                 315                 320

Gln Arg Asp Asp Val Val Leu Thr Cys Gln Val Lys His Asp Gly Gln
                325                 330                 335

Leu Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln Lys
            340                 345                 350

Asp Gln Ser Ser Asp Ala Thr Pro Leu Glu Ile Tyr Ile Trp Ala Pro
        355                 360                 365
```

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
370 375 380

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
385 390 395 400

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
405 410 415

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
420 425

<210> 4
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 4

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
35 40 45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser
100 105 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser

```
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
                245                 250                 255

Gly Ser Thr Val Thr Val Ser Ser Gly Ala Ala Ala Leu Glu Lys Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Glu Phe Ile
305                 310                 315                 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
                325                 330                 335

Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp
```

```
            340                 345                 350

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
        355                 360                 365

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
    370                 375                 380

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
385                 390                 395                 400

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
                405                 410                 415

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
            420                 425                 430

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
        435                 440                 445

Met Gln Ala Leu Pro Pro Arg
    450                 455
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<210> 5
<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 5

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
            20                  25                  30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
        35                  40                  45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60
```

```
Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser
            100                 105                 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
                245                 250                 255

Gly Ser Thr Val Thr Val Ser Ser Gly Ala Ala Ala Leu Glu Lys Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285
```

```
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Glu Phe Ile
305                 310                 315                 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
                325                 330                 335

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

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
        355                 360                 365

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
    370                 375                 380

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
385                 390                 395                 400

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
                405                 410                 415

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
            420                 425                 430

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
        435                 440                 445

Met Gln Ala Leu Pro Pro Arg Val Asp Gly Ser Gly Ala Thr Asn Phe
    450                 455                 460

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Ser
465                 470                 475                 480

Arg Met Pro Val Pro Ala Ser Trp Pro His Pro Pro Gly Pro Phe Leu
                485                 490                 495

Leu Leu Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu
            500                 505                 510
```

```
Leu Gln Met Ile Gln Pro Glu Lys Leu Leu Leu Val Thr Val Gly Lys
        515                 520                 525

Thr Ala Thr Leu His Cys Thr Val Thr Ser Leu Leu Pro Val Gly Pro
    530                 535                 540

Val Leu Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn
545                 550                 555                 560

Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu Thr
                565                 570                 575

Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro
            580                 585                 590

Ala Asp Val Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro
        595                 600                 605

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

Ala Lys Pro Ser Ala Pro Val Val Leu Gly Pro Ala Ala Arg Thr Thr
625                 630                 635                 640

Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
                645                 650                 655

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
            660                 665                 670

Phe Gln Thr Asn Val Asp Pro Thr Gly Gln Ser Val Ala Tyr Ser Ile
        675                 680                 685

Arg Ser Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln
    690                 695                 700

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
705                 710                 715                 720

Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu
                725                 730                 735
```

```
Val Thr Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys
            740                 745                 750

Gln Val Arg Lys Phe Tyr Pro Gln Ser Leu Gln Leu Thr Trp Ser Glu
        755                 760                 765

Asn Gly Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn
    770                 775                 780

Lys Asp Gly Thr Tyr Asn Trp Thr Ser Trp Phe Leu Val Asn Ile Ser
785                 790                 795                 800

Asp Gln Arg Asp Asp Val Val Leu Thr Cys Gln Val Lys His Asp Gly
                805                 810                 815

Gln Leu Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln
            820                 825                 830

Lys Asp Gln Ser Ser Asp Ala Thr Pro Leu Glu Phe Trp Val Leu Val
        835                 840                 845

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
    850                 855                 860

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
865                 870                 875                 880

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
                885                 890                 895

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
            900                 905                 910
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<210> 6
<211> 907
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 6

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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1               5                   10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
            20                  25                  30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
        35                  40                  45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser
            100                 105                 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
```

225 230 235 240

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
245 250 255

Gly Ser Thr Val Thr Val Ser Ser Gly Ala Ala Ala Leu Glu Lys Pro
260 265 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
275 280 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
290 295 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Glu Phe Ile
305 310 315 320

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
325 330 335

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

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
355 360 365

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
370 375 380

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
385 390 395 400

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
405 410 415

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
420 425 430

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
435 440 445

Met Gln Ala Leu Pro Pro Arg Val Asp Gly Ser Gly Ala Thr Asn Phe

```
    450                 455                 460

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
465                 470                 475                 480

Pro Val Pro Ala Ser Trp Pro His Pro Pro Gly Pro Phe Leu Leu Leu
                485                 490                 495

Thr Leu Leu Leu Gly Leu Thr Glu Val Ala Gly Glu Glu Glu Leu Gln
            500                 505                 510

Met Ile Gln Pro Glu Lys Leu Leu Leu Val Thr Val Gly Lys Thr Ala
        515                 520                 525

Thr Leu His Cys Thr Val Thr Ser Leu Leu Pro Val Gly Pro Val Leu
    530                 535                 540

Trp Phe Arg Gly Val Gly Pro Gly Arg Glu Leu Ile Tyr Asn Gln Lys
545                 550                 555                 560

Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu Thr Lys Arg
                565                 570                 575

Asn Asn Met Asp Phe Ser Ile Arg Ile Ser Ser Ile Thr Pro Ala Asp
            580                 585                 590

Val Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Glu Asn
        595                 600                 605

Val Glu Phe Lys Ser Gly Pro Gly Thr Glu Met Ala Leu Gly Ala Lys
    610                 615                 620

Pro Ser Ala Pro Val Val Leu Gly Pro Ala Ala Arg Thr Thr Pro Glu
625                 630                 635                 640

His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg Asp
                645                 650                 655

Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe Gln
            660                 665                 670

Thr Asn Val Asp Pro Thr Gly Gln Ser Val Ala Tyr Ser Ile Arg Ser
```

675 680 685

Thr Ala Arg Val Val Leu Asp Pro Trp Asp Val Arg Ser Gln Val Ile
690 695 700

Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg Gly Thr
705 710 715 720

Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu Val Thr
725 730 735

Gln Gln Pro Met Arg Val Gly Asn Gln Val Asn Val Thr Cys Gln Val
740 745 750

Arg Lys Phe Tyr Pro Gln Ser Leu Gln Leu Thr Trp Ser Glu Asn Gly
755 760 765

Asn Val Cys Gln Arg Glu Thr Ala Ser Thr Leu Thr Glu Asn Lys Asp
770 775 780

Gly Thr Tyr Asn Trp Thr Ser Trp Phe Leu Val Asn Ile Ser Asp Gln
785 790 795 800

Arg Asp Asp Val Val Leu Thr Cys Gln Val Lys His Asp Gly Gln Leu
805 810 815

Ala Val Ser Lys Arg Leu Ala Leu Glu Val Thr Val His Gln Lys Asp
820 825 830

Gln Ser Ser Asp Ala Thr Pro Leu Glu Ile Tyr Ile Trp Ala Pro Leu
835 840 845

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
850 855 860

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
865 870 875 880

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
885 890 895

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu

900 905

<210> 7
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 7

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 8
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 8

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 9
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 9

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 10
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 10

Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
1 5 10 15

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
20 25 30

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
35 40

<210> 11
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 11

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
1 5 10 15

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
20 25 30

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
35 40 45

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
50 55 60

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
65 70 75 80

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

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 12
<211> 1086
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 12
atgcctgtcc cagcctcctg gccccatcct cctggtcctt tcctgcttct gactctactg
60

ctgggactta cagaagtggc aggtgaggag gagctacaga tgattcagcc tgagaagctc
120

ctgttggtca cagttggaaa gacagccact ctgcactgca ctgtgacctc cctgcttccc
180

gtgggacccg tcctgtggtt cagaggagtt ggaccaggcc gggaattaat ctacaatcaa
240

aaagaaggcc acttccccag ggtaacaaca gtttcagacc tcacaaagag aaacaacatg
300

gacttttcca tccgcatcag tagcatcacc ccagcagatg tcggcacata ctactgtgtg
360

aagtttcgaa aagggagccc tgagaacgtg gagtttaagt ctggaccagg cactgagatg
420

gctttgggtg ccaaaccctc tgcccccgtg gtattgggcc ctgcggcgag gaccacacct
480

gagcatacag tgagtttcac ctgtgagtcc catggcttct ctcccagaga catcaccctg
540

aaatggttca aaaatgggaa tgagctctca gacttccaga ccaacgtgga ccccacagga
600

cagagtgtgg cctacagcat ccgcagcaca gccagggtgg tactggaccc ctgggacgtt
660

cgctctcagg tcatctgcga ggtggcccat gtcaccttgc agggggaccc tcttcgtggg
720

actgccaact tgtctgaggc catccgagtt ccacccacct tggaggttac tcaacagccc
780

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<211> 1290
<212> DNA
<213> Artificial Sequence

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120

ctgttggtca cagttggaaa gacagccact ctgcactgca ctgtgacctc cctgcttccc
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gtgggacccg tcctgtggtt cagaggagtt ggaccaggcc gggaattaat ctacaatcaa
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gacttttcca tccgcatcag tagcatcacc ccagcagatg tcggcacata ctactgtgtg
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420

gctttgggtg ccaaaccctc tgcccccgtg gtattgggcc ctgcggcgag gaccacacct
480

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660

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<211> 1284
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120

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420

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<220>
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<211> 2736
<212> DNA
<213> Artificial Sequence

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<211> 2724
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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<211> 123
<212> DNA
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<220>
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<211> 126
<212> DNA
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<210> 22
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
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gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc
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<210> 23
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 23

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His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
35 40 45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro

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    50                  55                  60

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser
            100                 105                 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
                245                 250                 255

Gly Ser Thr Val Thr Val Ser Ser Gly Ala Ala Ala Leu Glu Lys Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
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275 280 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
290 295 300

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

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
325 330 335

Ile Thr Leu Tyr Cys Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
340 345 350

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
355 360 365

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
370 375 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385 390 395 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
405 410 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
420 425 430

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
435 440 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
450 455 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
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485 490 495

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<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 24

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Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 25

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
35 40 45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser

```
            100                 105                 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
                245                 250                 255

Gly Ser Thr Val Thr Val Ser Ser
            260
```

<210> 26
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 26

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
            20                  25                  30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser
        35                  40                  45

Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser
            100                 105                 110

Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser
        115                 120                 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
                165                 170                 175

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
            180                 185                 190

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
        195                 200                 205

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
    210                 215                 220

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240
```

```
Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
                245                 250                 255

Gly Ser Thr Val Thr Val Ser Ser Gly Ala Ala Ala Leu Glu Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460
```

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 27
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 27

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser
130 135 140

Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser

```
145                 150                 155                 160

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

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ser Leu Lys Thr Arg Leu
            180                 185                 190

Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Val Leu Thr Met Thr
        195                 200                 205

Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Ser Ser
225                 230                 235                 240

Val Thr Val Ser Ser Leu Glu Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
305                 310                 315                 320

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
                325                 330                 335

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
            340                 345                 350

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
        355                 360                 365

Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
```

370 375 380

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
385 390 395 400

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
405 410 415

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
420 425 430

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
435 440 445

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
450 455 460

Gln Ala Leu Pro Pro Arg
465 470

<210> 28
<211> 696
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 28

Asp Ile Gln Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10 15

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
20 25 30

Arg Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
35 40 45

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

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
65 70 75 80

```
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Ser
                85                  90                  95

Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Thr
            100                 105                 110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Ser
        115                 120                 125

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
    130                 135                 140

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Tyr
145                 150                 155                 160

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                165                 170                 175

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Phe Val Pro Lys Phe
            180                 185                 190

Gln Gly Arg Ala Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
        195                 200                 205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
    210                 215                 220

Lys Thr Gly Gly Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240

Leu Glu Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
    290                 295                 300
```

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys Glu Phe Phe Trp Val Leu Val Val Val
465 470 475 480

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
485 490 495

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr
500 505 510

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
515 520 525

```
Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Val Lys Arg
    530                 535                 540

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
545                 550                 555                 560

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
                565                 570                 575

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
            580                 585                 590

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
        595                 600                 605

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
    610                 615                 620

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
625                 630                 635                 640

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
                645                 650                 655

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
            660                 665                 670

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
        675                 680                 685

His Met Gln Ala Leu Pro Pro Arg
    690                 695
```

<210> 29
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 29

```
Asp Ile Gln Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
```

```
1               5                   10                  15

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
            20                  25                  30

Arg Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
        35                  40                  45

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

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
65                  70                  75                  80

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Ser
                85                  90                  95

Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Thr
            100                 105                 110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Ser
        115                 120                 125

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
    130                 135                 140

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Tyr
145                 150                 155                 160

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                165                 170                 175

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Phe Val Pro Lys Phe
            180                 185                 190

Gln Gly Arg Ala Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
        195                 200                 205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
    210                 215                 220

Lys Thr Gly Gly Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
```

225 230 235 240

Leu Glu Ala Pro Pro Arg Ala Ser Ala Leu Pro Ala Pro Pro Thr Gly
245 250 255

Ser Ala Leu Pro Asp Pro Gln Thr Ala Ser Ala Leu Pro Asp Pro Pro
260 265 270

Ala Ala Ser Ala Leu Pro Glu Phe Phe Trp Val Leu Val Val Val Gly
275 280 285

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
290 295 300

Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met
305 310 315 320

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
325 330 335

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Val Lys Arg Gly
340 345 350

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
355 360 365

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
370 375 380

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
385 390 395 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu

450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg
500

<210> 30
<211> 277
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 30
atcccacagt gcatacgtgg gctccaacag gtcctcttgt cgagccacag tgcatacgtg
60

ggctccaaca ggtcctcttg tcgagccaca gtgcatacgt gggctccaac aggtcctctt
120

gtcgagccac agtgcatacg tgggctccaa caggtcctct tgtcgagcca cagtgcatac
180

gtgggctcca acaggtcctc ttgtcgagat ctggtaggcg tgtacggtgg gaggtctata
240

taagcagagc tcgtttagtg aaccgtcaga tcactag
277

<210> 31
<211> 2778
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 31
gacatccaga tgacccagag cccaagcagc ctgagcgcca gcgtgggtga cagagtgacc
60

atcacctgta gtaccagttc gagtgtaagt tacatgcact ggtaccagca gaagccaggt
120

aaggctccaa ggctgctgat ctacagcaca tccaacctgg cttctggtgt gccaagcaga
180

ttcagcggta gcggtagcgg taccgacttc accttcacca tcagcagcct ccagccagag
240

gacatcgcca cctactactg ccatcagtgg agtagttatc ccacgttcgg ccaagggacc
300

aaggtggaaa tcaaaggatc cacttccggt tcaggaaagc ccgggagtgg tgaaggtagc
360

actaaaggcc aggtccagct gcaggagagc ggtccaggtc ttgtgagacc tagccagacc
420

ctgagcctga cctgcaccgt gtctggcttc accatcagca gtggttatag ctggcactgg
480

gtgagacagc cacctggacg aggtcttgag tggattggat acatacagta cagtggtatc
540

actaactaca acccctctct caaaagtaga gtgacaatgc tggtagacac cagcaagaac
600

cagttcagcc tgagactcag cagcgtgaca gccgccgaca ccgcggtcta ttattgtgca
660

agagaagact atgattacca ctggtacttc gatgtctggg gtcaaggcag cacggtcacc
720

gtctcctcag gtgcggccgc cctcgagacc acgacgccag cgccgcgacc accaacaccg
780

gcgcccacca tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg
840

gggggcgcag tgcacacgag ggggctggac ttcgcctgtg atatctacat ctgggcgccc
900

ttggccggga cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg
960

ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact
1020

caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg
1080

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc
1140

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc
1200

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat
1260

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc
1320

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc
1380

tacgacgccc ttcacatgca ggccctgccc cctcgcgtcg acggaagcgg agctactaac
1440

ttcagcctgc tgaagcaggc tggagacgtg gaggagaacc ctggacctat gcctgtccca
1500

gcctcctggc cccatcctcc tggtcctttc ctgcttctga ctctactgct gggacttaca
1560

gaagtggcag gtgaggagga gctacagatg attcagcctg agaagctcct gttggtcaca
1620

gttggaaaga cagccactct gcactgcact gtgacctccc tgcttcccgt gggacccgtc
1680

ctgtggttca gaggagttgg accaggccgg gaattaatct acaatcaaaa agaaggccac
1740

ttccccaggg taacaacagt ttcagacctc acaaagagaa acaacatgga cttttccatc
1800

cgcatcagta gcatcacccc agcagatgtc ggcacatact actgtgtgaa gtttcgaaaa
1860

gggagccctg agaacgtgga gtttaagtct ggaccaggca ctgagatggc tttgggtgcc
1920

aaaccctctg cccccgtggt attgggccct gcggcgagga ccacacctga gcatacagtg
1980

agtttcacct gtgagtccca tggcttctct cccagagaca tcaccctgaa atggttcaaa
2040

aatgggaatg agctctcaga cttccagacc aacgtggacc ccacaggaca gagtgtggcc
2100

tacagcatcc gcagcacagc cagggtggta ctggacccct gggacgttcg ctctcaggtc
2160

atctgcgagg tggcccatgt caccttgcag ggggaccctc ttcgtgggac tgccaacttg
2220

tctgaggcca tccgagttcc acccaccttg gaggttactc aacagcccat gagggtgggg
2280

aaccaggtaa acgtcacctg ccaggtgagg aagttctacc cccagagcct acagctgacc
2340

tggtcggaga atggaaacgt gtgccagaga gaaacagcct cgacccttac agagaacaag
2400

gatggtacct acaactggac aagctggttc ctggtgaaca tatctgacca aagggatgat
2460

gtggtcctca cctgccaggt gaagcatgat gggcagctgg cggtcagcaa acgccttgcc
2520

ctagaggtca cagtccacca gaaggaccag agctcagatg ctacccctct tgagttctgg
2580

gtgctggtcg tggtgggtgg cgtgctggcc tgctacagcc tgctggtgac agtggccttc
2640

atcatctttt gggtgaggag caagcggagc agaggcggcc acagcgacta catgaacatg
2700

actccccgcc gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac
2760

ttcgcagcct atcgctcc
2778

<210> 32
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 32
atggctctgc cagtgacagc tctgctgctg cctctggctc tgctgctgca cgcagctaga
60

cccgacatcc agatgaccca gagcccttct tctctgagcg ccagcgtggg agacagagtg
120

accatcactt gcagggccag ccaggacatc agcaagtacc tgaattggta ccagcagaag
180

ccaggcaagg cccctagact gctgatctac cacacaagca gactgcacag cggagtgcct
240

agcagattca gcggcagcgg aagcggaacc gactacaccc tgaccatcag cagcctgcag
300

ccagaggact tcgccaccta ctactgccag cagggcaaca cactgcctta caccttcggc
360

ggaggcacaa gactggagat caagggcagc acaagcggaa gcggcaaacc aggaagcgga
420

gaaggaagca ccaagggaca ggtgcagctg caggaaagcg gaccaggact ggtgaagcct
480

tctcagaccc tgagcctgac ttgcaccgtg tcaggagtgt ccctgccaga ttacggcgtg
540

tcttggatca gacagccccc aggaaaggcc ctggagtggc tgggagtgat ttggggaagc
600

gagaccacct actacaacag cagcctgaag acccggctga ccatcagcaa ggacaacagc
660

aagaaccagg tggtgctgac catgaccaac atggaccccg tggacaccgc cacctactat
720

tgcgccaagc actactacta cggcggaagc tacgccatgg actattgggg ccagggaagc
780

agcgtgaccg tgtctagcct cgagaccacg acgccagcgc cgcgaccacc aacaccggcg
840

cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg
900

ggcgcagtgc acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg
960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc
1020

agaaagaaac tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa
1080

gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga
1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat
1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg
1260

gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa
1320

ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg
1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac
1440

gacgcccttc acatgcaggc cctgcccccc cgc
1473

<210> 33

<211> 1756
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 33
atcccacagt gcatacgtgg gctccaacag gtcctcttgt cgagccacag tgcatacgtg
60

ggctccaaca ggtcctcttg tcgagccaca gtgcatacgt gggctccaac aggtcctctt
120

gtcgagccac agtgcatacg tgggctccaa caggtcctct tgtcgagcca cagtgcatac
180

gtgggctcca acaggtcctc ttgtcgagat ctggtaggcg tgtacggtgg gaggtctata
240

taagcagagc tcgtttagtg aaccgtcaga tcactaggct agcatggctc tgccagtgac
300

agctctgctg ctgcctctgg ctctgctgct gcacgcagct agacccgaca tccagatgac
360

ccagagccct tcttctctga gcgccagcgt gggagacaga gtgaccatca cttgcagggc
420

cagccaggac atcagcaagt acctgaattg gtaccagcag aagccaggca aggcccctag
480

actgctgatc taccacacaa gcagactgca cagcggagtg cctagcagat tcagcggcag
540

cggaagcgga accgactaca ccctgaccat cagcagcctg cagccagagg acttcgccac
600

ctactactgc cagcagggca acacactgcc ttacaccttc ggcggaggca caagactgga
660

gatcaagggc agcacaagcg gaagcggcaa accaggaagc ggagaaggaa gcaccaaggg
720

acaggtgcag ctgcaggaaa gcggaccagg actggtgaag ccttctcaga ccctgagcct
780

gacttgcacc gtgtcaggag tgtccctgcc agattacggc gtgtcttgga tcagacagcc
840

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900

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1560

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<211> 1509
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<220>
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<210> 35
<211> 2088
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<213> Artificial Sequence

<220>
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<211> 804
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<220>
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<211> 41
<212> PRT
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<220>
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<400> 38

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Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40