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> ~~SIPOSequenceListing 1.0~~PatentIn version 3.5

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

<220>
<223> Synthesized construct

<400> 1

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
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

<210> 5
<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 5

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

<210> 6
<211> 907
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 6

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 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

atgagggtgg ggaaccaggt aaacgtcacc tgccaggtga ggaagttcta cccccagagc 840

ctacagctga cctggtcgga gaatggaaac gtgtgccaga gagaaacagc ctcgacccct 900

acagagaaca aggatggtac ctacaactgg acaagctggt tcctggtgaa catatctgac 960

caaagggatg atgtggtcct cacctgccag gtgaagcatg atgggcagct ggcggtcagc 1020

aaacgccttg ccctagaggt cacagtccac cagaaggacc agagctcaga tgctacccct 1080

ctcgag 1086

<210> 13
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 13
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

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cgctctcagg tcatctgcga ggtggcccat gtcaccttgc agggggaccc tcttcgtggg 720

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<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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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

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cagagtgtgg cctacagcat ccgcagcaca gccagggtgg tactggaccc ctgggacgtt 660

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tttatgagac cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa 1260

gaagaagaag gaggatgtga actg 1284

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<211> 1365
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthesized construct

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agacgtggcc gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc 1200

ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 1260

ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc 1320

aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgc 1365

<210> 16
<211> 2736
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgcgtcga cggaagcgga 1380

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<210> 17
<211> 2724
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

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gaggacatcg ccacctacta ctgccatcag tggagtagtt atcccacgtt cggccaaggg 360

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atgagaccag tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa 2700

gaagaaggag gatgtgaact gtaa 2724

<210> 18
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 18
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gccttcatca tcttttgggt g 81

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

<220>
<223> Synthesized construct

<400> 19
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acccttact gc 72

<210> 20
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 20
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ggccccaccc ggaagcacta ccagccctac gcccctccca gggacttcgc cgcctaccgg 120

agc 123

<210> 21
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 21
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actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 22
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 22
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<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
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 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
465 470 475 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 24
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 24

Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr

1 5 10 15

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
20 25 30

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 25
<211> 264
<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
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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
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

cccaggaaag gccctggagt ggctgggagt gatttgggga agcgagacca cctactacaa 900

cagcagcctg aagacccggc tgaccatcag caaggacaac agcaagaacc aggtggtgct 960

gaccatgacc aacatggacc ccgtggacac cgccacctac tattgcgcca agcactacta 1020

ctacggcgga agctacgcca tggactattg gggccaggga agcagcgtga ccgtgtctag 1080

cctcgagacc acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca 1140

gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag tgcacacgag 1200

ggggctggac ttcgcctgtg atatctacat ctgggcgccc ttggccggga cttgtggggt 1260

ccttctcctg tcactggtta tcacccttta ctgcaaacgg ggcagaaaga aactcctgta 1320

tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag atggctgtag 1380

ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt tcagcaggag 1440

cgcagacgcc cccgcgtaca agcagggcca gaaccagctc tataacgagc tcaatctagg 1500

acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg agatgggggg 1560

aaagccgaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga aagataagat 1620

ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca aggggcacga 1680

tggcctttac cagggtctca gtacagccac caaggacacc tacgacgccc ttcacatgca 1740

ggccctgccc cctcgc 1756

<210> 34
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 34
gacatccagg atatccagct gacacagtcc cctagctccc tgagcgcctc cgtgggcgac 60

agggtgacca tcacatgcag cgcctctagc tccgtgagat tcatccactg gtaccagcag 120

aagcccggca aggcccctaa gaggctgatc tatgatacct ctaagctggc cagcggagtg 180

ccctcccgct tctctggcag cggctccggc accgacttta ccctgacaat ctctagcctg 240

cagccagagg attttgccac atactattgc cagcagtggt cctctagccc cttcaccttt 300

ggccagggca caaaggtgga gatcaaggga tctaccagcg gatccggcaa gcctggatct 360

ggagagggca gcacaaaggg ctccgaggtg cagctggtgg agtccggagg aggactggtg 420

cagccaggag gatctctgag gctgagctgt gcagcctccg gcttcaacat caaggactac 480

tatatccact gggtgagaca ggcacctggc aagggactgg agtgggtggc atggatcgac 540

cctgagaatg gcgataccga gttcgtgcca aagtttcagg gcagggccac aatctctgcc 600

gacaccagca agaacacagc ctacctgcag atgaatagcc tgcgcgccga ggataccgcc 660

gtgtactatt gtaagacagg aggattttgg ggacagggca ccctggtgac agtgtcctct 720

ctcgaggcac cacctcgggc cagcgccctg cctgcaccac ccaccggctc cgccctgcca 780

gaccctcaga cagcatctgc cctgccagat cctccagcag caagcgccct gcccgaattc 840

ttctgggtgc tggtcgtggt gggtggcgtg ctggcctgct acagcctgct ggtgacagtg 900

gccttcatca tcttttgggt gaggagcaag cggagcagag gcggccacag cgactacatg 960

aacatgactc cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca 1020

cgcgacttcg cagcctatcg ctccgttaaa cggggcagaa agaaactcct gtatatattc 1080

aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg tagctgccga 1140

tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgcagac 1200

gcccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 1260

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<400> 38

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35 40