SEQUENCE LISTING

<110> Wellstat ImmunoTherapeutics, LLC

<120> COMPLEMENT FACTOR B ANALOGS AND THEIR USES

<130> 21002-PCT

<150> US 61/482,827
<151> 2011-05-05

<150> US 61/497,835
<151> 2011-06-16

<150> US 61/568,518
<151> 2011-12-08

<160> 27

<170> PatentIn version 3.5

<210> 1
<211> 764
<212> PRT
<213> Homo sapiens

<400> 1

```
Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1               5                  10                  15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
            20                  25                  30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
        35                  40                  45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
    50                  55                  60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65                  70                  75                  80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
                85                  90                  95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
            100                 105                 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
        115                 120                 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
    130                 135                 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145                 150                 155                 160
```

```
Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                165                 170                 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Lys Arg Lys Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly
        275                 280                 285

Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430
```

```
Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700
```

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705 710 715 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
725 730 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 2
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 2

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
35 40 45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175

```
Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Ser Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445
```

```
Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720
```

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
725 730 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 3
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 3

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
35 40 45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175

```
Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Ser Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445
```

```
Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720
```

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
725 730 735

His Ala Arg Asn Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 4
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 4

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
35 40 45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
180 185 190

```
Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460
```

```
Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735
```

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 5
<211> 7754
<212> DNA
<213> Artificial Sequence

<220>
<223> hfB3 expression construct

<400> 5
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt acttaatacg actcactata ggctagcctc gagaattcac gcgtggtacc 1080

tctagagtcg actagctcct gccccaggcc cagcttctct cctgccttcc aacgccatgg 1140

gctccaacct gtccccccag ctgtgcctga tgcctttcat cctgggcctg ctgtctggcg 1200

gcgtgaccac cacccttgg tccctggcca ggcctcaggg ctcctgctcc ctggagggcg 1260

tggagatcaa gggcggctcc ttccggctgc tgcaggaagg ccaggctctg gagtacgtgt 1320

gcccttccgg cttctaccct taccctgtgc agacaaggac ctgtaggtcc accggctctt 1380

ggtccacact gaaaacccag gaccagaaaa ccgtccggaa ggccgagtgc cgggccatcc 1440

actgccctcg gcctcacgac ttcgagaacg gcgagtactg gcctcggtcc ccttactaca 1500

acgtgtccga cgagatctcc ttccactgct acgacggcta caccctgcgg ggctccgcca 1560

acaggacctg ccaggtcaac ggccggtggt ccggccagac cgccatctgc gacaacggcg 1620

ctggctactg ctccaaccct ggcatcccta tcggcacccg gaaggtcggc tcccagtacc 1680

ggctggagga ctccgtgacc taccactgct ccagaggcct gaccctgaga ggctcccagc 1740

ggcgcacctg tcaggaaggt ggcagctggt ctggcaccga accatcttgc caggactcct 1800

tcatgtacga cacccctcag gaagtggccg aggccttcct gtcctccctg accgagacaa 1860

tcgagggcgt ggacgccgag gatggccacg gccctggcga gcagcaggcc gctgccatcg 1920

tgctggaccc ctccggctcc atgaacatct acctggtgct ggacggctcc ggcagcatcg 1980

gcgcctccga cttcaccggc gccaagaagt gcctggtcaa cctgatcgag aaggtggcct 2040

cctacggcgt gaagcctaga tacggcctgg tgacctacgc cacctaccct aagatctggg 2100

tgaaggtgtc cgaggccgac tcctccaacg ccgactgggt gaccaagcag ctgaacgaga 2160

tcaactacga ggaccacaag ctgaagtccg gcaccaacac caagaaggcc ctgcaggccg 2220

tctactccat gatgtcctgg cctgacgacg tgcctcctga gggctggaac cggacccggc 2280

acgtgattat cctgatgacc gacggcctgc acaacatggg cggcgaccct atcaccgtga 2340

tcgacgagat ccgggacctg ctgtacatcg gcaaggaccg gaagaaccct cgggaggact 2400

acctggacgt gtacgtgttc ggcgtgggcc ctctggtgaa ccaggtcaac atcaacgccc 2460

tggcctccaa gaaggacaac gagcagcacg tgttcaaggt caaggacatg gagaacctgg 2520

aggacgtgtt ctaccagatg atcgatgagt cccagtccct gagcctgtgc ggcatggtct 2580

gggagcaccg caagggaacc gactaccaca agcagccttg gcaggccaag atctccgtga 2640

tccggccttc caagggccac gagtcctgca tgggcgccgt ggtgtccgag tacttcgtgc 2700

tgaccgccgc tcactgcttc accgtggacg acaaggaaca ctccatcaaa gtctccgtgg 2760

gcggcgagaa gcgggacctg gagatcgagg tggtgctgtt ccaccctaac tacaacatca 2820

acggcaagaa ggaagccggc atccctgagt tctacgacta cgacgtggcc ctgatcaagc 2880

tgaagaataa gctgaagtat ggccagacca tccggcctat ctgcctgcct tgcaccgagg 2940

gcaccaccag ggccctgcgg ctgcctccta ccaccacctg ccagcagcag aaggaagagc 3000

tgctgcctgc ccaggacatc aaggccctgt tcgtgtccga ggaagagaag aagctgaccc 3060

ggaaggaagt gtacatcaag aacggcgaca agaagggcag ctgcgagcgg gacgcccagt 3120

acgcccctgg ctacgataag gtcaaggata tctccgaggt ggtgaccct cggttcctgt 3180

gcaccggcgg agtgtccccc tacgccgacc ctaacacctg cagaggcgac tctggcggcc 3240

ctctgatcgt gcacaagcgg tcccggttca tccaggtcgg cgtgatctcc tggggcgtgg 3300

tggacgtgtg caagaaccag aagcggcaga agcaggtccc cgcccacgcc cgggacttcc 3360

acatcaacct gttccaggtg ctgccttggc tgaaggaaaa gctgcaggat gaggacctgg 3420

gcttcctgtg aggggtttcc tgctggacag gggcgtggga ttgacgcccc tctccctccc 3480

ccccccctaa cgttactggc cgaagccgct tggaataagg ccggtgtgcg tttgtctata 3540

tgttattttc caccatattg ccgtcttttg gcaatgtgag ggcccggaaa cctggccctg 3600

tcttcttgac gagcattcct aggggtcttt cccctctcgc caaaggaatg caaggtctgt 3660

tgaatgtcgt gaaggaagca gttcctctgg aagcttcttg aagacaaaca acgtctgtag 3720

cgacccttg caggcagcgg aacccccac ctggcgacag gtgcctctgc ggccaaaagc 3780

cacgtgtata agatacacct gcaaaggcgg cacaacccca gtgccacgtt gtgagttgga 3840

tagttgtgga aagagtcaaa tggctctcct caagcgtatt caacaagggg ctgaaggatg 3900

cccagaaggt accccattgt atgggatctg atctggggcc tcggtgcaca tgctttacat 3960

gtgtttagtc gaggttaaaa aaacgtctag gcccccccgaa ccacggggac gtggttttcc 4020

tttgaaaaac acgatgataa gcttgccaca acccgggata attcctgcag ccaatatggg 4080

atcggccatt gaacaagatg gattgcacgc aggttctccg gccgcttggg tggagaggct 4140

attcggctat gactgggcac aacagacaat cggctgctct gatgccgccg tgttccggct 4200

gtcagcgcag gggcgcccgg ttctttttgt caagaccgac ctgtccggtg ccctgaatga 4260

actgcaggac gaggcagcgc ggctatcgtg gctggccacg acgggcgttc cttgcgcagc 4320

tgtgctcgac gttgtcactg aagcgggaag ggactggctg ctattgggcg aagtgccggg 4380

gcaggatctc ctgtcatctc accttgctcc tgccgagaaa gtatccatca tggctgatgc 4440

aatgcggcgg ctgcatacgc ttgatccggc tacctgccca ttcgaccacc aagcgaaaca 4500

tcgcatcgag cgagcacgta ctcggatgga agccggtctt gtcgatcagg atgatctgga 4560

cgaagagcat caggggctcg cgccagccga actgttcgcc aggctcaagg cgcgcatgcc 4620

cgacggcgat gatctcgtcg tgacccatgg cgatgcctgc ttgccgaata tcatggtgga 4680

aaatggccgc ttttctggat tcatcgactg tggccggctg ggtgtggcgg accgctatca 4740

ggacatagcg ttggctaccc gtgatattgc tgaagagctt ggcggcgaat gggctgaccg 4800

cttcctcgtg ctttacggta tcgccgctcc cgattcgcag cgcatcgcct tctatcgcct 4860

tcttgacgag ttcttctgag ctagtcgacc cgggcggcct cgagaataaa caatcattat 4920

tttcattgga tctgtgtgtt ggtttttgt gtgggcttgg gggaggggga ggccagaatg 4980

actccaagag ctacaggaag gcaggtcaga gaccccactg gacaaacagt ggctggactc 5040

tgcaccataa cacacaatca acaggggagt gagctggatc gagctgctcg agatccgggc 5100

tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg cagcctgaat 5160

ggcgaatgga cgcgccctgt agcggcgcat taagcgcggc gggtgtggtg gttacgcgca 5220

gcgtgaccgc tacacttgcc agcgccctag cgcccgctcc tttcgctttc ttcccttcct 5280

ttctcgccac gttcgccggc tttccccgtc aagctctaaa tcgggggctc cctttagggt 5340

tccgatttag tgctttacgg cacctcgacc ccaaaaaact tgattagggt gatggttcac 5400

gtagtgggcc atcgccctga tagacggttt ttcgcccttt gacgttggag tccacgttct 5460

ttaatagtgg actcttgttc caaactggaa caacactcaa ccctatctcg gtctattctt 5520

ttgatttata agggattttg ccgatttcgg cctattggtt aaaaaatgag ctgatttaac 5580

aaaaatttaa cgcgaatttt aacaaaatat taacgcttac aatttcctga tgcggtattt 5640

tctccttacg catctgtgcg gtatttcaca ccgcatatgg tgcactctca gtacaatctg 5700

ctctgatgcc gcatagttaa gccagccccg acacccgcca acacccgctg acgcgccctg 5760

acgggcttgt ctgctcccgg catccgctta cagacaagct gtgaccgtct ccgggagctg 5820

catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg agacgaaagg gcctcgtgat 5880

acgcctattt ttataggtta atgtcatgat aataatggtt tcttagacgt caggtggcac 5940

ttttcgggga aatgtgcgcg gaacccctat ttgtttattt ttctaaatac attcaaatat 6000

gtatccgctc atgagacaat aaccctgata aatgcttcaa taatattgaa aaaggaagag 6060

tatgagtatt caacatttcc gtgtcgccct tattcccttt tttgcggcat tttgccttcc 6120

tgtttttgct cacccagaaa cgctggtgaa agtaaaagat gctgaagatc agttgggtgc 6180

acgagtgggt tacatcgaac tggatctcaa cagcggtaag atccttgaga gttttcgccc 6240

cgaagaacgt tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc 6300

ccgtattgac gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt 6360

ggttgagtac tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt 6420

atgcagtgct gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat 6480

cggaggaccg aaggagctaa ccgcttttt gcacaacatg ggggatcatg taactcgcct 6540

tgatcgttgg gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat 6600

gcctgtagca atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc 6660

ttcccggcaa caattaatag actggatgga ggcggataaa gttgcaggac cacttctgcg 6720

ctcggccctt ccggctggct ggtttattgc tgataaatct ggagccggtg agcgtgggtc 6780

tcgcggtatc attgcagcac tggggccaga tggtaagccc tcccgtatcg tagttatcta 6840

cacgacgggg agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc 6900

ctcactgatt aagcattggt aactgtcaga ccaagtttac tcatatatac tttagattga 6960

tttaaaactt cattttaat ttaaaaggat ctaggtgaag atccttttg ataatctcat 7020

gaccaaaatc ccttaacgtg agttttcgtt ccactgagcg tcagaccccg tagaaaagat 7080

caaaggatct tcttgagatc ctttttttct gcgcgtaatc tgctgcttgc aaacaaaaaa 7140

accaccgcta ccagcggtgg tttgtttgcc ggatcaagag ctaccaactc ttttccgaa 7200

ggtaactggc ttcagcagag cgcagatacc aaatactgtt cttctagtgt agccgtagtt 7260

aggccaccac ttcaagaact ctgtagcacc gcctacatac ctcgctctgc taatcctgtt 7320

accagtggct gctgccagtg gcgataagtc gtgtcttacc gggttggact caagacgata 7380

gttaccggat aaggcgcagc ggtcgggctg aacgggggt tcgtgcacac agcccagctt 7440

ggagcgaacg acctacaccg aactgagata cctacagcgt gagctatgag aaagcgccac 7500

gcttcccgaa gggagaaagg cggacaggta tccggtaagc ggcagggtcg gaacaggaga 7560

gcgcacgagg gagcttccag ggggaaacgc ctggtatctt tatagtcctg tcgggtttcg 7620

ccacctctga cttgagcgtc gatttttgtg atgctcgtca gggggggcgga gcctatggaa 7680

aaacgccagc aacgcggcct ttttacggtt cctggccttt tgctggcctt ttgctcacat 7740

ggctcgacag atct 7754

<210> 6
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
caccggcgcc aagaagagcc tggtcaacct gatc 34

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
gatcaggttg accaggctct tcttggcgcc ggtg 34

<210> 8
<211> 7754
<212> DNA
<213> Artificial Sequence

<220>
<223> expression construct

<400> 8
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt acttaatacg actcactata ggctagcctc gagaattcac gcgtggtacc 1080

tctagagtcg actagctcct gccccaggcc cagcttctct cctgccttcc aacgccatgg 1140

gctccaacct gtccccccag ctgtgcctga tgcctttcat cctgggcctg ctgtctggcg 1200

gcgtgaccac cacccttgg tccctggcca ggcctcaggg ctcctgctcc ctggagggcg 1260

tggagatcaa gggcggctcc ttccggctgc tgcaggaagg ccaggctctg gagtacgtgt 1320

gcccttccgg cttctaccct taccctgtgc agacaaggac ctgtaggtcc accggctctt 1380

ggtccacact gaaaacccag gaccagaaaa ccgtccggaa ggccgagtgc cgggccatcc 1440

actgccctcg gcctcacgac ttcgagaacg gcgagtactg gcctcggtcc ccttactaca 1500

acgtgtccga cgagatctcc ttccactgct acgacggcta caccctgcgg ggctccgcca 1560

acaggacctg ccaggtcaac ggccggtggt ccggccagac cgccatctgc gacaacggcg 1620

ctggctactg ctccaaccct ggcatcccta tcggcacccg gaaggtcggc tcccagtacc 1680

ggctggagga ctccgtgacc taccactgct ccagaggcct gaccctgaga ggctcccagc 1740

ggcgcacctg tcaggaaggt ggcagctggt ctggcaccga accatcttgc caggactcct 1800

tcatgtacga cacccctcag gaagtggccg aggccttcct gtcctccctg accgagacaa 1860

tcgagggcgt ggacgccgag gatggccacg gccctggcga gcagcaggcc gctgccatcg 1920

tgctggaccc ctccggctcc atgaacatct acctggtgct ggacggctcc ggcagcatcg 1980

gcgcctccga cttcaccggc gccaagaaga gcctggtcaa cctgatcgag aaggtggcct 2040

cctacggcgt gaagcctaga tacggcctgg tgacctacgc cacctaccct aagatctggg 2100

tgaaggtgtc cgaggccgac tcctccaacg ccgactgggt gaccaagcag ctgaacgaga 2160

tcaactacga ggaccacaag ctgaagtccg gcaccaacac caagaaggcc ctgcaggccg 2220

tctactccat gatgtcctgg cctgacgacg tgcctcctga gggctggaac cggacccggc 2280

acgtgattat cctgatgacc gacggcctgc acaacatggg cggcgaccct atcaccgtga 2340

tcgacgagat ccgggacctg ctgtacatcg gcaaggaccg gaagaaccct cgggaggact 2400

acctggacgt gtacgtgttc ggcgtgggcc ctctggtgaa ccaggtcaac atcaacgccc 2460

tggcctccaa gaaggacaac gagcagcacg tgttcaaggt caaggacatg gagaacctgg 2520

aggacgtgtt ctaccagatg atcgatgagt cccagtccct gagcctgtgc ggcatggtct 2580

gggagcaccg caagggaacc gactaccaca agcagccttg gcaggccaag atctccgtga 2640

tccggccttc caagggccac gagtcctgca tgggcgccgt ggtgtccgag tacttcgtgc 2700

tgaccgccgc tcactgcttc accgtggacg acaaggaaca ctccatcaaa gtctccgtgg 2760

gcggcgagaa gcgggacctg gagatcgagg tggtgctgtt ccaccctaac tacaacatca 2820

acggcaagaa ggaagccggc atccctgagt tctacgacta cgacgtggcc ctgatcaagc 2880

tgaagaataa gctgaagtat ggccagacca tccggcctat ctgcctgcct tgcaccgagg 2940

gcaccaccag ggccctgcgg ctgcctccta ccaccacctg ccagcagcag aaggaagagc 3000

tgctgcctgc ccaggacatc aaggccctgt tcgtgtccga ggaagagaag aagctgaccc 3060

ggaaggaagt gtacatcaag aacggcgaca agaagggcag ctgcgagcgg gacgcccagt 3120

acgcccctgg ctacgataag gtcaaggata tctccgaggt ggtgacccct cggttcctgt 3180

gcaccggcgg agtgtccccc tacgccgacc ctaacacctg cagaggcgac tctggcggcc 3240

ctctgatcgt gcacaagcgg tcccggttca tccaggtcgg cgtgatctcc tggggcgtgg 3300

tggacgtgtg caagaaccag aagcggcaga agcaggtccc cgcccacgcc cgggacttcc 3360

acatcaacct gttccaggtg ctgccttggc tgaaggaaaa gctgcaggat gaggacctgg 3420

gcttcctgtg aggggtttcc tgctggacag gggcgtggga ttgacgcccc tctccctccc 3480

ccccccctaa cgttactggc cgaagccgct tggaataagg ccggtgtgcg tttgtctata 3540

tgttattttc caccatattg ccgtcttttg gcaatgtgag ggcccggaaa cctggccctg 3600

tcttcttgac gagcattcct aggggtcttt cccctctcgc caaaggaatg caaggtctgt 3660

tgaatgtcgt gaaggaagca gttcctctgg aagcttcttg aagacaaaca acgtctgtag 3720

cgacccttttg caggcagcgg aacccccccac ctggcgacag gtgcctctgc ggccaaaagc 3780

cacgtgtata agatacacct gcaaaggcgg cacaacccca gtgccacgtt gtgagttgga 3840

tagttgtgga aagagtcaaa tggctctcct caagcgtatt caacaagggg ctgaaggatg 3900

cccagaaggt accccattgt atgggatctg atctggggcc tcggtgcaca tgctttacat 3960

gtgtttagtc gaggttaaaa aaacgtctag gccccccgaa ccacggggac gtggttttcc 4020

tttgaaaaac acgatgataa gcttgccaca acccgggata attcctgcag ccaatatggg 4080

atcggccatt gaacaagatg gattgcacgc aggttctccg gccgcttggg tggagaggct 4140

attcggctat gactgggcac aacagacaat cggctgctct gatgccgccg tgttccggct 4200

gtcagcgcag gggcgcccgg ttctttttgt caagaccgac ctgtccggtg ccctgaatga 4260

actgcaggac gaggcagcgc ggctatcgtg gctggccacg acgggcgttc cttgcgcagc 4320

tgtgctcgac gttgtcactg aagcgggaag ggactggctg ctattgggcg aagtgccggg 4380

gcaggatctc ctgtcatctc accttgctcc tgccgagaaa gtatccatca tggctgatgc 4440

aatgcggcgg ctgcatacgc ttgatccggc tacctgccca ttcgaccacc aagcgaaaca 4500

tcgcatcgag cgagcacgta ctcggatgga agccggtctt gtcgatcagg atgatctgga 4560

cgaagagcat caggggctcg cgccagccga actgttcgcc aggctcaagg cgcgcatgcc 4620

cgacggcgat gatctcgtcg tgacccatgg cgatgcctgc ttgccgaata tcatggtgga 4680

aaatggccgc ttttctggat tcatcgactg tggccggctg ggtgtggcgg accgctatca 4740

ggacatagcg ttggctaccc gtgatattgc tgaagagctt ggcggcgaat gggctgaccg 4800

cttcctcgtg ctttacggta tcgccgctcc cgattcgcag cgcatcgcct tctatcgcct 4860

tcttgacgag ttcttctgag ctagtcgacc cgggcggcct cgagaataaa caatcattat 4920

tttcattgga tctgtgtgtt ggtttttgt gtgggcttgg gggaggggga ggccagaatg 4980

actccaagag ctacaggaag gcaggtcaga gaccccactg gacaaacagt ggctggactc 5040

tgcaccataa cacacaatca acaggggagt gagctggatc gagctgctcg agatccgggc 5100

tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg cagcctgaat 5160

ggcgaatgga cgcgccctgt agcggcgcat taagcgcggc gggtgtggtg gttacgcgca 5220

gcgtgaccgc tacacttgcc agcgccctag cgcccgctcc tttcgctttc ttcccttcct 5280

ttctcgccac gttcgccggc tttccccgtc aagctctaaa tcgggggctc cctttagggt 5340

tccgatttag tgctttacgg cacctcgacc ccaaaaaact tgattagggt gatggttcac 5400

gtagtgggcc atcgccctga tagacggttt ttcgcccttt gacgttggag tccacgttct 5460

ttaatagtgg actcttgttc caaactggaa caacactcaa ccctatctcg gtctattctt 5520

ttgatttata agggattttg ccgatttcgg cctattggtt aaaaaatgag ctgatttaac 5580

aaaaatttaa cgcgaatttt aacaaaatat taacgcttac aatttcctga tgcggtattt 5640

tctccttacg catctgtgcg gtatttcaca ccgcatatgg tgcactctca gtacaatctg 5700

ctctgatgcc gcatagttaa gccagccccg acacccgcca acacccgctg acgcgccctg 5760

acgggcttgt ctgctcccgg catccgctta cagacaagct gtgaccgtct ccgggagctg 5820

catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg agacgaaagg gcctcgtgat 5880

acgcctattt ttataggtta atgtcatgat aataatggtt tcttagacgt caggtggcac 5940

ttttcgggga aatgtgcgcg gaacccctat ttgtttattt ttctaaatac attcaaatat 6000

gtatccgctc atgagacaat aaccctgata aatgcttcaa taatattgaa aaaggaagag 6060

tatgagtatt caacatttcc gtgtcgccct tattcccttt tttgcggcat tttgccttcc 6120

tgtttttgct cacccagaaa cgctggtgaa agtaaaagat gctgaagatc agttgggtgc 6180

acgagtgggt tacatcgaac tggatctcaa cagcggtaag atccttgaga gttttcgccc 6240

cgaagaacgt tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc 6300

ccgtattgac gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt 6360

ggttgagtac tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt 6420

atgcagtgct gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat 6480

cggaggaccg aaggagctaa ccgcttttt gcacaacatg ggggatcatg taactcgcct 6540

tgatcgttgg gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat 6600

gcctgtagca atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc 6660

ttcccggcaa caattaatag actggatgga ggcggataaa gttgcaggac cacttctgcg 6720

ctcggccctt ccggctggct ggtttattgc tgataaatct ggagccggtg agcgtgggtc 6780

tcgcggtatc attgcagcac tggggccaga tggtaagccc tcccgtatcg tagttatcta 6840

cacgacgggg agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc 6900

ctcactgatt aagcattggt aactgtcaga ccaagtttac tcatatatac tttagattga 6960

tttaaaactt catttttaat ttaaaaggat ctaggtgaag atccttttg ataatctcat 7020

gaccaaaatc ccttaacgtg agttttcgtt ccactgagcg tcagaccccg tagaaaagat 7080

caaaggatct tcttgagatc ctttttttct gcgcgtaatc tgctgcttgc aaacaaaaaa 7140

accaccgcta ccagcggtgg tttgtttgcc ggatcaagag ctaccaactc tttttccgaa 7200

ggtaactggc ttcagcagag cgcagatacc aaatactgtt cttctagtgt agccgtagtt 7260

aggccaccac ttcaagaact ctgtagcacc gcctacatac ctcgctctgc taatcctgtt 7320

accagtggct gctgccagtg gcgataagtc gtgtcttacc gggttggact caagacgata 7380

gttaccggat aaggcgcagc ggtcgggctg aacgggggt tcgtgcacac agcccagctt 7440

ggagcgaacg acctacaccg aactgagata cctacagcgt gagctatgag aaagcgccac 7500

gcttcccgaa gggagaaagg cggacaggta tccggtaagc ggcagggtcg gaacaggaga 7560

gcgcacgagg gagcttccag ggggaaacgc ctggtatctt tatagtcctg tcgggtttcg 7620

ccacctctga cttgagcgtc gatttttgtg atgctcgtca gggggggcgga gcctatggaa 7680

aaacgccagc aacgcggcct ttttacggtt cctggccttt tgctggcctt ttgctcacat 7740

ggctcgacag atct 7754

<210> 9
<211> 23
<212> PRT
<213> Homo sapiens

<400> 9

Ile Gly Ala Ser Asn Phe Thr Gly Ala Lys Lys Cys Leu Val Asn Leu
1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 10
<211> 23
<212> PRT
<213> Mus musculus

<400> 10

Ile Gly Ser Ser Asn Phe Thr Gly Ala Lys Arg Cys Leu Thr Asn Leu
1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 11
<211> 23
<212> PRT
<213> Rattus norvegicus

<400> 11

Ile Gly Ala Ser Asn Phe Thr Gly Ala Lys Arg Cys Leu Ala Asn Leu

1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 12
<211> 23
<212> PRT
<213> Sus scrofa

<400> 12

Ile Gly Ala Arg Asn Phe Thr Gly Ala Lys Asn Cys Leu Lys Asp Phe
1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 13
<211> 23
<212> PRT
<213> Macaca mulatta

<400> 13

Ile Gly Ala Gly Asn Phe Thr Gly Ala Lys Lys Cys Leu Val Asn Leu
1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 14
<211> 23
<212> PRT
<213> Ovis aries

<400> 14

Val Gly Ala His Asn Phe Thr Gly Ala Lys Asn Cys Leu Arg Asp Phe
1 5 10 15

Ile Glu Lys Val Ala Ser Tyr
20

<210> 15
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gtccccgccc acgcccggaa cttccacatc aacctgttcc 40

<210> 16
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
ggaacaggtt gatgtggaag ttccgggcgt gggcggggac 40

<210> 17
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 17

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
35 40 45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
180 185 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
195 200 205

```
Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480
```

```
Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735

His Ala Arg Asn Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
            740                 745                 750
```

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 18
<211> 8465
<212> DNA
<213> Artificial Sequence

<220>
<223> expression construct

<400> 18
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt acttaatacg actcactata ggctagcgaa ttcacgcgtg gtacctctag 1080

agtcgactag ctcctgcccc aggcccagct tctctcctgc cttccaacgc catgggctcc 1140

aacctgtccc cccagctgtg cctgatgcct ttcatcctgg gcctgctgtc tggcggcgtg 1200

accaccaccc cttggtccct ggccaggcct cagggctcct gctccctgga gggcgtggag 1260

atcaagggcg gctccttccg gctgctgcag gaaggccagg ctctggagta cgtgtgccct 1320

tccggcttct acccttaccc tgtgcagaca aggacctgta ggtccaccgg ctcttggtcc 1380

acactgaaaa cccaggacca gaaaaccgtc cggaaggccg agtgccgggc catccactgc 1440

cctcggcctc acgacttcga gaacggcgag tactggcctc ggtcccctta ctacaacgtg 1500

tccgacgaga tctccttcca ctgctacgac ggctacaccc tgcggggctc cgccaacagg 1560

acctgccagg tcaacggccg gtggtccggc cagaccgcca tctgcgacaa cggcgctggc 1620

tactgctcca accctggcat ccctatcggc acccggaagg tcggctccca gtaccggctg 1680

gaggactccg tgacctacca ctgctccaga ggcctgaccc tgagaggctc ccagcggcgc 1740

acctgtcagg aaggtggcag ctggtctggc accgaaccat cttgccagga ctccttcatg 1800

tacgacaccc ctcaggaagt ggccgaggcc ttcctgtcct ccctgaccga gacaatcgag 1860

ggcgtggacg ccgaggatgg ccacggccct ggcgagcagc aggccgctgc catcgtgctg 1920

gacccctccg gctccatgaa catctacctg gtgctggacg gctccggcag catcggcgcc 1980

tccgacttca ccggcgccaa gaagtgcctg gtcaacctga tcgagaaggt ggcctcctac 2040

ggcgtgaagc ctagatacgg cctggtgacc tacgccacct accctaagat ctgggtgaag 2100

gtgtccgagg ccgactcctc caacgccgac tgggtgacca agcagctgaa cgagatcaac 2160

tacgaggacc acaagctgaa gtccggcacc aacaccaaga aggccctgca ggccgtctac 2220

tccatgatgt cctggcctga cgacgtgcct cctgagggct ggaaccggac ccggcacgtg 2280

attatcctga tgaccgacgg cctgcacaac atgggcggcg accctatcac cgtgatcgac 2340

gagatccggg acctgctgta catcggcaag gaccggaaga accctcggga ggactacctg 2400

gacgtgtacg tgttcggcgt gggccctctg gtgaaccagg tcaacatcaa cgccctggcc 2460

tccaagaagg acaacgagca gcacgtgttc aaggtcaagg acatggagaa cctggaggac 2520

gtgttctacc agatgatcga tgagtcccag tccctgagcc tgtgcggcat ggtctgggag 2580

caccgcaagg gaaccgacta ccacaagcag ccttggcagg ccaagatctc cgtgatccgg 2640

ccttccaagg gccacgagtc ctgcatgggc gccgtggtgt ccgagtactt cgtgctgacc 2700

gccgctcact gcttcaccgt ggacgacaag gaacactcca tcaaagtctc cgtgggcggc 2760

gagaagcggg acctggagat cgaggtggtg ctgttccacc ctaactacaa catcaacggc 2820

aagaaggaag ccggcatccc tgagttctac gactacgacg tggccctgat caagctgaag 2880

aataagctga agtatggcca gaccatccgg cctatctgcc tgccttgcac cgagggcacc 2940

accagggccc tgcggctgcc tcctaccacc acctgccagc agcagaagga agagctgctg 3000

cctgcccagg acatcaaggc cctgttcgtg tccgaggaag agaagaagct gacccggaag 3060

gaagtgtaca tcaagaacgg cgacaagaag ggcagctgcg agcgggacgc ccagtacgcc 3120

cctggctacg ataaggtcaa ggatatctcc gaggtggtga cccctcggtt cctgtgcacc 3180

ggcggagtgt ccccctacgc cgaccctaac acctgcagag gcgactctgg cggccctctg 3240

atcgtgcaca agcggtcccg gttcatccag gtcggcgtga tctcctgggg cgtggtggac 3300

gtgtgcaaga accagaagcg gcagaagcag gtccccgccc acgcccggga cttccacatc 3360

aacctgttcc aggtgctgcc ttggctgaag gaaaagctgc aggatgagga cctgggcttc 3420

ctgagatctc ccccatgccc atcatgccca gcacctgagt tcctgggggg accatcagtc 3480

ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 3540

tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 3600

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 3660

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 3720

tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 3780

gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 3840

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 3900

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 3960

gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg 4020

aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc 4080

ctctccctgt ctccgggtaa atgagtgcta gcctcgagaa ttcacgcgtg gtacctctag 4140

agtcgatcta gggcggccaa ttccgcccct ctccctcccc ccccccctaac gttactggcc 4200

gaagccgctt ggaataaggc cggtgtgcgt ttgtctatat gttattttcc accatattgc 4260

cgtcttttgg caatgtgagg gcccggaaac ctggccctgt cttcttgacg agcattccta 4320

ggggtctttc ccctctcgcc aaaggaatgc aaggtctgtt gaatgtcgtg aaggaagcag 4380

ttcctctgga agcttcttga agacaaacaa cgtctgtagc gacccttttgc aggcagcgga 4440

acccccccacc tggcgacagg tgcctctgcg gccaaaagcc acgtgtataa gatacacctg 4500

caaaggcggc acaaccccag tgccacgttg tgagttggat agttgtggaa agagtcaaat 4560

ggctctcctc aagcgtattc aacaaggggc tgaaggatgc ccagaaggta ccccattgta 4620

tgggatctga tctggggcct cggtgcacat gctttacatg tgtttagtcg aggttaaaaa 4680

aacgtctagg ccccccgaac cacggggacg tggttttcct ttgaaaaaca cgatgataag 4740

cttgccacaa cccgggataa ttcctgcagc caatatggga tcggccattg aacaagatgg 4800

attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttcggctatg actgggcaca 4860

acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgcagg ggcgcccggt 4920

tctttttgtc aagaccgacc tgtccggtgc cctgaatgaa ctgcaggacg aggcagcgcg 4980

gctatcgtgg ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg ttgtcactga 5040

agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc tgtcatctca 5100

ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc tgcatacgct 5160

tgatccggct acctgcccat tcgaccacca agcgaaacat cgcatcgagc gagcacgtac 5220

tcggatggaa gccggtcttg tcgatcagga tgatctggac gaagagcatc aggggctcgc 5280

gccagccgaa ctgttcgcca ggctcaaggc gcgcatgccc gacggcgatg atctcgtcgt 5340

gacccatggc gatgcctgct tgccgaatat catggtggaa aatggccgct tttctggatt 5400

catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt tggctacccg 5460

tgatattgct gaagagcttg gcggcgaatg ggctgaccgc ttcctcgtgc tttacggtat 5520

cgccgctccc gattcgcagc gcatcgcctt ctatcgcctt cttgacgagt tcttctgagg 5580

ggatcaattc tctagtcgac ccgggcggcc tcgagaataa acaatcatta ttttcattgg 5640

atctgtgtgt tggtttttg tgtgggcttg ggggaggggg aggccagaat gactccaaga 5700

gctacaggaa ggcaggtcag agaccccact ggacaaacag tggctggact ctgcaccata 5760

acacacaatc aacaggggag tgagctggat cgagctgctc gagatccggg ctggcgtaat 5820

agcgaagagg cccgcaccga tcgcccttcc caacagttgc gcagcctgaa tggcgaatgg 5880

acgcgccctg tagcggcgca ttaagcgcgg cgggtgtggt ggttacgcgc agcgtgaccg 5940

ctacacttgc cagcgcccta gcgcccgctc ctttcgcttt cttcccttcc tttctcgcca 6000

cgttcgccgg ctttccccgt caagctctaa atcgggggct ccctttaggg ttccgattta 6060

gtgctttacg gcacctcgac cccaaaaaac ttgattaggg tgatggttca cgtagtgggc 6120

catcgccctg atagacggtt tttcgccctt tgacgttgga gtccacgttc tttaatagtg 6180

gactcttgtt ccaaactgga acaacactca accctatctc ggtctattct tttgatttat 6240

aagggatttt gccgatttcg gcctattggt taaaaaatga gctgatttaa caaaaattta 6300

acgcgaattt taacaaaata ttaacgctta caatttcctg atgcggtatt ttctccttac 6360

gcatctgtgc ggtatttcac accgcatatg gtgcactctc agtacaatct gctctgatgc 6420

cgcatagtta agccagcccc gacacccgcc aacacccgct gacgcgccct gacgggcttg 6480

tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct gcatgtgtca 6540

gaggttttca ccgtcatcac cgaaacgcgc gagacgaaag ggcctcgtga tacgcctatt 6600

tttataggtt aatgtcatga taataatggt ttcttagacg tcaggtggca cttttcgggg 6660

aaatgtgcgc ggaacccta tttgtttatt tttctaaata cattcaaata tgtatccgct 6720

catgagacaa taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat 6780

tcaacatttc cgtgtcgccc ttattccctt ttttgcggca ttttgccttc ctgtttttgc 6840

tcacccagaa acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg 6900

ttacatcgaa ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg 6960

ttttccaatg atgagcactt ttaaagttct gctatgtggc gcggtattat cccgtattga 7020

cgccgggcaa gagcaactcg gtcgccgcat acactattct cagaatgact tggttgagta 7080

ctcaccagtc acagaaaagc atcttacgga tggcatgaca gtaagagaat tatgcagtgc 7140

tgccataacc atgagtgata acactgcggc caacttactt ctgacaacga tcggaggacc 7200

gaaggagcta accgcttttt tgcacaacat gggggatcat gtaactcgcc ttgatcgttg 7260

ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctgtagc 7320

aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca 7380

acaattaata gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct 7440

tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat 7500

cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg 7560

gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat 7620

taagcattgg taactgtcag accaagttta ctcatatata ctttagattg atttaaaact 7680

tcatttttaa tttaaaagga tctaggtgaa gatccttttt gataatctca tgaccaaaat 7740

ccccttaacgt gagttttcgt tccactgagc gtcagacccc gtagaaaaga tcaaaggatc 7800

ttcttgagat cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct 7860

accagcggtg gtttgtttgc cggatcaaga gctaccaact ctttttccga aggtaactgg 7920

cttcagcaga gcgcagatac caaatactgt tcttctagtg tagccgtagt taggccacca 7980

cttcaagaac tctgtagcac cgcctacata cctcgctctg ctaatcctgt taccagtggc 8040

tgctgccagt ggcgataagt cgtgtcttac cgggttggac tcaagacgat agttaccgga 8100

taaggcgcag cggtcgggct gaacgggggg ttcgtgcaca gcccagct tggagcgaac 8160

gacctacacc gaactgagat acctacagcg tgagctatga gaaagcgcca cgcttcccga 8220

agggagaaag gcggacaggt atccggtaag cggcagggtc ggaacaggag agcgcacgag 8280

ggagcttcca gggggaaacg cctggtatct ttatagtcct gtcgggtttc gccacctctg 8340

acttgagcgt cgatttttgt gatgctcgtc agggggggcgg agcctatgga aaaacgccag 8400

caacgcggcc tttttacggt tcctggcctt ttgctggcct tttgctcaca tggctcgaca 8460

gatct 8465

<210> 19
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
gcgcaccggt gctagcgaat tcggcgacaa gaagggcagc tgcga 45

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
gcgcagatct caggaagccc aggtcctcat 30

<210> 21
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog with Fc domain

<400> 21

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

```
Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
        35                  40                  45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
    50                  55                  60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65                  70                  75                  80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
                85                  90                  95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
            100                 105                 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
        115                 120                 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
    130                 135                 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145                 150                 155                 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                165                 170                 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300
```

```
Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575
```

```
Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
            740                 745                 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu Arg Ser Pro Pro
        755                 760                 765

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
    770                 775                 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785                 790                 795                 800

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
                805                 810                 815

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            820                 825                 830

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
        835                 840                 845
```

```
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    850                 855                 860

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
865                 870                 875                 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                885                 890                 895

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            900                 905                 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        915                 920                 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    930                 935                 940

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
945                 950                 955                 960

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                965                 970                 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            980                 985                 990
```

<210> 22
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 22

```
Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1               5                   10                  15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
            20                  25                  30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
        35                  40                  45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
    50                  55                  60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65                  70                  75                  80
```

```
Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
                85                  90                  95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
            100                 105                 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
        115                 120                 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
    130                 135                 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145                 150                 155                 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                165                 170                 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Ser Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350
```

```
Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620
```

```
Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
            740                 745                 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu Arg Ser Pro Pro
        755                 760                 765

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
    770                 775                 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785                 790                 795                 800

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
                805                 810                 815

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            820                 825                 830

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
        835                 840                 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    850                 855                 860

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
865                 870                 875                 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                885                 890                 895
```

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
900 905 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
915 920 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
930 935 940

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
945 950 955 960

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
965 970 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985 990

<210> 23
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 23

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1 5 10 15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20 25 30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
35 40 45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140

```
Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145                 150                 155                 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                165                 170                 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Ser Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415
```

```
Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685
```

```
Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735

His Ala Arg Asn Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
            740                 745                 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu Arg Ser Pro Pro
        755                 760                 765

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
    770                 775                 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785                 790                 795                 800

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
                805                 810                 815

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            820                 825                 830

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
        835                 840                 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    850                 855                 860

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
865                 870                 875                 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                885                 890                 895

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            900                 905                 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        915                 920                 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    930                 935                 940

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
945                 950                 955                 960
```

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
965 970 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985 990

<210> 24
<211> 6860
<212> DNA
<213> Artificial Sequence

<220>
<223> expression construct

<400> 24
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt acttaatacg actcactata ggctagcgcc accatgggct ccaacctgtc 1080

cccccagctg tgcctgatgc ctttcatcct gggcctgctg tctggcggcg tgaccaccac 1140

cccttggtcc ctggccaggc ctcagggctc ctgctccctg gagggcgtgg agatcaaggg 1200

cggctccttc cggctgctgc aggaaggcca ggctctggag tacgtgtgcc cttccggctt 1260

ctaccttac cctgtgcaga caaggacctg taggtccacc ggctcttggt ccacactgaa 1320

aacccaggac cagaaaaccg tccggaaggc cgagtgccgg gccatccact gccctcggcc 1380

tcacgacttc gagaacggcg agtactggcc tcggtcccct tactacaacg tgtccgacga 1440

gatctccttc cactgctacg acggctacac cctgcggggc tccgccaaca ggacctgcca 1500

ggtcaacggc cggtggtccg gccagaccgc catctgcgac aacggcgctg gctactgctc 1560

caaccctggc atccctatcg gcacccggaa ggtcggctcc cagtaccggc tggaggactc 1620

cgtgacctac cactgctcca gaggcctgac cctgagaggc tcccagcggc gcacctgtca 1680

ggaaggtggc agctggtctg gcaccgaacc atcttgccag gactccttca tgtacgacac 1740

ccctcaggaa gtggccgagg ccttcctgtc ctccctgacc gagacaatcg agggcgtgga 1800

cgccgaggat ggccacggcc ctggcgagca gcaggccgct gccatcgtgc tggacccctc 1860

cggctccatg aacatctacc tggtgctgga cggctccggc agcatcggcg cctccgactt 1920

caccggcgcc aagaagagcc tggtcaacct gatcgagaag gtggcctcct acggcgtgaa 1980

gcctagatac ggcctggtga cctacgccac ctaccctaag atctgggtga aggtgtccga 2040

ggccgactcc tccaacgccg actgggtgac caagcagctg aacgagatca actacgagga 2100

ccacaagctg aagtccggca ccaacaccaa gaaggccctg caggccgtct actccatgat 2160

gtcctggcct gacgacgtgc ctcctgaggg ctggaaccgg acccggcacg tgattatcct 2220

gatgaccgac ggcctgcaca acatgggcgg cgaccctatc accgtgatcg acgagatccg 2280

ggacctgctg tacatcggca aggaccggaa gaaccctcgg gaggactacc tggacgtgta 2340

cgtgttcggc gtgggccctc tggtgaacca ggtcaacatc aacgccctgg cctccaagaa 2400

ggacaacgag cagcacgtgt tcaaggtcaa ggacatggag aacctggagg acgtgttcta 2460

ccagatgatc gatgagtccc agtccctgag cctgtgcggc atgtgataag ctagcctcga 2520

gaattcacgc gtggtacctc tagagtcgac cctctagggc ggccaattcc gcccctctcc 2580

ctccccccccc cctaacgtta ctggccgaag ccgcttggaa taaggccggt gtgcgtttgt 2640

ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc ggaaacctgg 2700

ccctgtcttc ttgacgagca ttcctagggg tctttcccct ctcgccaaag gaatgcaagg 2760

tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac aaacaacgtc 2820

tgtagcgacc ctttgcaggc agcggaaccc cccacctggc gacaggtgcc tctgcggcca 2880

aaagccacgt gtataagata cacctgcaaa ggcggcacaa ccccagtgcc acgttgtgag 2940

ttggatagtt gtggaaagag tcaaatggct ctcctcaagc gtattcaaca aggggctgaa 3000

ggatgcccag aaggtacccc attgtatggg atctgatctg gggcctcggt gcacatgctt 3060

tacatgtgtt tagtcgaggt taaaaaaacg tctaggcccc ccgaaccacg gggacgtggt 3120

tttcctttga aaaacacgat gataagcttg ccacaacccg ggataattcc tgcagccaat 3180

atgggatcgg ccattgaaca agatggattg cacgcaggtt ctccggccgc ttgggtggag 3240

aggctattcg gctatgactg ggcacaacag acaatcggct gctctgatgc cgccgtgttc 3300

cggctgtcag cgcaggggcg cccggttctt tttgtcaaga ccgacctgtc cggtgccctg 3360

aatgaactgc aggacgaggc agcgcggcta tcgtggctgg ccacgacggg cgttccttgc 3420

gcagctgtgc tcgacgttgt cactgaagcg ggaagggact ggctgctatt gggcgaagtg 3480

ccggggcagg atctcctgtc atctcacctt gctcctgccg agaaagtatc catcatggct 3540

gatgcaatgc ggcggctgca tacgcttgat ccggctacct gcccattcga ccaccaagcg 3600

aaacatcgca tcgagcgagc acgtactcgg atggaagccg gtcttgtcga tcaggatgat 3660

ctggacgaag agcatcaggg gctcgcgcca gccgaactgt tcgccaggct caaggcgcgc 3720

atgcccgacg gcgatgatct cgtcgtgacc catggcgatg cctgcttgcc gaatatcatg 3780

gtggaaaatg gccgcttttc tggattcatc gactgtggcc ggctgggtgt ggcggaccgc 3840

tatcaggaca tagcgttggc tacccgtgat attgctgaag agcttggcgg cgaatgggct 3900

gaccgcttcc tcgtgcttta cggtatcgcc gctcccgatt cgcagcgcat cgccttctat 3960

cgccttcttg acgagttctt ctgaggggat caattctggg cggcctcgag aataaacaat 4020

cattattttc attggatctg tgtgttggtt ttttgtgtgg gcttggggga gggggaggcc 4080

agaatgactc caagagctac aggaaggcag gtcagagacc ccactggaca aacagtggct 4140

ggactctgca ccataacaca caatcaacag gggagtgagc tggatcgagc tgctcgagat 4200

ccgggctggc gtaatagcga agaggcccgc accgatcgcc cttcccaaca gttgcgcagc 4260

ctgaatggcg aatggacgcg ccctgtagcg gcgcattaag cgcggcgggt gtggtggtta 4320

cgcgcagcgt gaccgctaca cttgccagcg ccctagcgcc cgctcctttc gctttcttcc 4380

cttcctttct cgccacgttc gccggctttc cccgtcaagc tctaaatcgg gggctccctt 4440

tagggttccg atttagtgct ttacggcacc tcgaccccaa aaaacttgat tagggtgatg 4500

gttcacgtag tgggccatcg ccctgataga cggtttttcg ccctttgacg ttggagtcca 4560

cgttctttaa tagtggactc ttgttccaaa ctggaacaac actcaaccct atctcggtct 4620

attcttttga tttataaggg attttgccga tttcggccta ttggttaaaa aatgagctga 4680

tttaacaaaa atttaacgcg aattttaaca aaatattaac gcttacaatt tcctgatgcg 4740

gtattttctc cttacgcatc tgtgcggtat ttcacaccgc atatggtgca ctctcagtac 4800

aatctgctct gatgccgcat agttaagcca gccccgacac ccgccaacac ccgctgacgc 4860

gccctgacgg gcttgtctgc tcccggcatc cgcttacaga caagctgtga ccgtctccgg 4920

gagctgcatg tgtcagaggt tttcaccgtc atcaccgaaa cgcgcgagac gaaagggcct 4980

cgtgatacgc ctatttttat aggttaatgt catgataata atggtttctt agacgtcagg 5040

tggcactttt cggggaaatg tgcgcggaac ccctatttgt ttatttttct aaatacattc 5100

aaatatgtat ccgctcatga gacaataacc ctgataaatg cttcaataat attgaaaaag 5160

gaagagtatg agtattcaac atttccgtgt cgcccttatt cccttttttg cggcattttg 5220

ccttcctgtt tttgctcacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt 5280

gggtgcacga gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt 5340

tcgccccgaa gaacgttttc caatgatgag cacttttaaa gttctgctat gtggcgcggt 5400

attatcccgt attgacgccg ggcaagagca actcggtcgc cgcatacact attctcagaa 5460

tgacttggtt gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag 5520

agaattatgc agtgctgcca taaccatgag tgataacact gcggccaact tacttctgac 5580

aacgatcgga ggaccgaagg agctaaccgc ttttttgcac aacatggggg atcatgtaac 5640

tcgccttgat cgttgggaac cggagctgaa tgaagccata ccaaacgacg agcgtgacac 5700

cacgatgcct gtagcaatgg caacaacgtt gcgcaaacta ttaactggcg aactacttac 5760

tctagcttcc cggcaacaat taatagactg gatggaggcg gataaagttg caggaccact 5820

tctgcgctcg gcccttccgg ctggctggtt tattgctgat aaatctggag ccggtgagcg 5880

tgggtctcgc ggtatcattg cagcactggg gccagatggt aagccctccc gtatcgtagt 5940

tatctacacg acggggagtc aggcaactat ggatgaacga aatagacaga tcgctgagat 6000

aggtgcctca ctgattaagc attggtaact gtcagaccaa gtttactcat atatacttta 6060

gattgattta aaacttcatt tttaatttaa aaggatctag gtgaagatcc tttttgataa 6120

tctcatgacc aaaatccctt aacgtgagtt ttcgttccac tgagcgtcag accccgtaga 6180

aaagatcaaa ggatcttctt gagatccttt ttttctgcgc gtaatctgct gcttgcaaac 6240

aaaaaaacca ccgctaccag cggtggtttg tttgccggat caagagctac caactctttt 6300

tccgaaggta actggcttca gcagagcgca gataccaaat actgttcttc tagtgtagcc 6360

gtagttaggc caccacttca agaactctgt agcaccgcct acatacctcg ctctgctaat 6420

cctgttacca gtggctgctg ccagtggcga taagtcgtgt cttaccgggt tggactcaag 6480

acgatagtta ccggataagg cgcagcggtc gggctgaacg gggggttcgt gcacacagcc 6540

cagcttggag cgaacgacct acaccgaact gagataccta cagcgtgagc tatgagaaag 6600

cgccacgctt cccgaaggga gaaaggcgga caggtatccg gtaagcggca gggtcggaac 6660

aggagagcgc acgagggagc ttccaggggg aaacgcctgg tatctttata gtcctgtcgg 6720

gtttcgccac ctctgacttg agcgtcgatt tttgtgatgc tcgtcagggg ggcggagcct 6780

atggaaaaac gccagcaacg cggccttttt acggttcctg gcctttgct ggccttttgc 6840

tcacatggct cgacagatct 6860

<210> 25
<211> 8435
<212> DNA
<213> Artificial Sequence

<220>
<223> expression construct

<400> 25
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc 660

cgccccgttg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcactagaag ctttattgcg gtagtttatc acagttaaat 780

tgctaacgca gtcagtgctt ctgacacaac agtctcgaac ttaagctgca gaagttggtc 840

gtgaggcact gggcaggtaa gtatcaaggt tacaagacag gtttaaggag accaatagaa 900

actgggcttg tcgagacaga gaagactctt gcgtttctga taggcaccta ttggtcttac 960

tgacatccac tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta 1020

aggctagagt acttaatacg actcactata ggctagctcc tgccccaggc ccagcttctc 1080

tcctgccttc caacgccatg ggctccaacc tgtcccccca gctgtgcctg atgcctttca 1140

tcctgggcct gctgtctggc ggcgtgacca ccacccttg gtccctggcc aggcctcagg 1200

gctcctgctc cctggagggc gtggagatca agggcggctc cttccggctg ctgcaggaag 1260

gccaggctct ggagtacgtg tgcccttccg gcttctaccc ttaccctgtg cagacaagga 1320

cctgtaggtc caccggctct tggtccacac tgaaaaccca ggaccagaaa accgtccgga 1380

aggccgagtg ccgggccatc cactgccctc ggcctcacga cttcgagaac ggcgagtact 1440

ggcctcggtc cccttactac aacgtgtccg acgagatctc cttccactgc tacgacggct 1500

acaccctgcg gggctccgcc aacaggacct gccaggtcaa cggccggtgg tccggccaga 1560

ccgccatctg cgacaacggc gctggctact gctccaaccc tggcatccct atcggcaccc 1620

ggaaggtcgg ctcccagtac cggctggagg actccgtgac ctaccactgc tccagaggcc 1680

tgaccctgag aggctcccag cggcgcacct gtcaggaagg tggcagctgg tctggcaccg 1740

aaccatcttg ccaggactcc ttcatgtacg acacccctca ggaagtggcc gaggccttcc 1800

tgtcctccct gaccgagaca atcgagggcg tggacgccga ggatggccac ggccctggcg 1860

agcagcaggc cgctgccatc gtgctggacc cctccggctc catgaacatc tacctggtgc 1920

tggacggctc cggcagcatc ggcgcctccg acttcaccgg cgccaagaag agcctggtca 1980

acctgatcga gaaggtggcc tcctacggcg tgaagcctag atacggcctg gtgacctacg 2040

ccacctaccc taagatctgg gtgaaggtgt ccgaggccga ctcctccaac gccgactggg 2100

tgaccaagca gctgaacgag atcaactacg aggaccacaa gctgaagtcc ggcaccaaca 2160

ccaagaaggc cctgcaggcc gtctactcca tgatgtcctg gcctgacgac gtgcctcctg 2220

agggctggaa ccggacccgg cacgtgatta tcctgatgac cgacggcctg cacaacatgg 2280

gcggcgaccc tatcaccgtg atcgacgaga tccgggacct gctgtacatc ggcaaggacc 2340

ggaagaaccc tcgggaggac tacctggacg tgtacgtgtt cggcgtgggc cctctggtga 2400

accaggtcaa catcaacgcc ctggcctcca agaaggacaa cgagcagcac gtgttcaagg 2460

tcaaggacat ggagaacctg gaggacgtgt tctaccagat gatcgatgag tcccagtccc 2520

tgagcctgtg cggcatggtc tgggagcacc gcaagggaac cgactaccac aagcagcctt 2580

ggcaggccaa gatctccgtg atccggcctt ccaagggcca cgagtcctgc atgggcgccg 2640

tggtgtccga gtacttcgtg ctgaccgccg ctcactgctt caccgtggac gacaaggaac 2700

actccatcaa agtctccgtg ggcggcgaga agcgggacct ggagatcgag gtggtgctgt 2760

tccaccctaa ctacaacatc aacggcaaga aggaagccgg catccctgag ttctacgact 2820

acgacgtggc cctgatcaag ctgaagaata agctgaagta tggccagacc atccggccta 2880

tctgcctgcc ttgcaccgag ggcaccacca gggccctgcg gctgcctcct accaccacct 2940

gccagcagca gaaggaagag ctgctgcctg cccaggacat caaggccctg ttcgtgtccg 3000

aggaagagaa gaagctgacc cggaaggaag tgtacatcaa gaacggcgac aagaagggca 3060

gctgcgagcg ggacgcccag tacgcccctg gctacgataa ggtcaaggat atctccgagg 3120

tggtgacccc tcggttcctg tgcaccggcg gagtgtcccc ctacgccgac cctaacacct 3180

gcagaggcga ctctggcggc cctctgatcg tgcacaagcg gtcccggttc atccaggtcg 3240

gcgtgatctc ctggggcgtg gtggacgtgt gcaagaacca gaagcggcag aagcaggtcc 3300

ccgcccacgc ccgggacttc cacatcaacc tgttccaggt gctgccttgg ctgaaggaaa 3360

agctgcagga tgaggacctg ggcttcctga gatccaacac caaggtggac aagagagttg 3420

agtccaaata tggtccccca tccccatcat ccccagcacc tgagttcctg gggggaccat 3480

cagtcttcct gttcccccca aaacccaagg acactctcat gatctcccgg acccctgagg 3540

tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc aactggtacg 3600

tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag ttcaacagca 3660

cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt 3720

acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc atctccaaag 3780

ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag gaggagatga 3840

ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc gacatcgccg 3900

tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgctgg 3960

actccgacgg ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg 4020

aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac tacacacaga 4080

agagcctctc cctgtctctg ggtaaatgag tctagacagg ggcgtgggat tgacgcccct 4140

ctccctcccc ccccccctaac gttactggcc gaagccgctt ggaataaggc cggtgtgcgt 4200

ttgtctatat gttattttcc accatattgc cgtcttttgg caatgtgagg gcccggaaac 4260

ctggccctgt cttcttgacg agcattccta ggggtctttc ccctctcgcc aaaggaatgc 4320

aaggtctgtt gaatgtcgtg aaggaagcag ttcctctgga agcttcttga agacaaacaa 4380

cgtctgtagc gacccttttgc aggcagcgga acccccccacc tggcgacagg tgcctctgcg 4440

gccaaaagcc acgtgtataa gatacacctg caaaggcggc acaaccccag tgccacgttg 4500

tgagttggat agttgtggaa agagtcaaat ggctctcctc aagcgtattc aacaaggggc 4560

tgaaggatgc ccagaaggta ccccattgta tgggatctga tctggggcct cggtgcacat 4620

gctttacatg tgtttagtcg aggttaaaaa aacgtctagg ccccccgaac cacggggacg 4680

tggttttcct ttgaaaaaca cgatgataag cttgccacaa cccgggataa ttcctgcagc 4740

caatatggga tcggccattg aacaagatgg attgcacgca ggttctccgg ccgcttgggt 4800

ggagaggcta ttcggctatg actgggcaca acagacaatc ggctgctctg atgccgccgt 4860

gttccggctg tcagcgcagg ggcgcccggt tctttttgtc aagaccgacc tgtccggtgc 4920

cctgaatgaa ctgcaggacg aggcagcgcg gctatcgtgg ctggccacga cgggcgttcc 4980

ttgcgcagct gtgctcgacg ttgtcactga agcgggaagg gactggctgc tattgggcga 5040

agtgccgggg caggatctcc tgtcatctca ccttgctcct gccgagaaag tatccatcat 5100

ggctgatgca atgcggcggc tgcatacgct tgatccggct acctgcccat tcgaccacca 5160

agcgaaacat cgcatcgagc gagcacgtac tcggatggaa gccggtcttg tcgatcagga 5220

tgatctggac gaagagcatc aggggctcgc gccagccgaa ctgttcgcca ggctcaaggc 5280

gcgcatgccc gacggcgatg atctcgtcgt gacccatggc gatgcctgct tgccgaatat 5340

catggtggaa aatggccgct tttctggatt catcgactgt ggccggctgg gtgtggcgga 5400

ccgctatcag gacatagcgt tggctacccg tgatattgct gaagagcttg gcggcgaatg 5460

ggctgaccgc ttcctcgtgc tttacggtat cgccgctccc gattcgcagc gcatcgcctt 5520

ctatcgcctt cttgacgagt tcttctgagg ggatcaattc tctagtcgac ccgggcggcc 5580

tcgagaataa acaatcatta ttttcattgg atctgtgtgt tggtttttg tgtgggcttg 5640

ggggaggggg aggccagaat gactccaaga gctacaggaa ggcaggtcag agaccccact 5700

ggacaaacag tggctggact ctgcaccata acacacaatc aacaggggag tgagctggat 5760

cgagctgctc gagatccggg ctggcgtaat agcgaagagg cccgcaccga tcgcccttcc 5820

caacagttgc gcagcctgaa tggcgaatgg acgcgccctg tagcggcgca ttaagcgcgg 5880

cgggtgtggt ggttacgcgc agcgtgaccg ctacacttgc cagcgcccta gcgcccgctc 5940

ctttcgcttt cttcccttcc tttctcgcca cgttcgccgg ctttccccgt caagctctaa 6000

atcgggggct ccctttaggg ttccgattta gtgctttacg gcacctcgac cccaaaaaac 6060

ttgattaggg tgatggttca cgtagtgggc catcgccctg atagacggtt tttcgccctt 6120

tgacgttgga gtccacgttc tttaatagtg gactcttgtt ccaaactgga acaacactca 6180

accctatctc ggtctattct tttgatttat aagggatttt gccgatttcg gcctattggt 6240

taaaaaatga gctgatttaa caaaaattta acgcgaattt taacaaaata ttaacgctta 6300

caatttcctg atgcggtatt ttctccttac gcatctgtgc ggtatttcac accgcatatg 6360

gtgcactctc agtacaatct gctctgatgc cgcatagtta agccagcccc gacacccgcc 6420

aacacccgct gacgcgccct gacgggcttg tctgctcccg gcatccgctt acagacaagc 6480

tgtgaccgtc tccgggagct gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc 6540

gagacgaaag ggcctcgtga tacgcctatt tttataggtt aatgtcatga taataatggt 6600

ttcttagacg tcaggtggca cttttcgggg aaatgtgcgc ggaacccctа tttgtttatt 6660

tttctaaata cattcaaata tgtatccgct catgagacaa taaccctgat aaatgcttca 6720

ataatattga aaaaggaaga gtatgagtat tcaacatttc cgtgtcgccc ttattccctt 6780

ttttgcggca ttttgccttc ctgtttttgc tcacccagaa acgctggtga aagtaaaaga 6840

tgctgaagat cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa 6900

gatccttgag agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct 6960

gctatgtggc gcggtattat cccgtattga cgccgggcaa gagcaactcg gtcgccgcat 7020

acactattct cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga 7080

tggcatgaca gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc 7140

caacttactt ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat 7200

gggggatcat gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa 7260

cgacgagcgt gacaccacga tgcctgtagc aatggcaaca acgttgcgca aactattaac 7320

tggcgaacta cttactctag cttcccggca acaattaata gactggatgg aggcggataa 7380

agttgcagga ccacttctgc gctcggccct tccggctggc tggtttattg ctgataaatc 7440

tggagccggt gagcgtgggt ctcgcggtat cattgcagca ctggggccag atggtaagcc 7500

ctcccgtatc gtagttatct acacgacggg gagtcaggca actatggatg aacgaaatag 7560

acagatcgct gagataggtg cctcactgat taagcattgg taactgtcag accaagttta 7620

ctcatatata ctttagattg atttaaaact tcatttttaa tttaaaagga tctaggtgaa 7680

gatccttttt gataatctca tgaccaaaat cccttaacgt gagttttcgt tccactgagc 7740

gtcagacccc gtagaaaaga tcaaaggatc ttcttgagat cctttttttc tgcgcgtaat 7800

ctgctgcttg caaacaaaaa aaccaccgct accagcggtg gtttgtttgc cggatcaaga 7860

gctaccaact ctttttccga aggtaactgg cttcagcaga gcgcagatac caaatactgt 7920

tcttctagtg tagccgtagt taggccacca cttcaagaac tctgtagcac cgcctacata 7980

cctcgctctg ctaatcctgt taccagtggc tgctgccagt ggcgataagt cgtgtcttac 8040

cgggttggac tcaagacgat agttaccgga taaggcgcag cggtcgggct gaacgggggg 8100

ttcgtgcaca cagcccagct tggagcgaac gacctacacc gaactgagat acctacagcg 8160

tgagctatga gaaagcgcca cgcttcccga agggagaaag gcggacaggt atccggtaag 8220

cggcagggtc ggaacaggag agcgcacgag ggagcttcca gggggaaacg cctggtatct 8280

ttatagtcct gtcgggtttc gccacctctg acttgagcgt cgatttttgt gatgctcgtc 8340

agggggggcgg agcctatgga aaaacgccag caacgcggcc tttttacggt tcctggcctt 8400

ttgctggcct tttgctcaca tggctcgaca gatct 8435

<210> 26
<211> 1003

<212> PRT
<213> Artificial Sequence

<220>
<223> complement factor B protein analog

<400> 26

```
Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1               5                  10                  15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
            20                  25                  30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
        35                  40                  45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
    50                  55                  60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65                  70                  75                  80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
                85                  90                  95

Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
            100                 105                 110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
        115                 120                 125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
    130                 135                 140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145                 150                 155                 160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                165                 170                 175

Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
            180                 185                 190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
        195                 200                 205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
    210                 215                 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225                 230                 235                 240
```

```
Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                245                 250                 255

Gln Ala Ala Ala Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260                 265                 270

Leu Val Leu Asp Gly Ser Gly Ser Ile Gly Ala Ser Asp Phe Thr Gly
        275                 280                 285

Ala Lys Lys Ser Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
    290                 295                 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305                 310                 315                 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                325                 330                 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
            340                 345                 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
        355                 360                 365

Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
    370                 375                 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385                 390                 395                 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                405                 410                 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
            420                 425                 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
        435                 440                 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
    450                 455                 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465                 470                 475                 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                485                 490                 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
            500                 505                 510
```

```
Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
        515                 520                 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
    530                 535                 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545                 550                 555                 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                565                 570                 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
            580                 585                 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
        595                 600                 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
    610                 615                 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625                 630                 635                 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
                645                 650                 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
            660                 665                 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
        675                 680                 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
    690                 695                 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705                 710                 715                 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
                725                 730                 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
            740                 745                 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu Arg Ser Asn Thr
        755                 760                 765

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser
    770                 775                 780
```

```
Ser Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
785                 790                 795                 800


Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                805                 810                 815


Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            820                 825                 830


Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        835                 840                 845


Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    850                 855                 860


Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
865                 870                 875                 880


Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                885                 890                 895


Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            900                 905                 910


Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        915                 920                 925


Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    930                 935                 940


Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
945                 950                 955                 960


Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                965                 970                 975


Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            980                 985                 990


Thr Gln Lys Ser Leu Ser Leu Ser  Leu Gly Lys
        995                 1000


<210>  27
<211>  238
<212>  PRT
<213>  Homo sapiens

<400>  27

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
1               5                   10                  15


Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
```

```
            20                  25                  30

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        35                  40                  45

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
    50                  55                  60

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
65                  70                  75                  80

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                85                  90                  95

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            100                 105                 110

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
        115                 120                 125

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    130                 135                 140

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
145                 150                 155                 160

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                165                 170                 175

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            180                 185                 190

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
        195                 200                 205

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    210                 215                 220

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
225                 230                 235
```