SEQUENCE LISTING

<110> HCW BIOLOGICS, INC.

<120> MULTI-CHAIN CHIMERIC POLYPEPTIDES AND USES THEREOF

<130> 47039-0005WO1

<140>
<141>

<150> 62/881,088
<151> 2019-07-31

<150> 62/817,241
<151> 2019-03-12

<150> 62/817,230
<151> 2019-03-12

<150> 62/816,683
<151> 2019-03-11

<150> 62/749,506
<151> 2018-10-23

<150> 62/749,007
<151> 2018-10-22

<150> 62/746,832
<151> 2018-10-17

<150> 62/725,043
<151> 2018-08-30

<150> 62/725,010
<151> 2018-08-30

<150> 62/724,969
<151> 2018-08-30

<160> 226

<170> PatentIn version 3.5

<210> 1
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Tissue factor"

<400> 1
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
1   5   10   15

Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
            20   25   30

Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
        35   40   45

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
    50   55   60

Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
65   70   75   80

Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
                85   90   95

Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
            100   105   110

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

Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
    130   135   140

Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
145   150   155   160

Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
                165   170   175

```
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
            180                 185                 190


Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
        195                 200                 205


Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu
    210                 215


<210> 2
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Tissue factor"

<400> 2
agcggcacaa ccaacacagt cgctgcctat aacctcactt ggaagagcac caacttcaaa       60

accatcctcg aatgggaacc caaacccgtt aaccaagttt acaccgtgca gatcagcacc      120

aagtccggcg actggaagtc caaatgtttc tataccaccg acaccgagtg cgatctcacc      180

gatgagatcg tgaaagatgt gaaacagacc tacctcgccc gggtgtttag ctaccccgcc      240

ggcaatgtgg agagcactgg ttccgctggc gagcctttat acgagaacag ccccgaattt      300

acccccttacc tcgagaccaa tttaggacag cccaccatcc aaagctttga gcaagttggc      360

acaaaggtga atgtgacagt ggaggacgag cggactttag tgcggcggaa caacaccttt      420

ctcagcctcc gggatgtgtt cggcaaagat ttaatctaca cactgtatta ctggaagtcc      480

tcttcctccg gcaagaagac agctaaaacc aacacaaacg agtttttaat cgacgtggat      540

aaaggcgaaa actactgttt cagcgtgcaa gctgtgatcc cctcccggac cgtgaatagg      600

aaaagcaccg atagccccgt tgagtgcatg ggccaagaaa agggcgagtt ccgggag         657


<210> 3
<211> 219
<212> PRT
```

<213> Homo sapiens

<220>
<221> source
<223> /note="Tissue factor"

<400> 3
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
1   5   10   15

Thr Asn Phe Ala Thr Ala Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
            20   25   30

Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
        35   40   45

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Ala Leu Thr Asp Glu Ile Val
    50   55   60

Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
65   70   75   80

Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
                85   90   95

Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
            100   105   110

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

Asp Glu Arg Thr Leu Val Ala Arg Asn Asn Thr Ala Leu Ser Leu Arg
    130   135   140

Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
145   150   155   160

Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
                165   170   175

```
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
            180                 185                 190


Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
        195                 200                 205


Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu
    210                 215


<210> 4
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Tissue factor"

<400> 4
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
1               5                   10                  15


Thr Asn Phe Ala Thr Ala Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
            20                  25                  30


Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Ala Lys Ser Lys
        35                  40                  45


Cys Phe Tyr Thr Thr Asp Thr Glu Cys Ala Leu Thr Asp Glu Ile Val
    50                  55                  60


Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
65                  70                  75                  80


Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Ala Glu Asn
                85                  90                  95


Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
```

```
            100                 105                 110

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

Asp Glu Arg Thr Leu Val Ala Arg Asn Asn Thr Ala Leu Ser Leu Arg
    130                 135                 140

Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
145                 150                 155                 160

Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
                165                 170                 175

Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
            180                 185                 190

Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
        195                 200                 205

Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu
    210                 215


<210> 5
<211> 223
<212> PRT
<213> Mus musculus

<220>
<221> source
<223> /note="Tissue factor"

<400> 5
Ala Gly Ile Pro Glu Lys Ala Phe Asn Leu Thr Trp Ile Ser Thr Asp
1               5                   10                  15

Phe Lys Thr Ile Leu Glu Trp Gln Pro Lys Pro Thr Asn Tyr Thr Tyr
            20                  25                  30
```

```
Thr Val Gln Ile Ser Asp Arg Ser Arg Asn Trp Lys Asn Lys Cys Phe
        35                  40                  45

Ser Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp
    50                  55                  60

Val Thr Trp Ala Tyr Glu Ala Lys Val Leu Ser Val Pro Arg Arg Asn
65                  70                  75                  80

Ser Val His Gly Asp Gly Asp Gln Leu Val Ile His Gly Glu Glu Pro
                85                  90                  95

Pro Phe Thr Asn Ala Pro Lys Phe Leu Pro Tyr Arg Asp Thr Asn Leu
            100                 105                 110

Gly Gln Pro Val Ile Gln Gln Phe Glu Gln Asp Gly Arg Lys Leu Asn
        115                 120                 125

Val Val Val Lys Asp Ser Leu Thr Leu Val Arg Lys Asn Gly Thr Phe
    130                 135                 140

Leu Thr Leu Arg Gln Val Phe Gly Lys Asp Leu Gly Tyr Ile Ile Thr
145                 150                 155                 160

Tyr Arg Lys Gly Ser Ser Thr Gly Lys Lys Thr Asn Ile Thr Asn Thr
                165                 170                 175

Asn Glu Phe Ser Ile Asp Val Glu Glu Gly Val Ser Tyr Cys Phe Phe
            180                 185                 190

Val Gln Ala Met Ile Phe Ser Arg Lys Thr Asn Gln Asn Ser Pro Gly
        195                 200                 205

Ser Ser Thr Val Cys Thr Glu Gln Trp Lys Ser Phe Leu Gly Glu
    210                 215                 220
```

<210> 6

<211> 224
<212> PRT
<213> Rattus rattus

<220>
<221> source
<223> /note="Tissue factor"

<400> 6
Ala Gly Thr Pro Pro Gly Lys Ala Phe Asn Leu Thr Trp Ile Ser Thr
1   5   10   15

Asp Phe Lys Thr Ile Leu Glu Trp Gln Pro Lys Pro Thr Asn Tyr Thr
            20   25   30

Tyr Thr Val Gln Ile Ser Asp Arg Ser Arg Asn Trp Lys Tyr Lys Cys
        35   40   45

Thr Gly Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
    50   55   60

Asp Val Asn Trp Thr Tyr Glu Ala Arg Val Leu Ser Val Pro Trp Arg
65   70   75   80

Asn Ser Thr His Gly Lys Glu Thr Leu Phe Gly Thr His Gly Glu Glu
                85   90   95

Pro Pro Phe Thr Asn Ala Arg Lys Phe Leu Pro Tyr Arg Asp Thr Lys
            100   105   110

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

Lys Val Thr Val Lys Asp Ser Phe Thr Leu Val Arg Lys Asn Gly Thr
    130   135   140

Phe Leu Thr Leu Arg Gln Val Phe Gly Asn Asp Leu Gly Tyr Ile Leu
145   150   155   160

Thr Tyr Arg Lys Asp Ser Ser Thr Gly Arg Lys Thr Asn Thr Thr His
165 170 175

Thr Asn Glu Phe Leu Ile Asp Val Glu Lys Gly Val Ser Tyr Cys Phe
180 185 190

Phe Ala Gln Ala Val Ile Phe Ser Arg Lys Thr Asn His Lys Ser Pro
195 200 205

Glu Ser Ile Thr Lys Cys Thr Glu Gln Trp Lys Ser Val Leu Gly Glu
210 215 220

<210> 7
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Linker sequence"

<400> 7
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Linker sequence"

<400> 8
ggcggtggag gatccggagg aggtggctcc ggcggcggag gatct 45

<210> 9
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-2"

<400> 9
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1   5   10   15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
            20   25   30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
        35   40   45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
    50   55   60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65   70   75   80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                85   90   95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
            100   105   110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115   120   125

Ile Ser Thr Leu Thr
    130

<210> 10
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source

<223> /note="IL-3"

<400> 10
Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp Val Asn Cys
1   5   10   15

Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
            20   25   30

Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
        35   40   45

Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
    50   55   60

Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
65   70   75   80

Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
                85   90   95

Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
            100   105   110

Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
        115   120   125

Ser Leu Ala Ile Phe
    130

<210> 11
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-7"

<400> 11

```
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1               5                   10                  15


Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
            20                  25                  30


Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
        35                  40                  45


Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
    50                  55                  60


Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80


Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95


Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110


Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125


Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140


Ile Leu Met Gly Thr Lys Glu His
145                 150


<210> 12
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-8"
```

<400> 12
Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys
1   5   10   15

Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu
            20   25   30

Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val
        35   40   45

Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp
    50   55   60

Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
65   70   75

<210> 13
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-10"

<400> 13
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1   5   10   15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20   25   30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35   40   45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50   55   60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65   70   75   80

```
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95


Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110


Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125


Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140


Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160


<210> 14
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-15"

<400> 14
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1               5                   10                  15


Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
            20                  25                  30


Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
        35                  40                  45


Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
    50                  55                  60


Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
```

65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser

<210> 15
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-17"

<400> 15
Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser Glu Asp Lys
1 5 10 15

Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His Asn Arg Asn
20 25 30

Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser Thr
35 40 45

Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro Ser
50 55 60

Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala Asp
65 70 75 80

Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile
85 90 95

```
Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
            100                 105                 110


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


His His Val Ala
    130


<210> 16
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-18"

<400> 16
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1               5                   10                  15


Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
            20                  25                  30


Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
        35                  40                  45


Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
    50                  55                  60


Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65                  70                  75                  80


Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
                85                  90                  95


Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
            100                 105                 110
```

Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
        115   120   125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
    130   135   140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145   150   155

<210> 17
<211> 352
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="PDGF-DD"

<400> 17
Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg
1   5   10   15

Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr
            20   25   30

Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser
        35   40   45

Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg
    50   55   60

Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln
65   70   75   80

Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val
                85   90   95

Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp
            100   105   110

```
Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln
        115                 120                 125

Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly
    130                 135                 140

Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala
145                 150                 155                 160

Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser
                165                 170                 175

Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu
            180                 185                 190

Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr
        195                 200                 205

Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp
    210                 215                 220

Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val
225                 230                 235                 240

Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro
                245                 250                 255

Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val
            260                 265                 270

Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys
        275                 280                 285

Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys
    290                 295                 300
```

```
Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile
305                 310                 315                 320


Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu
                325                 330                 335


Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg
            340                 345                 350


<210> 18
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="SCF"

<400> 18
Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr
1               5                   10                  15


Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr
            20                  25                  30


Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met
        35                  40                  45


Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser
    50                  55                  60


Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
65                  70                  75                  80


Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys
                85                  90                  95


Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro
            100                 105                 110
```

```
Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
        115                 120                 125

Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu
    130                 135                 140

Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
145                 150                 155                 160

Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn
                165                 170                 175

Arg Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala
            180                 185                 190

Met Ala Leu Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly
        195                 200                 205

Ala Leu Tyr Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu
    210                 215                 220

Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu
225                 230                 235                 240

Lys Glu Arg Glu Phe Gln Glu Val
                245
```

<210> 19
<211> 209
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="FLT3L"

<400> 19
```
Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala
```

```
1               5                   10                  15

Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
            20                  25                  30

Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
        35                  40                  45

Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
    50                  55                  60

Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
65                  70                  75                  80

Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
                85                  90                  95

Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
            100                 105                 110

Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
        115                 120                 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser
    130                 135                 140

Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu
145                 150                 155                 160

Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala
                165                 170                 175

Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly
            180                 185                 190

Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu
        195                 200                 205
```

His

<210> 20
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="MICA"

<400> 20
Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val Leu Ser Trp Asp Gly
1   5   10   15

Ser Val Gln Ser Gly Phe Leu Thr Glu Val His Leu Asp Gly Gln Pro
            20   25   30

Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala Lys Pro Gln Gly Gln
        35   40   45

Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp Asp Arg Glu Thr Arg
    50   55   60

Asp Leu Thr Gly Asn Gly Lys Asp Leu Arg Met Thr Leu Ala His Ile
65   70   75   80

Lys Asp Gln Lys Glu Gly Leu His Ser Leu Gln Glu Ile Arg Val Cys
                85   90   95

Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser Gln His Phe Tyr Tyr
            100   105   110

Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Lys Glu Trp Thr
        115   120   125

Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Arg Asn

```
    130                 135                 140

Phe Leu Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr His Ala Met
145                 150                 155                 160

His Ala Asp Cys Leu Gln Glu Leu Arg Arg Tyr Leu Lys Ser Gly Val
                165                 170                 175

Val Leu Arg Arg Thr Val Pro Pro Met Val Asn Val Thr Arg Ser Glu
            180                 185                 190

Ala Ser Glu Gly Asn Ile Thr Val Thr Cys Arg Ala Ser Gly Phe Tyr
        195                 200                 205

Pro Trp Asn Ile Thr Leu Ser Trp Arg Gln Asp Gly Val Ser Leu Ser
    210                 215                 220

His Asp Thr Gln Gln Trp Gly Asp Val Leu Pro Asp Gly Asn Gly Thr
225                 230                 235                 240

Tyr Gln Thr Trp Val Ala Thr Arg Ile Cys Gln Gly Glu Glu Gln Arg
                245                 250                 255

Phe Thr Cys Tyr Met Glu His Ser Gly Asn His Ser Thr His Pro Val
            260                 265                 270

Pro Ser Gly Lys Val Leu Val Leu Gln Ser His Trp Gln Thr Phe His
        275                 280                 285

Val Ser Ala Val Ala Ala Ala Ala Ile Phe Val Ile Ile Ile Phe Tyr
    290                 295                 300

Val Arg Cys Cys Lys Lys Lys Thr Ser Ala Ala Glu Gly Pro Glu Leu
305                 310                 315                 320

Val Ser Leu Gln Val Leu Asp Gln His Pro Val Gly Thr Ser Asp His
                325                 330                 335
```

```
Arg Asp Ala Thr Gln Leu Gly Phe Gln Pro Leu Met Ser Asp Leu Gly
            340                 345                 350


Ser Thr Gly Ser Thr Glu Gly Ala
        355                 360


<210> 21
<211> 361
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="MICB"

<400> 21
Ala Glu Pro His Ser Leu Arg Tyr Asn Leu Met Val Leu Ser Gln Asp
1               5                   10                  15


Glu Ser Val Gln Ser Gly Phe Leu Ala Glu Gly His Leu Asp Gly Gln
            20                  25                  30


Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg Arg Ala Lys Pro Gln Gly
        35                  40                  45


Gln Trp Ala Glu Asp Val Leu Gly Ala Lys Thr Trp Asp Thr Glu Thr
    50                  55                  60


Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu Arg Arg Thr Leu Thr His
65                  70                  75                  80


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


Cys Glu Ile His Glu Asp Ser Ser Thr Arg Gly Ser Arg His Phe Tyr
            100                 105                 110


Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Gln Glu Ser
```

```
        115                 120                 125

Thr Val Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Thr
    130                 135                 140

Asn Phe Trp Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr Arg Ala
145                 150                 155                 160

Met Gln Ala Asp Cys Leu Gln Lys Leu Gln Arg Tyr Leu Lys Ser Gly
                165                 170                 175

Val Ala Ile Arg Arg Thr Val Pro Pro Met Val Asn Val Thr Cys Ser
            180                 185                 190

Glu Val Ser Glu Gly Asn Ile Thr Val Thr Cys Arg Ala Ser Ser Phe
        195                 200                 205

Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg Gln Asp Gly Val Ser Leu
    210                 215                 220

Ser His Asn Thr Gln Gln Trp Gly Asp Val Leu Pro Asp Gly Asn Gly
225                 230                 235                 240

Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile Arg Gln Gly Glu Glu Gln
                245                 250                 255

Arg Phe Thr Cys Tyr Met Glu His Ser Gly Asn His Gly Thr His Pro
            260                 265                 270

Val Pro Ser Gly Lys Val Leu Val Leu Gln Ser Gln Arg Thr Asp Phe
        275                 280                 285

Pro Tyr Val Ser Ala Ala Met Pro Cys Phe Val Ile Ile Ile Ile Leu
    290                 295                 300

Cys Val Pro Cys Cys Lys Lys Lys Thr Ser Ala Ala Glu Gly Pro Glu
305                 310                 315                 320
```

Leu Val Ser Leu Gln Val Leu Asp Gln His Pro Val Gly Thr Gly Asp
325 330 335

His Arg Asp Ala Ala Gln Leu Gly Phe Gln Pro Leu Met Ser Ala Thr
340 345 350

Gly Ser Thr Gly Ser Thr Glu Gly Ala
355 360

<210> 22
<211> 190
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP1"

<400> 22
Trp Val Asp Thr His Cys Leu Cys Tyr Asp Phe Ile Ile Thr Pro Lys
1 5 10 15

Ser Arg Pro Glu Pro Gln Trp Cys Glu Val Gln Gly Leu Val Asp Glu
20 25 30

Arg Pro Phe Leu His Tyr Asp Cys Val Asn His Lys Ala Lys Ala Phe
35 40 45

Ala Ser Leu Gly Lys Lys Val Asn Val Thr Lys Thr Trp Glu Glu Gln
50 55 60

Thr Glu Thr Leu Arg Asp Val Val Asp Phe Leu Lys Gly Gln Leu Leu
65 70 75 80

Asp Ile Gln Val Glu Asn Leu Ile Pro Ile Glu Pro Leu Thr Leu Gln
85 90 95

Ala Arg Met Ser Cys Glu His Glu Ala His Gly His Gly Arg Gly Ser

```
            100                 105                 110

Trp Gln Phe Leu Phe Asn Gly Gln Lys Phe Leu Leu Phe Asp Ser Asn
        115                 120                 125

Asn Arg Lys Trp Thr Ala Leu His Pro Gly Ala Lys Lys Met Thr Glu
    130                 135                 140

Lys Trp Glu Lys Asn Arg Asp Val Thr Met Phe Phe Gln Lys Ile Ser
145                 150                 155                 160

Leu Gly Asp Cys Lys Met Trp Leu Glu Glu Phe Leu Met Tyr Trp Glu
                165                 170                 175

Gln Met Leu Asp Pro Thr Lys Pro Pro Ser Leu Ala Pro Gly
            180                 185                 190
```

<210> 23
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP2"

<400> 23

```
Gly Arg Ala Asp Pro His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro
1               5                   10                  15

Lys Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp
            20                  25                  30

Glu Lys Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro
        35                  40                  45

Val Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala
    50                  55                  60
```

```
Gln Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
65                  70                  75                  80


Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu
                85                  90                  95


Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly
            100                 105                 110


Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu Phe Asp Ser
        115                 120                 125


Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys
    130                 135                 140


Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe
145                 150                 155                 160


Ser Met Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met
                165                 170                 175


Asp Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Leu Ala Met Ser
            180                 185                 190


<210> 24
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP3"

<400> 24
Asp Ala His Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu Pro Arg
1               5                   10                  15


His Gly Gln Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn
            20                  25                  30
```

```
Phe Leu Ser Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His
        35                  40                  45

Leu Glu Glu Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu
    50                  55                  60

Met Leu Arg Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr
65                  70                  75                  80

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

Met Ser Cys Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln
            100                 105                 110

Phe Ser Phe Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg
        115                 120                 125

Lys Trp Thr Val Val His Ala Gly Ala Arg Arg Met Lys Glu Lys Trp
    130                 135                 140

Glu Lys Asp Ser Gly Leu Thr Thr Phe Phe Lys Met Val Ser Met Arg
145                 150                 155                 160

Asp Cys Lys Ser Trp Leu Arg Asp Phe Leu Met His Arg Lys Lys Arg
                165                 170                 175

Leu Glu Pro Thr Ala Pro Pro Thr Met Ala Pro Gly
            180                 185
```

<210> 25
<211> 233
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP4"

<400> 25
His Ser Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly
1   5   10   15

Gln Pro Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu
            20   25   30

Gln Tyr Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly
        35   40   45

Lys Lys Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu
    50   55   60

Gly Glu Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro
65   70   75   80

Gln Ile Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Glu Met Phe Cys
                85   90   95

Gln Arg Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr
            100   105   110

Asn Gly Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr
        115   120   125

Val Ile Asn His Glu Ala Ser Lys Ile Lys Glu Thr Trp Lys Lys Asp
    130   135   140

Arg Gly Leu Glu Lys Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp
145   150   155   160

His Trp Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Glu Pro
                165   170   175

Thr Val Ser Pro Val Asn Ala Ser Asp Ile His Trp Ser Ser Ser Ser
            180   185   190

```
Leu Pro Asp Arg Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Val Leu
        195                 200                 205


Met Gly Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Glu Trp Gln
    210                 215                 220


Ala Gly Leu Trp Pro Leu Arg Thr Ser
225                 230


<210> 26
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP5"

<400> 26
Gly Leu Ala Asp Pro His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro
1               5                   10                  15


Lys Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp
            20                  25                  30


Glu Lys Thr Phe Leu His Tyr Asp Cys Gly Ser Lys Thr Val Thr Pro
        35                  40                  45


Val Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala
    50                  55                  60


Gln Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
65                  70                  75                  80


Leu Asp Ile Gln Leu Glu Asn Tyr Ile Pro Lys Glu Pro Leu Thr Leu
                85                  90                  95


Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Gly Ser Gly
            100                 105                 110
```

Ser Trp Gln Leu Ser Phe Asp Gly Gln Ile Phe Leu Leu Phe Asp Ser
        115   120   125

Glu Asn Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys
    130   135   140

Glu Lys Trp Glu Asn Asp Lys Asp Met Thr Met Ser Phe His Tyr Ile
145   150   155   160

Ser Met Gly Asp Cys Thr Gly Trp Leu Glu Asp Phe Leu Met Gly Met
                165   170   175

Asp Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Pro Thr Met Ser Ser
            180   185   190

Gly

<210> 27
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="ULBP6"

<400> 27
Arg Arg Asp Asp Pro His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro
1   5   10   15

Lys Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp
            20   25   30

Glu Lys Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro
        35   40   45

Val Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Met Ala Trp Lys Ala

```
    50                  55                  60

Gln Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
65                  70                  75                  80

Leu Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu
                85                  90                  95

Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly
            100                 105                 110

Ser Trp Gln Phe Ser Ile Asp Gly Gln Thr Phe Leu Leu Phe Asp Ser
        115                 120                 125

Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys
    130                 135                 140

Glu Lys Trp Glu Asn Asp Lys Asp Val Ala Met Ser Phe His Tyr Ile
145                 150                 155                 160

Ser Met Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met
                165                 170                 175

Asp Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Leu Ala Met Ser Ser
            180                 185                 190

Gly
```

<210> 28
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL15Ralpha"

<400> 28

```
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
1               5                   10                  15


Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            20                  25                  30


Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        35                  40                  45


Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    50                  55                  60


Arg
65


<210> 29
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL15Ralpha"

<400> 29
attacatgcc cccctcccat gagcgtggag cacgccgaca tctgggtgaa gagctatagc       60

ctctacagcc gggagaggta tatctgtaac agcggcttca agaggaaggc cggcaccagc      120

agcctcaccg agtgcgtgct gaataaggct accaacgtgg ctcactggac aacaccctct      180

ttaaagtgca tccgg                                                       195


<210> 30
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-15"

<400> 30
```

aactgggtga acgtcatcag cgatttaaag aagatcgaag atttaattca gtccatgcat 60

atcgacgcca ctttatacac agaatccgac gtgcacccct cttgtaaggt gaccgccatg 120

aaatgttttt tactggagct gcaagttatc tctttagaga gcggagacgc tagcatccac 180

gacaccgtgg agaatttaat cattttagcc aataactctt tatccagcaa cggcaacgtg 240

acagagtccg gctgcaagga gtgcgaagag ctggaggaga agaacatcaa ggagtttctg 300

caatcctttg tgcacattgt ccagatgttc atcaatacct cc 342

<210> 31
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 32
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 32
atgaaatggg tgacctttat ttctttactg ttcctcttta gcagcgccta ctcc 54

<210> 33
<211> 54
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 33
atgaagtggg tcacatttat ctctttactg ttcctcttct ccagcgccta cagc 54

<210> 34
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 34
atgaaatggg tgacctttat ttctttactg ttcctcttta gcagcgccta ctcc 54

<210> 35
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 35
Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Leu Gly Val Asn Cys
1 5 10 15

<210> 36
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 36
Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp
1   5   10   15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile
            20   25   30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser
        35   40   45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly
    50   55

<210> 37
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 37
Met Pro Asn His Gln Ser Gly Ser Pro Thr Gly Ser Ser Asp Leu Leu
1   5   10   15

Leu Ser Gly Lys Lys Gln Arg Pro His Leu Ala Leu Arg Arg Lys Arg
            20   25   30

Arg Arg Glu Met Arg Lys Ile Asn Arg Lys Val Arg Arg Met Asn Leu
        35   40   45

Ala Pro Ile Lys Glu Lys Thr Ala Trp Gln His Leu Gln Ala Leu Ile
    50   55   60

Ser Glu Ala Glu Glu Val Leu Lys Thr Ser Gln Thr Pro Gln Asn Ser
65   70   75   80

Leu Thr Leu Phe Leu Ala Leu Leu Ser Val Leu Gly Pro Pro Val Thr
85 90 95

Gly

<210> 38
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38
Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15

Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser
20 25 30

<210> 39
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic AviTag sequence"

<400> 39
Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
1 5 10 15

<210> 40
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 40
Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg
1   5   10   15

Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu
            20   25

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 41
Glu Glu Glu Glu Glu Glu Thr
1   5

<210> 42
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 42
Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg
1   5   10

<210> 43
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 43
Asp Tyr Lys Asp Asp Asp Asp Lys
1   5

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 44
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1   5

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 45
His His His His His
1   5

<210> 46
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 46

His His His His His His
1   5

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 47
His His His His His His His
1   5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 48
His His His His His His His His
1   5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 49
His His His His His His His His His
1   5

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 50
His His His His His His His His His His
1 5 10

<210> 51
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 51
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 52
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 52
Thr Lys Glu Asn Pro Arg Ser Asn Gln Glu Glu Ser Tyr Asp Asp Asn
1 5 10 15

Glu Ser

<210> 53
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 53
Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1 5 10 15

<210> 54
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 54
Met Asp Glu Lys Thr Thr Gly Trp Arg Gly Gly His Val Val Glu Gly
1 5 10 15

Leu Ala Gly Glu Leu Glu Gln Leu Arg Ala Arg Leu Glu His His Pro
20 25 30

Gln Gly Gln Arg Glu Pro
35

<210> 55
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 55

Ser Leu Ala Glu Leu Leu Asn Ala Gly Leu Gly Gly Ser
1   5   10

<210> 56
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 56
Thr Gln Asp Pro Ser Arg Val Gly
1   5

<210> 57
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 57
Pro Asp Arg Val Arg Ala Val Ser His Trp Ser Ser
1   5   10

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      Tag sequence"

<400> 58
Trp Ser His Pro Gln Phe Glu Lys
1   5

<210> 59
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 59
Cys Cys Pro Gly Cys Cys
1 5

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 60
Glu Val His Thr Asn Gln Asp Pro Leu Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 61
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
1 5 10

<210> 62
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 62
Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
1   5   10

<210> 63
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 63
Asp Leu Tyr Asp Asp Asp Asp Lys
1   5

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Tag sequence"

<400> 64
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1   5   10

<210> 65
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-18"

<400> 65
tacttcggca aactggaatc caagctgagc gtgatccgga atttaaacga ccaagttctg 60

tttatcgatc aaggtaaccg gcctctgttc gaggacatga ccgactccga ttgccgggac 120

aatgcccccc ggaccatctt cattatctcc atgtacaagg acagccagcc ccggggcatg 180

gctgtgacaa ttagcgtgaa gtgtgagaaa atcagcactt tatcttgtga gaacaagatc 240

atctccttta aggaaatgaa ccccccccgat aacatcaagg acaccaagtc cgatatcatc 300

ttcttccagc ggtccgtgcc cggtcacgat aacaagatgc agttcgaatc ctcctcctac 360

gagggctact ttttagcttg tgaaaaggag agggatttat tcaagctgat cctcaagaag 420

gaggacgagc tgggcgatcg ttccatcatg ttcaccgtcc aaaacgagga t 471

<210> 66
<211> 306
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-12Beta"

<400> 66
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

```
Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
            100                 105                 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
        115                 120                 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145                 150                 155                 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
```

275 280 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
290 295 300

Cys Ser
305

<210> 67
<211> 918
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-12Beta"

<400> 67
atttgggaac tgaagaagga cgtctacgtg gtcgaactgg actggtatcc cgatgctccc 60

ggcgaaatgg tggtgctcac ttgtgacacc cccgaagaag acggcatcac ttggaccctc 120

gatcagagca gcgaggtgct gggctccgga aagaccctca caatccaagt taaggagttc 180

ggagacgctg gccaatacac atgccacaag ggaggcgagg tgctcagcca ttccttatta 240

ttattacaca agaaggaaga cggaatctgg tccaccgaca ttttaaaaga tcagaaggag 300

cccaagaata agacctttt aaggtgtgag gccaaaaact acagcggtcg tttcacttgt 360

tggtggctga ccaccatttc caccgattta accttctccg tgaaaagcag ccggggaagc 420

tccgaccctc aaggtgtgac atgtggagcc gctaccctca gcgctgagag ggttcgtggc 480

gataacaagg aatacgagta cagcgtggag tgccaagaag atagcgcttg tcccgctgcc 540

gaagaatctt tacccattga ggtgatggtg gacgccgtgc acaaactcaa gtacgagaac 600

tacacctcct ccttctttat ccgggacatc attaagcccg atcctcctaa gaatttacag 660

ctgaagcctc tcaaaaatag ccggcaagtt gaggtctctt gggaatatcc cgacacttgg 720

agcacacccc acagctactt ctctttaacc ttttgtgtgc aagttcaagg taaaagcaag 780

cgggagaaga aagaccgggt gtttaccgac aaaaccagcg ccaccgtcat ctgtcggaag 840

aacgcctcca tcagcgtgag ggctcaagat cgttattact ccagcagctg gtccgagtgg 900

gccagcgtgc cttgttcc 918

<210> 68
<211> 197
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-12alpha"

<400> 68
Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu
1 5 10 15

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

Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr
65 70 75 80

Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
85 90 95

Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu
130 135 140

```
Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser
145                 150                 155                 160


Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
                165                 170                 175


Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser
            180                 185                 190


Tyr Leu Asn Ala Ser
        195


<210> 69
<211> 591
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-12alpha"

<400> 69
cgtaacctcc ccgtggctac ccccgatccc ggaatgttcc cttgtttaca ccacagccag       60

aatttactga gggccgtgag caacatgctg cagaaagcta ggcagacttt agaatttac       120

ccttgcacca gcgaggagat cgaccatgaa gatatcacca aggacaagac atccaccgtg      180

gaggcttgtt tacctctgga gctgacaaag aacgagtctt gtctcaactc tcgtgaaacc      240

agcttcatca caaatggctc ttgtttagct tcccggaaga cctccttttat gatggcttta     300

tgcctcagct ccatctacga ggatttaaag atgtaccaag tggagttcaa gaccatgaac      360

gccaagctgc tcatggaccc taaacggcag atctttttag accagaacat gctggctgtg      420

attgatgagc tgatgcaagc tttaaacttc aactccgaga ccgtccctca gaagtcctcc      480

ctcgaggagc ccgattttta caagacaaag atcaaactgt gcattttact ccacgccttt      540

aggatccggg ccgtgaccat tgaccgggtc atgagctatt taaacgccag c               591
```

<210> 70
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 70
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1 5 10 15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
100 105 110

Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
130 135 140

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

```
Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe
                165                 170                 175

Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr
            180                 185                 190

Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr
        195                 200                 205

Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val
    210                 215                 220

Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val
225                 230                 235                 240

Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu
                245                 250                 255

Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser
            260                 265                 270

Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg
        275                 280                 285

Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe
    290                 295                 300

Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser
305                 310                 315                 320

Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val
                325                 330                 335

Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser
            340                 345                 350
```

```
Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly
        355                 360                 365

Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp
    370                 375                 380

Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
385                 390                 395                 400

Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
                405                 410                 415

Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
            420                 425                 430

Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
        435                 440                 445

Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
    450                 455                 460

Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
465                 470                 475                 480

His Ile Val Gln Met Phe Ile Asn Thr Ser
                485                 490
```

<210> 71
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 71
tacttcggca aactggaatc caagctgagc gtgatccgga atttaaacga ccaagttctg 60

tttatcgatc aaggtaaccg gcctctgttc gaggacatga ccgactccga ttgccgggac 120

aatgcccccc ggaccatctt cattatctcc atgtacaagg acagccagcc ccggggcatg 180

gctgtgacaa ttagcgtgaa gtgtgagaaa atcagcactt tatcttgtga gaacaagatc 240

atctccttta aggaaatgaa ccccccccgat aacatcaagg acaccaagtc cgatatcatc 300

ttcttccagc ggtccgtgcc cggtcacgat aacaagatgc agttcgaatc ctcctcctac 360

gagggctact ttttagcttg tgaaaaggag agggatttat tcaagctgat cctcaagaag 420

gaggacgagc tgggcgatcg ttccatcatg ttcaccgtcc aaaacgagga tagcggcaca 480

accaacacag tcgctgccta taacctcact tggaagagca ccaacttcaa aaccatcctc 540

gaatgggaac ccaaacccgt taaccaagtt tacaccgtgc agatcagcac caagtccggc 600

gactggaagt ccaaatgttt ctataccacc gacaccgagt gcgatctcac cgatgagatc 660

gtgaaagatg tgaaacagac ctacctcgcc cgggtgttta gctaccccgc cggcaatgtg 720

gagagcactg gttccgctgg cgagccttta tacgagaaca gccccgaatt taccccttac 780

ctcgagacca atttaggaca gcccaccatc caaagctttg agcaagttgg cacaaaggtg 840

aatgtgacag tggaggacga gcggacttta gtgcggcgga acaacacctt tctcagcctc 900

cgggatgtgt tcggcaaaga tttaatctac acactgtatt actggaagtc ctcttcctcc 960

ggcaagaaga cagctaaaac caacacaaac gagtttttaa tcgacgtgga taaaggcgaa 1020

aactactgtt tcagcgtgca agctgtgatc ccctcccgga ccgtgaatag gaaaagcacc 1080

gatagccccg ttgagtgcat gggccaagaa aagggcgagt tccgggagaa ctgggtgaac 1140

gtcatcagcg atttaaagaa gatcgaagat ttaattcagt ccatgcatat cgacgccact 1200

ttatacacag aatccgacgt gcacccctct tgtaaggtga ccgccatgaa atgtttttta 1260

ctggagctgc aagttatctc tttagagagc ggagacgcta gcatccacga caccgtggag 1320

aatttaatca ttttagccaa taactcttta tccagcaacg gcaacgtgac agagtccggc 1380

tgcaaggagt gcgaagagct ggaggagaag aacatcaagg agtttctgca atcctttgtg 1440

cacattgtcc agatgttcat caatacctcc 1470

<210> 72
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 72
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn
20 25 30

Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe
35 40 45

Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile
50 55 60

Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val
65 70 75 80

Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn
85 90 95

Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp
100 105 110

Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp
115 120 125

Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala
130 135 140

Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp

```
145                 150                 155                 160

Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp Ser
                165                 170                 175

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
            180                 185                 190

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
        195                 200                 205

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
    210                 215                 220

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
225                 230                 235                 240

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

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
            260                 265                 270

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
        275                 280                 285

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
    290                 295                 300

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
305                 310                 315                 320

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
                325                 330                 335

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
            340                 345                 350
```

```
Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
        355                 360                 365

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
    370                 375                 380

Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
385                 390                 395                 400

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
                405                 410                 415

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
            420                 425                 430

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
        435                 440                 445

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
    450                 455                 460

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
465                 470                 475                 480

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
                485                 490                 495

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            500                 505
```

<210> 73
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 73
atgaagtggg tcacatttat ctctttactg ttcctcttct ccagcgccta cagctacttc 60

ggcaaactgg aatccaagct gagcgtgatc cggaatttaa acgaccaagt tctgtttatc 120

gatcaaggta accggcctct gttcgaggac atgaccgact ccgattgccg ggacaatgcc 180

ccccggacca tcttcattat ctccatgtac aaggacagcc agccccgggg catggctgtg 240

acaattagcg tgaagtgtga gaaaatcagc actttatctt gtgagaacaa gatcatctcc 300

tttaaggaaa tgaacccccc cgataacatc aaggacacca agtccgatat catcttcttc 360

cagcggtccg tgcccggtca cgataacaag atgcagttcg aatcctcctc ctacgagggc 420

tacttttag cttgtgaaaa ggagagggat ttattcaagc tgatcctcaa gaaggaggac 480

gagctgggcg atcgttccat catgttcacc gtccaaaacg aggatagcgg cacaaccaac 540

acagtcgctg cctataacct cacttggaag agcaccaact tcaaaaccat cctcgaatgg 600

gaacccaaac ccgttaacca agtttacacc gtgcagatca gcaccaagtc cggcgactgg 660

aagtccaaat gtttctatac caccgacacc gagtgcgatc tcaccgatga gatcgtgaaa 720

gatgtgaaac agacctacct cgcccgggtg tttagctacc ccgccggcaa tgtggagagc 780

actggttccg ctggcgagcc tttatacgag aacagccccg aatttacccc ttacctcgag 840

accaatttag gacagcccac catccaaagc tttgagcaag ttggcacaaa ggtgaatgtg 900

acagtggagg acgagcggac tttagtgcgg cggaacaaca cctttctcag cctccgggat 960

gtgttcggca aagatttaat ctacacactg tattactgga agtcctcttc ctccggcaag 1020

aagacagcta aaaccaacac aaacgagttt ttaatcgacg tggataaagg cgaaaactac 1080

tgtttcagcg tgcaagctgt gatcccctcc cggaccgtga ataggaaaag caccgatagc 1140

cccgttgagt gcatgggcca agaaaagggc gagttccggg agaactgggt gaacgtcatc 1200

agcgatttaa agaagatcga agatttaatt cagtccatgc atatcgacgc cactttatac 1260

acagaatccg acgtgcaccc ctcttgtaag gtgaccgcca tgaaatgttt tttactggag 1320

ctgcaagtta tctctttaga gagcggagac gctagcatcc acgacaccgt ggagaattta 1380

atcattttag ccaataactc tttatccagc aacggcaacg tgacagagtc cggctgcaag 1440

gagtgcgaag agctggagga gaagaacatc aaggagtttc tgcaatcctt tgtgcacatt 1500

gtccagatgt tcatcaatac ctcc 1524

<210> 74
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 74
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

```
Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145                 150                 155                 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
```

```
Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys
                325                 330                 335

Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln
            340                 345                 350

Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile
        355                 360                 365

Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys
    370                 375                 380

Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu
385                 390                 395                 400

Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser
                405                 410                 415

Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met
            420                 425                 430

Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro
        435                 440                 445

Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu
    450                 455                 460

Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser
465                 470                 475                 480

Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile
                485                 490                 495

Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met
            500                 505                 510
```

```
Ser Tyr Leu Asn Ala Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu
        515                 520                 525


His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg
    530                 535                 540


Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu
545                 550                 555                 560


Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr
                565                 570                 575


Pro Ser Leu Lys Cys Ile Arg
            580
```

<210> 75
<211> 1749
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 75

```
atttgggaac tgaagaagga cgtctacgtg gtcgaactgg actggtatcc cgatgctccc       60

ggcgaaatgg tggtgctcac ttgtgacacc cccgaagaag acggcatcac ttggaccctc      120

gatcagagca gcgaggtgct gggctccgga aagaccctca caatccaagt taaggagttc      180

ggagacgctg gccaatacac atgccacaag ggaggcgagg tgctcagcca ttccttatta      240

ttattacaca agaaggaaga cggaatctgg tccaccgaca ttttaaaaga tcagaaggag      300

cccaagaata agacctttt aaggtgtgag gccaaaaact acagcggtcg tttcacttgt      360

tggtggctga ccaccatttc caccgattta accttctccg tgaaaagcag ccggggaagc      420

tccgaccctc aaggtgtgac atgtggagcc gctaccctca gcgctgagag ggttcgtggc      480

gataacaagg aatacgagta cagcgtggag tgccaagaag atagcgcttg tcccgctgcc      540
```

gaagaatctt tacccattga ggtgatggtg gacgccgtgc acaaactcaa gtacgagaac 600

tacacctcct ccttctttat ccgggacatc attaagcccg atcctcctaa gaatttacag 660

ctgaagcctc tcaaaaatag ccggcaagtt gaggtctctt gggaatatcc cgacacttgg 720

agcacacccc acagctactt ctctttaacc ttttgtgtgc aagttcaagg taaaagcaag 780

cgggagaaga aagaccgggt gtttaccgac aaaaccagcg ccaccgtcat ctgtcggaag 840

aacgcctcca tcagcgtgag ggctcaagat cgttattact ccagcagctg gtccgagtgg 900

gccagcgtgc cttgttccgg cggtggagga tccggaggag gtggctccgg cggcggagga 960

tctcgtaacc tccccgtggc taccccgat cccggaatgt tcccttgttt acaccacagc 1020

cagaatttac tgagggccgt gagcaacatg ctgcagaaag ctaggcagac tttagaattt 1080

taccttgca ccagcgagga gatcgaccat gaagatatca ccaaggacaa gacatccacc 1140

gtggaggctt gtttacctct ggagctgaca aagaacgagt cttgtctcaa ctctcgtgaa 1200

accagcttca tcacaaatgg ctcttgttta gcttcccgga agacctcctt tatgatggct 1260

ttatgcctca gctccatcta cgaggattta aagatgtacc aagtggagtt caagaccatg 1320

aacgccaagc tgctcatgga ccctaaacgg cagatctttt tagaccagaa catgctggct 1380

gtgattgatg agctgatgca agctttaaac ttcaactccg agaccgtccc tcagaagtcc 1440

tccctcgagg agcccgattt ttacaagaca aagatcaaac tgtgcatttt actccacgcc 1500

tttaggatcc gggccgtgac cattgaccgg gtcatgagct atttaaacgc cagcattaca 1560

tgcccccctc ccatgagcgt ggagcacgcc gacatctggg tgaagagcta tagcctctac 1620

agccgggaga ggtatatctg taacagcggc ttcaagagga aggccggcac cagcagcctc 1680

accgagtgcg tgctgaataa ggctaccaac gtggctcact ggacaacacc ctctttaaag 1740

tgcatccgg 1749

<210> 76
<211> 601
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 76
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp
20 25 30

Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr
35 40 45

Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val
50 55 60

Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp
65 70 75 80

Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
85 90 95

Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile
100 105 110

Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu
115 120 125

Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile
130 135 140

Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp
145 150 155 160

Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
165 170 175

```
Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp
            180                 185                 190

Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val
        195                 200                 205

Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe
    210                 215                 220

Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys
225                 230                 235                 240

Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp
                245                 250                 255

Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln
            260                 265                 270

Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp
        275                 280                 285

Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val
    290                 295                 300

Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser
305                 310                 315                 320

Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                325                 330                 335

Gly Gly Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe
            340                 345                 350

Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met
        355                 360                 365

Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu
```

```
    370                 375                 380

Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu
385                 390                 395                 400

Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser
                405                 410                 415

Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys
            420                 425                 430

Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu
        435                 440                 445

Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met
    450                 455                 460

Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile
465                 470                 475                 480

Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln
                485                 490                 495

Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu
            500                 505                 510

Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg
        515                 520                 525

Val Met Ser Tyr Leu Asn Ala Ser Ile Thr Cys Pro Pro Pro Met Ser
    530                 535                 540

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
545                 550                 555                 560

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
                565                 570                 575
```

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
580 585 590

Thr Thr Pro Ser Leu Lys Cys Ile Arg
595 600

<210> 77
<211> 1803
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s sequence"

<400> 77
atgaaatggg tgacctttat ttctttactg ttcctcttta gcagcgccta ctccatttgg 60

gaactgaaga aggacgtcta cgtggtcgaa ctggactggt atcccgatgc tcccggcgaa 120

atggtggtgc tcacttgtga cacccccgaa gaagacggca tcacttggac cctcgatcag 180

agcagcgagg tgctgggctc cggaaagacc ctcacaatcc aagttaagga gttcggagac 240

gctggccaat acacatgcca caagggaggc gaggtgctca gccattcctt attattatta 300

cacaagaagg aagacggaat ctggtccacc gacattttaa aagatcagaa ggagcccaag 360

aataagacct ttttaaggtg tgaggccaaa aactacagcg gtcgtttcac ttgttggtgg 420

ctgaccacca tttccaccga tttaaccttc tccgtgaaaa gcagccgggg aagctccgac 480

cctcaaggtg tgacatgtgg agccgctacc ctcagcgctg agagggttcg tggcgataac 540

aaggaatacg agtacagcgt ggagtgccaa gaagatagcg cttgtcccgc tgccgaagaa 600

tctttaccca ttgaggtgat ggtggacgcc gtgcacaaac tcaagtacga gaactacacc 660

tcctccttct ttatccggga catcattaag cccgatcctc ctaagaattt acagctgaag 720

cctctcaaaa atagccggca agttgaggtc tcttgggaat atcccgacac ttggagcaca 780

ccccacagct acttctcttt aacctttgt gtgcaagttc aaggtaaaag caagcgggag 840

aagaaagacc gggtgtttac cgacaaaacc agcgccaccg tcatctgtcg gaagaacgcc 900

tccatcagcg tgagggctca agatcgttat tactccagca gctggtccga gtgggccagc 960

gtgccttgtt ccggcggtgg aggatccgga ggaggtggct ccggcggcgg aggatctcgt 1020

aacctccccg tggctacccc cgatcccgga atgttccctt gtttacacca cagccagaat 1080

ttactgaggg ccgtgagcaa catgctgcag aaagctaggc agactttaga attttaccct 1140

tgcaccagcg aggagatcga ccatgaagat atcaccaagg acaagacatc caccgtggag 1200

gcttgtttac ctctggagct gacaaagaac gagtcttgtc tcaactctcg tgaaaccagc 1260

ttcatcacaa atggctcttg tttagcttcc cggaagacct cctttatgat ggctttatgc 1320

ctcagctcca tctacgagga tttaaagatg taccaagtgg agttcaagac catgaacgcc 1380

aagctgctca tggaccctaa acggcagatc tttttagacc agaacatgct ggctgtgatt 1440

gatgagctga tgcaagcttt aaacttcaac tccgagaccg tccctcagaa gtcctccctc 1500

gaggagcccg atttttacaa gacaaagatc aaactgtgca ttttactcca cgcctttagg 1560

atccgggccg tgaccattga ccgggtcatg agctatttaa acgccagcat tacatgcccc 1620

cctcccatga gcgtggagca cgccgacatc tgggtgaaga gctatagcct ctacagccgg 1680

gagaggtata tctgtaacag cggcttcaag aggaaggccg gcaccagcag cctcaccgag 1740

tgcgtgctga ataaggctac caacgtggct cactggacaa caccctcttt aaagtgcatc 1800

cgg 1803

<210> 78
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-21"

<400> 78
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

```
Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
            20                  25                  30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
        35                  40                  45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
    50                  55                  60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65                  70                  75                  80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser
    130
```

<210> 79
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL7RA MCP insert sequence"

<400> 79
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg 60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc 120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcc 399

<210> 80
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 80
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
85 90 95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
100 105 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
115 120 125

```
Glu Tyr Asn Thr Ser Asn Pro Asp
    130                 135


<210> 81
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 81
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1               5                   10                  15


Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20                  25                  30


Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35                  40                  45


Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60


Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80


Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95


Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110


Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125


Glu Tyr Asn Thr Ser Asn Pro Asp
```

130 135

<210> 82
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 82
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcacgatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgat 408

<210> 83
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 83
attcctcccc acgtgcagaa gagcgtgaat aatgacatga tcgtgaccga taacaatggc 60

gccgtgaaat ttccccagct gtgcaaattc tgcgatgtga ggttttccac ctgcgacaac 120

cagaagtcct gtatgagcaa ctgcacaatc acctccatct gtgagaagcc tcaggaggtg 180

tgcgtggctg tctggcggaa gaatgacgag aatatcaccc tggaaaccgt ctgccacgat 240

cccaagctgc cctaccacga tttcatcctg gaagacgccg ccagccctaa gtgcatcatg 300

aaagagaaaa agaagcctgg cgagaccttt ttcatgtgct cctgcagcag cgacgaatgc 360

aacgacaata tcatctttag cgaggaatac aataccagca accccgac 408

<210> 84
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 84
aactgggtga atgtgatcag cgacctgaag aagatcgagg atctgatcca gagcatgcac 60

attgatgcca ccctgtacac agaatctgat gtgcacccta tccccccca tgtgcaaaag 120

agcgtgaaca acgatatgat cgtgaccgac aacaacggcg ccgtgaagtt tccccagctc 180

tgcaagttct gcgatgtcag gttcagcacc tgcgataatc agaagtcctg catgtccaac 240

tgcacgatca cctccatctg cgagaagccc caagaagtgt gcgtggccgt gtggcggaaa 300

aatgacgaga acatcaccct ggagaccgtg tgtcacgacc ccaagctccc ttatcacgac 360

ttcattctgg aggacgctgc ctcccccaaa tgcatcatga aggagaagaa gaagcccgga 420

gagaccttct ttatgtgttc ctgtagcagc gacgagtgta acgacaacat catcttcagc 480

gaagagtaca acaccagcaa ccctgatgga ggtggcggat ccggaggtgg aggttctggt 540

ggaggtggga gtattcctcc ccacgtgcag aagagcgtga ataatgacat gatcgtgacc 600

gataacaatg gcgccgtgaa atttccccag ctgtgcaaat tctgcgatgt gaggttttcc 660

acctgcgaca accagaagtc ctgtatgagc aactgcacaa tcacctccat ctgtgagaag 720

cctcaggagg tgtgcgtggc tgtctggcgg aagaatgacg agaatatcac cctggaaacc 780

gtctgccacg atcccaagct gccctaccac gatttcatcc tggaagacgc cgccagccct 840

aagtgcatca tgaaagagaa aaagaagcct ggcgagacct ttttcatgtg ctcctgcagc 900

agcgacgaat gcaacgacaa tatcatcttt agcgaggaat acaataccag caaccccgac 960

<210> 85
<211> 287

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="TGFRbetaRII"

<400> 85
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1   5   10   15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20   25   30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35   40   45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50   55   60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65   70   75   80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85   90   95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100   105   110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115   120   125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130   135   140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145   150   155   160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro

```
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp
        275                 280                 285


<210> 86
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21t15-TGFRs sequence"

<400> 86
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1               5                   10                  15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
            20                  25                  30
```

```
Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
        35                  40                  45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
    50                  55                  60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65                  70                  75                  80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn
    130                 135                 140

Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro
145                 150                 155                 160

Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly
                165                 170                 175

Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu
            180                 185                 190

Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val
        195                 200                 205

Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu
    210                 215                 220
```

```
Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn
225                 230                 235                 240

Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val
                245                 250                 255

Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr
            260                 265                 270

Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu
        275                 280                 285

Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn
    290                 295                 300

Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe
305                 310                 315                 320

Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr
                325                 330                 335

Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu
            340                 345                 350

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
        355                 360                 365

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
    370                 375                 380

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
385                 390                 395                 400

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
                405                 410                 415

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
```

420 425 430

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
435 440 445

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

Thr Ser
465

<210> 87
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-TGFRs sequence"

<400> 87
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg 60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc 120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcct ccggcaccac caataccgtg 420

gccgcttata acctcacatg gaagagcacc aacttcaaga caattctgga atgggaaccc 480

aagcccgtca atcaagttta caccgtgcag atctccacca aatccggaga ctggaagagc 540

aagtgcttct acacaacaga caccgagtgt gatttaaccg acgaaatcgt caaggacgtc 600

aagcaaacct atctggctcg ggtcttttcc taccccgctg gcaatgtcga gtccaccggc 660

tccgctggcg agcctctcta cgagaattcc cccgaattca ccccttattt agagaccaat 720

ttaggccagc ctaccatcca gagcttcgag caagttggca ccaaggtgaa cgtcaccgtc 780

gaggatgaaa ggactttagt gcggcggaat aacacatttt tatccctccg ggatgtgttc 840

ggcaaagacc tcatctacac actgtactat tggaagtcca gctcctccgg caaaaagacc 900

gctaagacca acaccaacga gtttttaatt gacgtggaca aaggcgagaa ctactgcttc 960

agcgtgcaag ccgtgatccc ttctcgtacc gtcaaccgga agagcacaga ttcccccgtt 1020

gagtgcatgg gccaagaaaa gggcgagttc cgggagaact gggtgaacgt catcagcgat 1080

ttaaagaaga tcgaagattt aattcagtcc atgcatatcg acgccacttt atacacagaa 1140

tccgacgtgc acccctcttg taaggtgacc gccatgaaat gtttttttact ggagctgcaa 1200

gttatctctt tagagagcgg agacgctagc atccacgaca ccgtggagaa tttaatcatt 1260

ttagccaata actctttatc cagcaacggc aacgtgacag agtccggctg caaggagtgc 1320

gaagagctgg aggagaagaa catcaaggag tttctgcaat cctttgtgca cattgtccag 1380

atgttcatca atacctcc 1398

<210> 88
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-TGFRs sequence"

<400> 88
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
20 25 30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
35 40 45

```
Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
    50                  55                  60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65                  70                  75                  80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
                85                  90                  95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
            100                 105                 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
        115                 120                 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ser Gly Thr Thr Asn Thr Val Ala Ala
145                 150                 155                 160

Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp
                165                 170                 175

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

Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys
        195                 200                 205

Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala
    210                 215                 220

Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala
225                 230                 235                 240

Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu
```

```
                245                 250                 255

Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr
            260                 265                 270

Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn
        275                 280                 285

Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr
    290                 295                 300

Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys
305                 310                 315                 320

Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr
                325                 330                 335

Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys
            340                 345                 350

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

Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
    370                 375                 380

Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp
385                 390                 395                 400

Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu
                405                 410                 415

Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr
            420                 425                 430

Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly
        435                 440                 445
```

Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
    450   455   460

Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe
465   470   475   480

Ile Asn Thr Ser

<210> 89
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21t15-TGFRs sequence"

<400> 89
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc 60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac 120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc 180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac 240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac 300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag 360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac 420

ctgtcctcca ggacccacgg ctccgaggac tcctccggca ccaccaatac cgtggccgct 480

tataacctca catggaagag caccaacttc aagacaattc tggaatggga acccaagccc 540

gtcaatcaag tttacaccgt gcagatctcc accaaatccg gagactggaa gagcaagtgc 600

ttctacacaa cagacaccga gtgtgattta accgacgaaa tcgtcaagga cgtcaagcaa 660

acctatctgg ctcgggtctt ttcctacccc gctggcaatg tcgagtccac cggctccgct 720

ggcgagcctc tctacgagaa ttcccccgaa ttcacccctt atttagagac caatttaggc 780

cagcctacca tccagagctt cgagcaagtt ggcaccaagg tgaacgtcac cgtcgaggat 840

gaaaggactt tagtgcggcg gaataacaca tttttatccc tccgggatgt gttcggcaaa 900

gacctcatct acacactgta ctattggaag tccagctcct ccggcaaaaa gaccgctaag 960

accaacacca acgagttttt aattgacgtg gacaaaggcg agaactactg cttcagcgtg 1020

caagccgtga tcccttctcg taccgtcaac cggaagagca cagattcccc cgttgagtgc 1080

atgggccaag aaaagggcga gttccgggag aactgggtga acgtcatcag cgatttaaag 1140

aagatcgaag atttaattca gtccatgcat atcgacgcca ctttatacac agaatccgac 1200

gtgcacccct cttgtaaggt gaccgccatg aaatgttttt tactggagct gcaagttatc 1260

tctttagaga gcggagacgc tagcatccac gacaccgtgg agaatttaat cattttagcc 1320

aataactctt tatccagcaa cggcaacgtg acagagtccg gctgcaagga gtgcgaagag 1380

ctggaggaga agaacatcaa ggagtttctg caatcctttg tgcacattgt ccagatgttc 1440

atcaatacct cc 1452

<210> 90
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-TGFRs sequence"

<400> 90
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

```
Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240
```

```
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350
```

<210> 91
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-TGFRs sequence"

<400> 91
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcacgatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgcaca 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga catcacgtgt cctcctccta tgtccgtgga acacgcagac 900

atctgggtca agagctacag cttgtactcc agggagcggt acatttgtaa ctctggtttc 960

aagcgtaaag ccggcacgtc cagcctgacg gagtgcgtgt tgaacaaggc cacgaatgtc 1020

gcccactgga caacccccag tctcaaatgt attaga 1056

<210> 92
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-TGFRs sequence"

<400> 92
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

```
Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50                  55                  60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240
```

```
Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255


Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270


Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285


Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300


Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320


Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335


Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350


Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365


Ile Arg
    370


<210> 93
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21t15-TGFRs sequence"

<400> 93
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc       60
```

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcac gatcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg cacaatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacatcac gtgtcctcct cctatgtccg tggaacacgc agacatctgg 960

gtcaagagct acagcttgta ctccagggag cggtacattt gtaactctgg tttcaagcgt 1020

aaagccggca cgtccagcct gacggagtgc gtgttgaaca aggccacgaa tgtcgcccac 1080

tggacaaccc ccagtctcaa atgtattaga 1110

<210> 94
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="IL-21"

<400> 94
caaggtcaag atcgccacat gattagaatg cgtcaactta tagatattgt tgatcagctg 60

aaaaattatg tgaatgactt ggtccctgaa tttctgccag ctccagaaga tgtagagaca 120

aactgtgagt ggtcagcttt ttcctgtttt cagaaggccc aactaaagtc agcaaataca 180

ggaaacaatg aaaggataat caatgtatca attaaaaagc tgaagaggaa accaccttcc 240

acaaatgcag ggagaagaca gaaacacaga ctaacatgcc cttcatgtga ttcttatgag 300

aaaaaaccac ccaaagaatt cctagaaaga ttcaaatcac ttctccaaaa gatgattcat 360

cagcatctgt cctctagaac acacggaagt gaagattcc 399

<210> 95
<211> 456
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-7 sequence"

<400> 95
gattgtgata ttgaaggtaa agatggcaaa caatatgaga gtgttctaat ggtcagcatc 60

gatcaattat tggacagcat gaaagaaatt ggtagcaatt gcctgaataa tgaatttaac 120

ttttttaaaa gacatatctg tgatgctaat aaggaaggta tgtttttatt ccgtgctgct 180

cgcaagttga ggcaatttct taaaatgaat agcactggtg attttgatct ccacttatta 240

aaagtttcag aaggcacaac aatactgttg aactgcactg gccaggttaa aggaagaaaa 300

ccagctgccc tgggtgaagc ccaaccaaca aagagtttgg aagaaaataa atctttaaag 360

gaacagaaaa aactgaatga cttgtgtttc ctaaagagac tattacaaga gataaaaact 420

tgttggaata aaattttgat gggcactaaa gaacac 456

<210> 96
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 96

```
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1               5                   10                  15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
            20                  25                  30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
        35                  40                  45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
    50                  55                  60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65                  70                  75                  80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn
    130                 135                 140

Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro
145                 150                 155                 160

Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly
                165                 170                 175

Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu
            180                 185                 190
```

```
Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val
        195                 200                 205

Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu
    210                 215                 220

Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn
225                 230                 235                 240

Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val
                245                 250                 255

Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr
            260                 265                 270

Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu
        275                 280                 285

Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn
    290                 295                 300

Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe
305                 310                 315                 320

Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr
                325                 330                 335

Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu
            340                 345                 350

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
        355                 360                 365

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
    370                 375                 380
```

```
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
385                 390                 395                 400


Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
                405                 410                 415


Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
            420                 425                 430


Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
        435                 440                 445


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


Thr Ser
465


<210> 97
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21t15-7s sequence"

<400> 97
caaggtcaag atcgccacat gattagaatg cgtcaactta tagatattgt tgatcagctg       60

aaaaattatg tgaatgactt ggtccctgaa tttctgccag ctccagaaga tgtagagaca      120

aactgtgagt ggtcagcttt ttcctgtttt cagaaggccc aactaaagtc agcaaataca      180

ggaaacaatg aaaggataat caatgtatca attaaaaagc tgaagaggaa accaccttcc      240

acaaatgcag ggagaagaca gaaacacaga ctaacatgcc cttcatgtga ttcttatgag      300

aaaaaaccac ccaaagaatt cctagaaaga ttcaaatcac ttctccaaaa gatgattcat      360

cagcatctgt cctctagaac acacggaagt gaagattcct caggcactac aaatactgtg      420
```

gcagcatata atttaacttg gaaatcaact aatttcaaga caattttgga gtgggaaccc 480

aaacccgtca atcaagtcta cactgttcaa ataagcacta agtcaggaga ttggaaaagc 540

aaatgctttt acacaacaga cacagagtgt gacctcaccg acgagattgt gaaggatgtg 600

aagcagacgt acttggcacg ggtcttctcc tacccggcag ggaatgtgga gagcaccggt 660

tctgctgggg agcctctgta tgagaactcc ccagagttca caccttacct ggagacaaac 720

ctcggacagc caacaattca gagttttgaa caggtgggaa caaaagtgaa tgtgaccgta 780

gaagatgaac ggactttagt cagaaggaac aacactttcc taagcctccg ggatgttttt 840

ggcaaggact taatttatac actttattat tggaaatctt caagttcagg aaagaaaaca 900

gccaaaacaa acactaatga gtttttgatt gatgtggata aaggagaaaa ctactgtttc 960

agtgttcaag cagtgattcc ctcccgaaca gttaaccgga agagtacaga cagcccggta 1020

gagtgtatgg gccaggagaa aggggaattc agagaaaact gggtgaacgt catcagcgat 1080

ttaaagaaga tcgaagattt aattcagtcc atgcatatcg acgccacttt atacacagaa 1140

tccgacgtgc acccctcttg taaggtgacc gccatgaaat gttttttact ggagctgcaa 1200

gttatctctt tagagagcgg agacgctagc atccacgaca ccgtggagaa tttaatcatt 1260

ttagccaata actctttatc cagcaacggc aacgtgacag agtccggctg caaggagtgc 1320

gaagagctgg aggagaagaa catcaaggag tttctgcaat cctttgtgca cattgtccag 1380

atgttcatca atacctcc 1398

<210> 98
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-7s sequence"

<400> 98
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

```
Ala Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp
            20                  25                  30

Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe
        35                  40                  45

Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe
    50                  55                  60

Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn
65                  70                  75                  80

Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro
                85                  90                  95

Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser
            100                 105                 110

Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe
        115                 120                 125

Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr
    130                 135                 140

His Gly Ser Glu Asp Ser Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr
145                 150                 155                 160

Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu
                165                 170                 175

Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser
            180                 185                 190

Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp
        195                 200                 205
```

```
Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg
    210                 215                 220

Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly
225                 230                 235                 240

Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr
                245                 250                 255

Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys
            260                 265                 270

Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn
        275                 280                 285

Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr
    290                 295                 300

Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr
305                 310                 315                 320

Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys
                325                 330                 335

Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser
            340                 345                 350

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

Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
    370                 375                 380

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
385                 390                 395                 400
```

```
His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
                405                 410                 415


Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
            420                 425                 430


Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
        435                 440                 445


Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
    450                 455                 460


Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
465                 470                 475                 480


Asn Thr Ser



<210> 99
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21t15-7s sequence"

<400> 99
atgggagtga aagttctttt tgcccttatt tgtattgctg tggccgaggc ccaaggtcaa       60

gatcgccaca tgattagaat gcgtcaactt atagatattg ttgatcagct gaaaaattat      120

gtgaatgact tggtccctga atttctgcca gctccagaag atgtagagac aaactgtgag      180

tggtcagctt tttcctgttt tcagaaggcc caactaaagt cagcaaatac aggaaacaat      240

gaaaggataa tcaatgtatc aattaaaaag ctgaagagga aaccaccttc cacaaatgca      300

gggagaagac agaaacacag actaacatgc ccttcatgtg attcttatga gaaaaaacca      360

cccaaagaat tcctagaaag attcaaatca cttctccaaa agatgattca tcagcatctg      420
```

tcctctagaa cacacggaag tgaagattcc tcaggcacta caaatactgt ggcagcatat 480

aatttaactt ggaaatcaac taatttcaag acaattttgg agtgggaacc caaacccgtc 540

aatcaagtct acactgttca aataagcact aagtcaggag attggaaaag caaatgcttt 600

tacacaacag acacagagtg tgacctcacc gacgagattg tgaaggatgt gaagcagacg 660

tacttggcac gggtcttctc ctacccggca gggaatgtgg agagcaccgg ttctgctggg 720

gagcctctgt atgagaactc cccagagttc acaccttacc tggagacaaa cctcggacag 780

ccaacaattc agagttttga acaggtggga acaaaagtga atgtgaccgt agaagatgaa 840

cggactttag tcagaaggaa caacactttc ctaagcctcc gggatgtttt tggcaaggac 900

ttaatttata cactttatta ttggaaatct tcaagttcag gaaagaaaac agccaaaaca 960

aacactaatg agtttttgat tgatgtggat aaaggagaaa actactgttt cagtgttcaa 1020

gcagtgattc cctcccgaac agttaaccgg aagagtacag acagcccggt agagtgtatg 1080

ggccaggaga aaggggaatt cagagaaaac tgggtgaacg tcatcagcga tttaaagaag 1140

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1200

caccctctt gtaaggtgac cgccatgaaa tgtttttttac tggagctgca agttatctct 1260

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat 1320

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg 1380

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc 1440

aatacctcc 1449

<210> 100
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-7s sequence"

<400> 100
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu

```
1               5                   10                  15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
            20                  25                  30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
        35                  40                  45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
    50                  55                  60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140

Ile Leu Met Gly Thr Lys Glu His Ile Thr Cys Pro Pro Pro Met Ser
145                 150                 155                 160

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
                165                 170                 175

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
            180                 185                 190

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
        195                 200                 205
```

Thr Thr Pro Ser Leu Lys Cys Ile Arg
210 215

<210> 101
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-7s sequence"

<400> 101
gattgtgata ttgaaggtaa agatggcaaa caatatgaga gtgttctaat ggtcagcatc 60

gatcaattat tggacagcat gaaagaaatt ggtagcaatt gcctgaataa tgaatttaac 120

ttttttaaaa gacatatctg tgatgctaat aaggaaggta tgtttttatt ccgtgctgct 180

cgcaagttga ggcaatttct taaaatgaat agcactggtg attttgatct ccacttatta 240

aaagtttcag aaggcacaac aatactgttg aactgcactg gccaggttaa aggaagaaaa 300

ccagctgccc tgggtgaagc ccaaccaaca aagagtttgg aagaaaataa atctttaaag 360

gaacagaaaa aactgaatga cttgtgtttc ctaaagagac tattacaaga gataaaaact 420

tgttggaata aaattttgat gggcactaaa gaacacatca cgtgccctcc ccccatgtcc 480

gtggaacacg cagacatctg ggtcaagagc tacagcttgt actccaggga gcggtacatt 540

tgtaactctg gtttcaagcg taaagccggc acgtccagcc tgacggagtg cgtgttgaac 600

aaggccacga atgtcgccca ctggacaacc cccagtctca aatgcattag a 651

<210> 102
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-7s sequence"

<400> 102
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1   5   10   15

Ala Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val
            20   25   30

Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly
        35   40   45

Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys
    50   55   60

Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu
65   70   75   80

Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu
                85   90   95

Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln
            100   105   110

Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys
        115   120   125

Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp
    130   135   140

Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn
145   150   155   160

Lys Ile Leu Met Gly Thr Lys Glu His Ile Thr Cys Pro Pro Pro Met
                165   170   175

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser
            180   185   190

Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr
195 200 205

Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His
210 215 220

Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
225 230

<210> 103
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21t15-7s sequence"

<400> 103
atgggagtga aagttctttt tgcccttatt tgtattgctg tggccgaggc cgattgtgat 60

attgaaggta aagatggcaa acaatatgag agtgttctaa tggtcagcat cgatcaatta 120

ttggacagca tgaaagaaat tggtagcaat tgcctgaata atgaatttaa ctttttttaaa 180

agacatatct gtgatgctaa taaggaaggt atgtttttat tccgtgctgc tcgcaagttg 240

aggcaatttc ttaaaatgaa tagcactggt gattttgatc tccacttatt aaaagtttca 300

gaaggcacaa caatactgtt gaactgcact ggccaggtta aaggaagaaa accagctgcc 360

ctgggtgaag cccaaccaac aaagagtttg gaagaaaata aatctttaaa ggaacagaaa 420

aaactgaatg acttgtgttt cctaaagaga ctattacaag agataaaaac ttgttggaat 480

aaaattttga tgggcactaa agaacacatc acgtgccctc cccccatgtc cgtggaacac 540

gcagacatct gggtcaagag ctacagcttg tactccaggg agcggtacat ttgtaactct 600

ggtttcaagc gtaaagccgg cacgtccagc ctgacggagt gcgtgttgaa caaggccacg 660

aatgtcgccc actggacaac ccccagtctc aaatgcatta ga 702

<210> 104
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 104
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
35 40 45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
50 55 60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65 70 75 80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
85 90 95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
100 105 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
115 120 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
130 135 140

Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr Val Ala
145 150 155 160

```
Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
                165                 170                 175

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
            180                 185                 190

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
        195                 200                 205

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
    210                 215                 220

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
225                 230                 235                 240

Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
                245                 250                 255

Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
            260                 265                 270

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
        275                 280                 285

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
    290                 295                 300

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
305                 310                 315                 320

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
                325                 330                 335

Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
            340                 345                 350
```

```
Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu
        355                 360                 365


Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
    370                 375                 380


Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
385                 390                 395                 400


Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
                405                 410                 415


Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
            420                 425                 430


Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
        435                 440                 445


Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
    450                 455                 460


Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
465                 470                 475                 480


Phe Ile Asn Thr Ser
                485


<210> 105
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-21s sequence"

<400> 105
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc       60
```

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac 120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc 180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg 240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa 300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag 360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc 420

tgctggaaca agatcctgat gggcaccaag gagcatagcg gcacaaccaa cacagtcgct 480

gcctataacc tcacttggaa gagcaccaac ttcaaaacca tcctcgaatg ggaacccaaa 540

cccgttaacc aagtttacac cgtgcagatc agcaccaagt ccggcgactg gaagtccaaa 600

tgtttctata ccaccgacac cgagtgcgat ctcaccgatg agatcgtgaa agatgtgaaa 660

cagacctacc tcgcccgggt gtttagctac cccgccggca atgtggagag cactggttcc 720

gctggcgagc ctttatacga gaacagcccc gaatttaccc cttacctcga gaccaattta 780

ggacagccca ccatccaaag ctttgagcaa gttggcacaa aggtgaatgt gacagtggag 840

gacgagcgga ctttagtgcg gcggaacaac acctttctca gcctccggga tgtgttcggc 900

aaagatttaa tctacacact gtattactgg aagtcctctt cctccggcaa gaagacagct 960

aaaaccaaca caaacgagtt tttaatcgac gtggataaag gcgaaaacta ctgtttcagc 1020

gtgcaagctg tgatcccctc ccggaccgtg aataggaaaa gcaccgatag ccccgttgag 1080

tgcatgggcc aagaaaaggg cgagttccgg gagaactggg tgaacgtcat cagcgattta 1140

aagaagatcg aagatttaat tcagtccatg catatcgacg ccactttata cacagaatcc 1200

gacgtgcacc cctcttgtaa ggtgaccgcc atgaaatgtt ttttactgga gctgcaagtt 1260

atctctttag agagcggaga cgctagcatc cacgacaccg tggagaattt aatcatttta 1320

gccaataact ctttatccag caacggcaac gtgacagagt ccggctgcaa ggagtgcgaa 1380

gagctggagg agaagaacat caaggagttt ctgcaatcct ttgtgcacat tgtccagatg 1440

ttcatcaata cctcc 1455

<210> 106
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 106
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
20 25 30

Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
35 40 45

Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
50 55 60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65 70 75 80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
85 90 95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
100 105 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
115 120 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
130 135 140

Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp

```
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr
                165                 170                 175

Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile
            180                 185                 190

Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile
        195                 200                 205

Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp
    210                 215                 220

Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr
225                 230                 235                 240

Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr
                245                 250                 255

Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro
            260                 265                 270

Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
        275                 280                 285

Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val
    290                 295                 300

Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp
305                 310                 315                 320

Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys
                325                 330                 335

Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly
            340                 345                 350
```

```
Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val
        355                 360                 365

Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys
    370                 375                 380

Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
385                 390                 395                 400

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                405                 410                 415

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            420                 425                 430

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        435                 440                 445

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    450                 455                 460

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
465                 470                 475                 480

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                485                 490                 495

Gln Met Phe Ile Asn Thr Ser
            500
```

<210> 107
<211> 1508
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 107
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc 60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag 120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc 180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa 240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg 300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct 360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag 420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg 480

aacaagatcc tgatgggcac caaggagcat agcggcacaa ccaacacagt cgctgcctat 540

aacctcactt ggaagagcac caacttcaaa accatcctcg aatgggaacc caaacccgtt 600

aaccaagttt acaccgtgca gatcagcacc aagtccggcg actggaagtc caaatgtttc 660

tataccaccg acaccgagtg cgatctcacc gatgagatcg tgaaagatgt gaaacagacc 720

tacctcgccc gggtgtttag ctaccccgcc ggcaatgtgg agagcactgg ttccgctggc 780

gagcctttat acgagaacag ccccgaattt acccccttacc tcgagaccaa tttaggacag 840

cccaccatcc aaagctttga gcaagttggc acaaaggtga atgtgacagt ggaggacgag 900

cggactttag tgcggcggaa caacaccttt ctcagcctcc gggatgtgtt cggcaaagat 960

ttaatctaca cactgtatta ctggaagtcc tcttcctccg gcaagaagac agctaaaacc 1020

aacacaaacg agtttttaat cgacgtggat aaaggcgaaa actactgttt cagcgtgcaa 1080

gctgtgatcc cctcccggac cgtgaatagg aaaagcaccg atagccccgt tgagtgcatg 1140

ggccaagaaa agggcgagtt ccgggagaac tgggtgaacg tcatcagcga tttaaagaag 1200

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1260

cacccctctt gtaaggtgac cgccatgaaa tgtttttttac tggagctgca agttatctct 1320

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat 1380

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg 1440

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc 1500

aatacctc 1508

<210> 108
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 108
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
20 25 30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
35 40 45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
50 55 60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65 70 75 80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
85 90 95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
100 105 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
115 120 125

Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu His
130 135 140

Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
145 150 155 160

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
165 170 175

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro
180 185 190

Ser Leu Lys Cys Ile Arg
195

<210> 109
<211> 594
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 109
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg 60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc 120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcca ttacatgccc ccctcccatg 420

agcgtggagc acgccgacat ctgggtgaag agctatagcc tctacagccg ggagaggtat 480

atctgtaaca gcggcttcaa gaggaaggcc ggcaccagca gcctcaccga gtgcgtgctg 540

aataaggcta ccaacgtggc tcactggaca acaccctctt taaagtgcat ccgg 594

<210> 110
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s sequence"

<400> 110
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
20 25 30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
35 40 45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
50 55 60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65 70 75 80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
85 90 95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
100 105 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
115 120 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg

```
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205

Thr Pro Ser Leu Lys Cys Ile Arg
    210                 215


<210> 111
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-21s sequence"

<400> 111
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc       60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac      120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc      180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac      240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac      300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag      360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac      420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccctcc catgagcgtg      480
```

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt 540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag 600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgg 648

<210> 112
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
CD16 LC sequence"

<400> 112
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
1 5 10 15

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

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

Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
50 55 60

Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
65 70 75 80

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His
100 105

<210> 113
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
CD16 LC sequence"

<400> 113
tccgagctga cccaggaccc tgctgtgtcc gtggctctgg gccagaccgt gaggatcacc 60

tgccagggcg actccctgag gtcctactac gcctcctggt accagcagaa gcccggccag 120

gctcctgtgc tggtgatcta cggcaagaac aacaggccct ccggcatccc tgacaggttc 180

tccggatcct cctccggcaa caccgcctcc ctgaccatca caggcgctca ggccgaggac 240

gaggctgact actactgcaa ctccagggac tcctccggca accatgtggt gttcggcggc 300

ggcaccaagc tgaccgtggg ccat 324

<210> 114
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
CD16 HC sequence"

<400> 114
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Arg
115

<210> 115
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
CD16 HC sequence"

<400> 115
gaggtgcagc tggtggagtc cggaggagga gtggtgaggc ctggaggctc cctgaggctg 60

agctgtgctg cctccggctt caccttcgac gactacggca tgtcctgggt gaggcaggct 120

cctggaaagg gcctggagtg ggtgtccggc atcaactgga acggcggatc caccggctac 180

gccgattccg tgaagggcag gttcaccatc agcagggaca acgccaagaa ctccctgtac 240

ctgcagatga actccctgag ggccgaggac accgccgtgt actactgcgc caggggcagg 300

tccctgctgt tcgactactg gggacagggc accctggtga ccgtgtccag g 351

<210> 116
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s16 sequence"

<400> 116
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1   5   10   15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
            20   25   30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
        35   40   45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
    50   55   60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65   70   75   80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
                85   90   95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
            100   105   110

Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
        115   120   125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
    130   135   140

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

Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe
                165   170   175

Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr
            180   185   190

```
Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr
        195                 200                 205

Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val
    210                 215                 220

Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val
225                 230                 235                 240

Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu
                245                 250                 255

Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser
            260                 265                 270

Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg
        275                 280                 285

Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe
    290                 295                 300

Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser
305                 310                 315                 320

Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val
                325                 330                 335

Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser
            340                 345                 350

Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly
        355                 360                 365

Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp
    370                 375                 380
```

```
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
385                 390                 395                 400


Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
                405                 410                 415


Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
            420                 425                 430


Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
        435                 440                 445


Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
    450                 455                 460


Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
465                 470                 475                 480


His Ile Val Gln Met Phe Ile Asn Thr Ser
                485                 490


<210> 117
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      18t15-12s16 sequence"

<400> 117
tacttcggca aactggaatc caagctgagc gtgatccgga atttaaacga ccaagttctg       60

tttatcgatc aaggtaaccg gcctctgttc gaggacatga ccgactccga ttgccgggac      120

aatgcccccc ggaccatctt cattatctcc atgtacaagg acagccagcc ccggggcatg      180

gctgtgacaa ttagcgtgaa gtgtgagaaa atcagcactt tatcttgtga gaacaagatc      240

atctccttta aggaaatgaa ccccccccgat aacatcaagg acaccaagtc cgatatcatc      300
```

ttcttccagc ggtccgtgcc cggtcacgat aacaagatgc agttcgaatc ctcctcctac 360

gagggctact ttttagcttg tgaaaaggag agggatttat tcaagctgat cctcaagaag 420

gaggacgagc tgggcgatcg ttccatcatg ttcaccgtcc aaaacgagga tagcggcaca 480

accaacacag tcgctgccta taacctcact tggaagagca ccaacttcaa aaccatcctc 540

gaatgggaac ccaaacccgt taaccaagtt tacaccgtgc agatcagcac caagtccggc 600

gactggaagt ccaaatgttt ctataccacc gacaccgagt gcgatctcac cgatgagatc 660

gtgaaagatg tgaaacagac ctacctcgcc cgggtgttta gctaccccgc cggcaatgtg 720

gagagcactg gttccgctgg cgagccttta tacgagaaca gccccgaatt taccccttac 780

ctcgagacca atttaggaca gcccaccatc caaagctttg agcaagttgg cacaaaggtg 840

aatgtgacag tggaggacga gcggacttta gtgcggcgga acaacacctt tctcagcctc 900

cgggatgtgt tcggcaaaga tttaatctac acactgtatt actggaagtc ctcttcctcc 960

ggcaagaaga cagctaaaac caacacaaac gagtttttaa tcgacgtgga taaaggcgaa 1020

aactactgtt tcagcgtgca agctgtgatc ccctcccgga ccgtgaatag gaaaagcacc 1080

gatagccccg ttgagtgcat gggccaagaa aagggcgagt tccgggagaa ctgggtgaac 1140

gtcatcagcg atttaaagaa gatcgaagat ttaattcagt ccatgcatat cgacgccact 1200

ttatacacag aatccgacgt gcacccctct tgtaaggtga ccgccatgaa atgtttttta 1260

ctggagctgc aagttatctc tttagagagc ggagacgcta gcatccacga caccgtggag 1320

aatttaatca ttttagccaa taactcttta tccagcaacg gcaacgtgac agagtccggc 1380

tgcaaggagt gcgaagagct ggaggagaag aacatcaagg agtttctgca atcctttgtg 1440

cacattgtcc agatgttcat caatacctcc 1470

<210> 118
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

18t15-12s16 sequence"

<400> 118
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1   5   10   15

Tyr Ser Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn
            20   25   30

Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe
        35   40   45

Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile
    50   55   60

Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val
65   70   75   80

Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn
                85   90   95

Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp
            100   105   110

Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp
        115   120   125

Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala
    130   135   140

Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp
145   150   155   160

Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp Ser
                165   170   175

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
            180   185   190

```
Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
        195                 200                 205

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
    210                 215                 220

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
225                 230                 235                 240

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

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
            260                 265                 270

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
        275                 280                 285

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
    290                 295                 300

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
305                 310                 315                 320

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
                325                 330                 335

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
            340                 345                 350

Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
        355                 360                 365

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
    370                 375                 380
```

```
Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
385                 390                 395                 400


Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
                405                 410                 415


Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
            420                 425                 430


Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
        435                 440                 445


Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
    450                 455                 460


Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
465                 470                 475                 480


Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
                485                 490                 495


Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            500                 505


<210> 119
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      18t15-12s16 sequence"

<400> 119
atgaagtggg tcacatttat ctctttactg ttcctcttct ccagcgccta cagctacttc       60

ggcaaactgg aatccaagct gagcgtgatc cggaatttaa acgaccaagt tctgtttatc      120

gatcaaggta accggcctct gttcgaggac atgaccgact ccgattgccg ggacaatgcc      180
```

ccccggacca tcttcattat ctccatgtac aaggacagcc agccccgggg catggctgtg 240

acaattagcg tgaagtgtga gaaaatcagc actttatctt gtgagaacaa gatcatctcc 300

tttaaggaaa tgaacccccc cgataacatc aaggacacca agtccgatat catcttcttc 360

cagcggtccg tgcccggtca cgataacaag atgcagttcg aatcctcctc ctacgagggc 420

tacttttag cttgtgaaaa ggagagggat ttattcaagc tgatcctcaa gaaggaggac 480

gagctgggcg atcgttccat catgttcacc gtccaaaacg aggatagcgg cacaaccaac 540

acagtcgctg cctataacct cacttggaag agcaccaact tcaaaaccat cctcgaatgg 600

gaacccaaac ccgttaacca agtttacacc gtgcagatca gcaccaagtc cggcgactgg 660

aagtccaaat gtttctatac caccgacacc gagtgcgatc tcaccgatga gatcgtgaaa 720

gatgtgaaac agacctacct cgcccgggtg tttagctacc ccgccggcaa tgtggagagc 780

actggttccg ctggcgagcc tttatacgag aacagccccg aatttacccc ttacctcgag 840

accaatttag gacagcccac catccaaagc tttgagcaag ttggcacaaa ggtgaatgtg 900

acagtggagg acgagcggac tttagtgcgg cggaacaaca cctttctcag cctccgggat 960

gtgttcggca aagatttaat ctacacactg tattactgga agtcctcttc ctccggcaag 1020

aagacagcta aaaccaacac aaacgagttt ttaatcgacg tggataaagg cgaaaactac 1080

tgtttcagcg tgcaagctgt gatcccctcc cggaccgtga ataggaaaag caccgatagc 1140

cccgttgagt gcatgggcca agaaaagggc gagttccggg agaactgggt gaacgtcatc 1200

agcgatttaa agaagatcga agatttaatt cagtccatgc atatcgacgc cactttatac 1260

acagaatccg acgtgcaccc ctcttgtaag gtgaccgcca tgaaatgttt tttactggag 1320

ctgcaagtta tctctttaga gagcggagac gctagcatcc acgacaccgt ggagaattta 1380

atcattttag ccaataactc tttatccagc aacggcaacg tgacagagtc cggctgcaag 1440

gagtgcgaag agctggagga gaagaacatc aaggagtttc tgcaatcctt tgtgcacatt 1500

gtccagatgt tcatcaatac ctcc 1524

<210> 120

<211> 823
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s16 sequence"

<400> 120
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145 150 155 160

```
Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320

Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys
                325                 330                 335

Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln
            340                 345                 350
```

```
Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile
        355                 360                 365

Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys
    370                 375                 380

Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu
385                 390                 395                 400

Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser
                405                 410                 415

Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met
            420                 425                 430

Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro
        435                 440                 445

Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu
    450                 455                 460

Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser
465                 470                 475                 480

Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile
                485                 490                 495

Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met
            500                 505                 510

Ser Tyr Leu Asn Ala Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu
        515                 520                 525

His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg
    530                 535                 540

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

```
545                 550                 555                 560

Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr
                565                 570                 575

Pro Ser Leu Lys Cys Ile Arg Ser Glu Leu Thr Gln Asp Pro Ala Val
            580                 585                 590

Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
        595                 600                 605

Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    610                 615                 620

Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
625                 630                 635                 640

Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
                645                 650                 655

Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg
            660                 665                 670

Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr
        675                 680                 685

Val Gly His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    690                 695                 700

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro
705                 710                 715                 720

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
                725                 730                 735

Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            740                 745                 750
```

```
Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp
        755                 760                 765


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
    770                 775                 780


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
785                 790                 795                 800


Tyr Cys Ala Arg Gly Arg Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly
                805                 810                 815


Thr Leu Val Thr Val Ser Arg
            820


<210> 121
<211> 2469
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      18t15-12s16 sequence"

<400> 121
atttgggaac tgaagaagga cgtctacgtg gtcgaactgg actggtatcc cgatgctccc       60

ggcgaaatgg tggtgctcac ttgtgacacc cccgaagaag acggcatcac ttggaccctc      120

gatcagagca gcgaggtgct gggctccgga aagaccctca caatccaagt taaggagttc      180

ggagacgctg gccaatacac atgccacaag ggaggcgagg tgctcagcca ttccttatta      240

ttattacaca agaaggaaga cggaatctgg tccaccgaca ttttaaaaga tcagaaggag      300

cccaagaata agacctttt aaggtgtgag gccaaaaact acagcggtcg tttcacttgt      360

tggtggctga ccaccatttc caccgattta accttctccg tgaaaagcag ccggggaagc      420

tccgaccctc aaggtgtgac atgtggagcc gctaccctca gcgctgagag ggttcgtggc      480
```

gataacaagg aatacgagta cagcgtggag tgccaagaag atagcgcttg tcccgctgcc 540

gaagaatctt tacccattga ggtgatggtg gacgccgtgc acaaactcaa gtacgagaac 600

tacacctcct ccttctttat ccgggacatc attaagcccg atcctcctaa gaatttacag 660

ctgaagcctc tcaaaaatag ccggcaagtt gaggtctctt gggaatatcc cgacacttgg 720

agcacacccc acagctactt ctctttaacc ttttgtgtgc aagttcaagg taaaagcaag 780

cgggagaaga aagaccgggt gtttaccgac aaaaccagcg ccaccgtcat ctgtcggaag 840

aacgcctcca tcagcgtgag ggctcaagat cgttattact ccagcagctg gtccgagtgg 900

gccagcgtgc cttgttccgg cggtggagga tccggaggag gtggctccgg cggcggagga 960

tctcgtaacc tccccgtggc taccccgat cccggaatgt tcccttgttt acaccacagc 1020

cagaatttac tgagggccgt gagcaacatg ctgcagaaag ctaggcagac tttagaattt 1080

taccttgca ccagcgagga gatcgaccat gaagatatca ccaaggacaa gacatccacc 1140

gtggaggctt gtttacctct ggagctgaca aagaacgagt cttgtctcaa ctctcgtgaa 1200

accagcttca tcacaaatgg ctcttgttta gcttcccgga agacctcctt tatgatggct 1260

ttatgcctca gctccatcta cgaggattta aagatgtacc aagtggagtt caagaccatg 1320

aacgccaagc tgctcatgga ccctaaacgg cagatctttt tagaccagaa catgctggct 1380

gtgattgatg agctgatgca agctttaaac ttcaactccg agaccgtccc tcagaagtcc 1440

tccctcgagg agcccgattt ttacaagaca aagatcaaac tgtgcatttt actccacgcc 1500

tttaggatcc gggccgtgac cattgaccgg gtcatgagct atttaaacgc cagcattaca 1560

tgcccccctc ccatgagcgt ggagcacgcc gacatctggg tgaagagcta tagcctctac 1620

agccgggaga ggtatatctg taacagcggc ttcaagagga aggccggcac cagcagcctc 1680

accgagtgcg tgctgaataa ggctaccaac gtggctcact ggacaacacc ctctttaaag 1740

tgcatccggt ccgagctgac ccaggaccct gctgtgtccg tggctctggg ccagaccgtg 1800

aggatcacct gccagggcga ctccctgagg tcctactacg cctcctggta ccagcagaag 1860

cccggccagg ctcctgtgct ggtgatctac ggcaagaaca acaggccctc cggcatccct 1920

gacaggttct ccggatcctc ctccggcaac accgcctccc tgaccatcac aggcgctcag 1980

gccgaggacg aggctgacta ctactgcaac tccagggact cctccggcaa ccatgtggtg 2040

ttcggcggcg gcaccaagct gaccgtgggc catggcggcg gcggctccgg aggcggcggc 2100

agcggcggag gaggatccga ggtgcagctg gtggagtccg gaggaggagt ggtgaggcct 2160

ggaggctccc tgaggctgag ctgtgctgcc tccggcttca ccttcgacga ctacggcatg 2220

tcctgggtga ggcaggctcc tggaaagggc ctggagtggg tgtccggcat caactggaac 2280

ggcggatcca ccggctacgc cgattccgtg aagggcaggt tcaccatcag cagggacaac 2340

gccaagaact ccctgtacct gcagatgaac tccctgaggg ccgaggacac cgccgtgtac 2400

tactgcgcca ggggcaggtc cctgctgttc gactactggg gacagggcac cctggtgacc 2460

gtgtccagg 2469

<210> 122
<211> 841
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s16 sequence"

<400> 122
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp
20 25 30

Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr
35 40 45

Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val
50 55 60

Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp
65 70 75 80

```
Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
                85                  90                  95

Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile
            100                 105                 110

Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu
        115                 120                 125

Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile
    130                 135                 140

Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp
145                 150                 155                 160

Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
                165                 170                 175

Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp
            180                 185                 190

Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val
        195                 200                 205

Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe
    210                 215                 220

Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys
225                 230                 235                 240

Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp
                245                 250                 255

Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln
            260                 265                 270
```

```
Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp
        275                 280                 285

Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val
    290                 295                 300

Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser
305                 310                 315                 320

Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                325                 330                 335

Gly Gly Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe
            340                 345                 350

Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met
        355                 360                 365

Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu
    370                 375                 380

Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu
385                 390                 395                 400

Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser
                405                 410                 415

Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys
            420                 425                 430

Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu
        435                 440                 445

Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met
    450                 455                 460
```

```
Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile
465                 470                 475                 480

Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln
                485                 490                 495

Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu
            500                 505                 510

Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg
        515                 520                 525

Val Met Ser Tyr Leu Asn Ala Ser Ile Thr Cys Pro Pro Pro Met Ser
    530                 535                 540

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
545                 550                 555                 560

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
                565                 570                 575

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
            580                 585                 590

Thr Thr Pro Ser Leu Lys Cys Ile Arg Ser Glu Leu Thr Gln Asp Pro
        595                 600                 605

Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly
    610                 615                 620

Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly
625                 630                 635                 640

Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
                645                 650                 655

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
```

```
            660                 665                 670

Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn
        675                 680                 685

Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys
    690                 695                 700

Leu Thr Val Gly His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
705                 710                 715                 720

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
                725                 730                 735

Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
            740                 745                 750

Phe Asp Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
        755                 760                 765

Leu Glu Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr
    770                 775                 780

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
785                 790                 795                 800

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
                805                 810                 815

Val Tyr Tyr Cys Ala Arg Gly Arg Ser Leu Leu Phe Asp Tyr Trp Gly
            820                 825                 830

Gln Gly Thr Leu Val Thr Val Ser Arg
        835                 840
```

<210> 123
<211> 2523

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
18t15-12s16 sequence"

<400> 123
atgaaatggg tgacctttat ttctttactg ttcctcttta gcagcgccta ctccatttgg 60

gaactgaaga aggacgtcta cgtggtcgaa ctggactggt atcccgatgc tcccggcgaa 120

atggtggtgc tcacttgtga caccccgaa gaagacggca tcacttggac cctcgatcag 180

agcagcgagg tgctgggctc cggaaagacc ctcacaatcc aagttaagga gttcggagac 240

gctggccaat acacatgcca caagggaggc gaggtgctca gccattcctt attattatta 300

cacaagaagg aagacggaat ctggtccacc gacattttaa aagatcagaa ggagcccaag 360

aataagacct ttttaaggtg tgaggccaaa aactacagcg gtcgtttcac ttgttggtgg 420

ctgaccacca tttccaccga tttaaccttc tccgtgaaaa gcagccgggg aagctccgac 480

cctcaaggtg tgacatgtgg agccgctacc ctcagcgctg agagggttcg tggcgataac 540

aaggaatacg agtacagcgt ggagtgccaa gaagatagcg cttgtcccgc tgccgaagaa 600

tctttaccca ttgaggtgat ggtggacgcc gtgcacaaac tcaagtacga gaactacacc 660

tcctccttct ttatccggga catcattaag cccgatcctc ctaagaattt acagctgaag 720

cctctcaaaa atagccggca agttgaggtc tcttgggaat atcccgacac ttggagcaca 780

ccccacagct acttctcttt aacctttgt gtgcaagttc aaggtaaaag caagcgggag 840

aagaaagacc gggtgtttac cgacaaaacc agcgccaccg tcatctgtcg gaagaacgcc 900

tccatcagcg tgagggctca agatcgttat tactccagca gctggtccga gtgggccagc 960

gtgccttgtt ccggcggtgg aggatccgga ggaggtggct ccggcggcgg aggatctcgt 1020

aacctccccg tggctacccc cgatcccgga atgttccctt gtttacacca cagccagaat 1080

ttactgaggg ccgtgagcaa catgctgcag aaagctaggc agactttaga attttaccct 1140

tgcaccagcg aggagatcga ccatgaagat atcaccaagg acaagacatc caccgtggag 1200

gcttgtttac ctctggagct gacaaagaac gagtcttgtc tcaactctcg tgaaaccagc 1260

ttcatcacaa atggctcttg tttagcttcc cggaagacct cctttatgat ggctttatgc 1320

ctcagctcca tctacgagga tttaaagatg taccaagtgg agttcaagac catgaacgcc 1380

aagctgctca tggaccctaa acggcagatc tttttagacc agaacatgct ggctgtgatt 1440

gatgagctga tgcaagcttt aaacttcaac tccgagaccg tccctcagaa gtcctccctc 1500

gaggagcccg atttttacaa gacaaagatc aaactgtgca ttttactcca cgcctttagg 1560

atccgggccg tgaccattga ccgggtcatg agctatttaa acgccagcat tacatgcccc 1620

cctcccatga gcgtggagca cgccgacatc tgggtgaaga gctatagcct ctacagccgg 1680

gagaggtata tctgtaacag cggcttcaag aggaaggccg gcaccagcag cctcaccgag 1740

tgcgtgctga ataaggctac caacgtggct cactggacaa caccctcttt aaagtgcatc 1800

cggtccgagc tgacccagga ccctgctgtg tccgtggctc tgggccagac cgtgaggatc 1860

acctgccagg gcgactccct gaggtcctac tacgcctcct ggtaccagca gaagcccggc 1920

caggctcctg tgctggtgat ctacggcaag aacaacaggc cctccggcat ccctgacagg 1980

ttctccggat cctcctccgg caacaccgcc tccctgacca tcacaggcgc tcaggccgag 2040

gacgaggctg actactactg caactccagg gactcctccg gcaaccatgt ggtgttcggc 2100

ggcggcacca agctgaccgt gggccatggc ggcggcggct ccggaggcgg cggcagcggc 2160

ggaggaggat ccgaggtgca gctggtggag tccggaggag gagtggtgag gcctggaggc 2220

tccctgaggc tgagctgtgc tgcctccggc ttcaccttcg acgactacgg catgtcctgg 2280

gtgaggcagg ctcctggaaa gggcctggag tgggtgtccg gcatcaactg gaacggcgga 2340

tccaccggct acgccgattc cgtgaagggc aggttcacca tcagcaggga caacgccaag 2400

aactccctgt acctgcagat gaactccctg agggccgagg acaccgccgt gtactactgc 2460

gccaggggca ggtccctgct gttcgactac tggggacagg gcaccctggt gaccgtgtcc 2520

agg 2523

<210> 124
<211> 456

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-7 sequence"

<400> 124
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc 60

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac 120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc 180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg 240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa 300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag 360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc 420

tgctggaaca agatcctgat gggcaccaag gagcat 456

<210> 125
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 125
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
35 40 45

```
Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
    50                  55                  60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140

Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr Val Ala
145                 150                 155                 160

Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
                165                 170                 175

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
            180                 185                 190

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
        195                 200                 205

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
    210                 215                 220

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
225                 230                 235                 240

Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
```

```
                245                 250                 255

Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
            260                 265                 270

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
        275                 280                 285

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
    290                 295                 300

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
305                 310                 315                 320

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
                325                 330                 335

Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
            340                 345                 350

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

Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
    370                 375                 380

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
385                 390                 395                 400

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
                405                 410                 415

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
            420                 425                 430

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
        435                 440                 445
```

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
    450   455   460

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
465   470   475   480

Phe Ile Asn Thr Ser
                485

<210> 126
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-16s21 sequence"

<400> 126
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc   60

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac   120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc   180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg   240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa   300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag   360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc   420

tgctggaaca agatcctgat gggcaccaag gagcatagcg gcacaaccaa cacagtcgct   480

gcctataacc tcacttggaa gagcaccaac ttcaaaacca tcctcgaatg ggaacccaaa   540

cccgttaacc aagtttacac cgtgcagatc agcaccaagt ccggcgactg gaagtccaaa   600

tgtttctata ccaccgacac cgagtgcgat ctcaccgatg agatcgtgaa agatgtgaaa   660

cagacctacc tcgcccgggt gtttagctac cccgccggca atgtggagag cactggttcc   720

gctggcgagc ctttatacga gaacagcccc gaatttaccc cttacctcga gaccaattta 780

ggacagccca ccatccaaag ctttgagcaa gttggcacaa aggtgaatgt gacagtggag 840

gacgagcgga ctttagtgcg gcggaacaac acctttctca gcctccggga tgtgttcggc 900

aaagatttaa tctacacact gtattactgg aagtcctctt cctccggcaa gaagacagct 960

aaaaccaaca caaacgagtt tttaatcgac gtggataaag gcgaaaacta ctgtttcagc 1020

gtgcaagctg tgatcccctc ccggaccgtg aataggaaaa gcaccgatag ccccgttgag 1080

tgcatgggcc aagaaaaggg cgagttccgg gagaactggg tgaacgtcat cagcgattta 1140

aagaagatcg aagatttaat tcagtccatg catatcgacg ccactttata cacagaatcc 1200

gacgtgcacc cctcttgtaa ggtgaccgcc atgaaatgtt ttttactgga gctgcaagtt 1260

atctctttag agagcggaga cgctagcatc cacgacaccg tggagaattt aatcatttta 1320

gccaataact ctttatccag caacggcaac gtgacagagt ccggctgcaa ggagtgcgaa 1380

gagctggagg agaagaacat caaggagttt ctgcaatcct ttgtgcacat tgtccagatg 1440

ttcatcaata cctcc 1455

<210> 127
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 127
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
20 25 30

Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
35 40 45

```
Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
    50                  55                  60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65                  70                  75                  80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
                85                  90                  95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
            100                 105                 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
        115                 120                 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
    130                 135                 140

Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr
                165                 170                 175

Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile
            180                 185                 190

Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile
        195                 200                 205

Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp
    210                 215                 220

Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr
225                 230                 235                 240
```

```
Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr
                245                 250                 255

Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro
            260                 265                 270

Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
        275                 280                 285

Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val
    290                 295                 300

Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp
305                 310                 315                 320

Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys
                325                 330                 335

Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly
            340                 345                 350

Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val
        355                 360                 365

Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys
    370                 375                 380

Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
385                 390                 395                 400

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                405                 410                 415

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            420                 425                 430

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
```

435 440 445

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
450 455 460

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
465 470 475 480

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
485 490 495

Gln Met Phe Ile Asn Thr Ser
500

<210> 128
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 128
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc 60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag 120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc 180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa 240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg 300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct 360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag 420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg 480

aacaagatcc tgatgggcac caaggagcat agcggcacaa ccaacacagt cgctgcctat 540

aacctcactt ggaagagcac caacttcaaa accatcctcg aatgggaacc caaacccgtt 600

aaccaagttt acaccgtgca gatcagcacc aagtccggcg actggaagtc caaatgtttc 660

tataccaccg acaccgagtg cgatctcacc gatgagatcg tgaaagatgt gaaacagacc 720

tacctcgccc gggtgtttag ctaccccgcc ggcaatgtgg agagcactgg ttccgctggc 780

gagcctttat acgagaacag ccccgaattt acccccttacc tcgagaccaa tttaggacag 840

cccaccatcc aaagctttga gcaagttggc acaaaggtga atgtgacagt ggaggacgag 900

cggactttag tgcggcggaa caacaccttt ctcagcctcc gggatgtgtt cggcaaagat 960

ttaatctaca cactgtatta ctggaagtcc tcttcctccg gcaagaagac agctaaaacc 1020

aacacaaacg agtttttaat cgacgtggat aaaggcgaaa actactgttt cagcgtgcaa 1080

gctgtgatcc cctcccggac cgtgaatagg aaaagcaccg atagccccgt tgagtgcatg 1140

ggccaagaaa agggcgagtt ccgggagaac tgggtgaacg tcatcagcga tttaaagaag 1200

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1260

caccctctt gtaaggtgac cgccatgaaa tgtttttttac tggagctgca agttatctct 1320

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat 1380

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg 1440

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc 1500

aatacctcc 1509

<210> 129
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 129
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
1 5 10 15

```
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
            20                  25                  30

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

Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
    50                  55                  60

Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
65                  70                  75                  80

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly Gly Gly
            100                 105                 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
        115                 120                 125

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

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val
145                 150                 155                 160

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

Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

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

```
    210                 215                 220

Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg
225                 230                 235                 240

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
                245                 250                 255

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            260                 265                 270

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        275                 280                 285

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    290                 295                 300

Arg Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp
305                 310                 315                 320

Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe
                325                 330                 335

Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe
            340                 345                 350

Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn
        355                 360                 365

Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro
    370                 375                 380

Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser
385                 390                 395                 400

Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe
                405                 410                 415
```

Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr
420 425 430

His Gly Ser Glu Asp Ser
435

<210> 130
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 130
tccgagctga cccaggaccc tgctgtgtcc gtggctctgg gccagaccgt gaggatcacc 60

tgccagggcg actccctgag gtcctactac gcctcctggt accagcagaa gcccggccag 120

gctcctgtgc tggtgatcta cggcaagaac aacaggccct ccggcatccc tgacaggttc 180

tccggatcct cctccggcaa caccgcctcc ctgaccatca caggcgctca ggccgaggac 240

gaggctgact actactgcaa ctccagggac tcctccggca accatgtggt gttcggcggc 300

ggcaccaagc tgaccgtggg ccatggcggc ggcggctccg gaggcggcgg cagcggcgga 360

ggaggatccg aggtgcagct ggtggagtcc ggaggaggag tggtgaggcc tggaggctcc 420

ctgaggctga gctgtgctgc ctccggcttc accttcgacg actacggcat gtcctgggtg 480

aggcaggctc ctggaaaggg cctggagtgg gtgtccggca tcaactggaa cggcggatcc 540

accggctacg ccgattccgt gaagggcagg ttcaccatca gcagggacaa cgccaagaac 600

tccctgtacc tgcagatgaa ctccctgagg gccgaggaca ccgccgtgta ctactgcgcc 660

aggggcaggt ccctgctgtt cgactactgg ggacagggca ccctggtgac cgtgtccagg 720

attacatgcc cccctcccat gagcgtggag cacgccgaca tctgggtgaa gagctatagc 780

ctctacagcc gggagaggta tatctgtaac agcggcttca agaggaaggc cggcaccagc 840

agcctcaccg agtgcgtgct gaataaggct accaacgtgg ctcactggac aacaccctct 900

ttaaagtgca tccggcaggg ccaggacagg cacatgatcc ggatgaggca gctcatcgac 960

atcgtcgacc agctgaagaa ctacgtgaac gacctggtgc ccgagtttct gcctgccccc 1020

gaggacgtgg agaccaactg cgagtggtcc gccttctcct gctttcagaa ggcccagctg 1080

aagtccgcca acaccggcaa caacgagcgg atcatcaacg tgagcatcaa gaagctgaag 1140

cggaagcctc cctccacaaa cgccggcagg aggcagaagc acaggctgac ctgccccagc 1200

tgtgactcct acgagaagaa gccccccaag gagttcctgg agaggttcaa gtccctgctg 1260

cagaagatga tccatcagca cctgtcctcc aggacccacg gctccgagga ctcc 1314

<210> 131
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 131
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
20 25 30

Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
35 40 45

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
50 55 60

Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
65 70 75 80

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala

```
                85                  90                  95

Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
            100                 105                 110

His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly
        115                 120                 125

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

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

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser
                165                 170                 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
            180                 185                 190

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg
        195                 200                 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
    210                 215                 220

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

Arg Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
                245                 250                 255

Ser Arg Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile
            260                 265                 270

Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn
        275                 280                 285
```

```
Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val
    290                 295                 300

Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys
305                 310                 315                 320

Cys Ile Arg Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu
                325                 330                 335

Ile Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro
            340                 345                 350

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

Ala Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly
    370                 375                 380

Asn Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys
385                 390                 395                 400

Pro Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys
                405                 410                 415

Pro Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu
            420                 425                 430

Arg Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser
        435                 440                 445

Arg Thr His Gly Ser Glu Asp Ser
    450                 455
```

<210> 132
<211> 1368
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-16s21 sequence"

<400> 132
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcctccgag 60

ctgacccagg accctgctgt gtccgtggct ctgggccaga ccgtgaggat cacctgccag 120

ggcgactccc tgaggtccta ctacgcctcc tggtaccagc agaagcccgg ccaggctcct 180

gtgctggtga tctacggcaa gaacaacagg ccctccggca tccctgacag gttctccgga 240

tcctcctccg gcaacaccgc ctccctgacc atcacaggcg ctcaggccga ggacgaggct 300

gactactact gcaactccag ggactcctcc ggcaaccatg tggtgttcgg cggcggcacc 360

aagctgaccg tgggccatgg cggcggcggc tccggaggcg gcggcagcgg cggaggagga 420

tccgaggtgc agctggtgga gtccggagga ggagtggtga ggcctggagg ctccctgagg 480

ctgagctgtg ctgcctccgg cttcaccttc gacgactacg gcatgtcctg ggtgaggcag 540

gctcctggaa agggcctgga gtgggtgtcc ggcatcaact ggaacggcgg atccaccggc 600

tacgccgatt ccgtgaaggg caggttcacc atcagcaggg acaacgccaa gaactccctg 660

tacctgcaga tgaactccct gagggccgag gacaccgccg tgtactactg cgccaggggc 720

aggtccctgc tgttcgacta ctggggacag ggcaccctgg tgaccgtgtc caggattaca 780

tgccccctc ccatgagcgt ggagcacgcc gacatctggg tgaagagcta tagcctctac 840

agccgggaga ggtatatctg taacagcggc ttcaagagga aggccggcac cagcagcctc 900

accgagtgcg tgctgaataa ggctaccaac gtggctcact ggacaacacc ctctttaaag 960

tgcatccggc agggccagga caggcacatg atccggatga ggcagctcat cgacatcgtc 1020

gaccagctga agaactacgt gaacgacctg gtgcccgagt ttctgcctgc ccccgaggac 1080

gtggagacca actgcgagtg gtccgccttc tcctgctttc agaaggccca gctgaagtcc 1140

gccaacaccg gcaacaacga gcggatcatc aacgtgagca tcaagaagct gaagcggaag 1200

cctccctcca caaacgccgg caggaggcag aagcacaggc tgacctgccc cagctgtgac 1260

tcctacgaga agaagccccc caaggagttc ctggagaggt tcaagtccct gctgcagaag 1320

atgatccatc agcacctgtc ctccaggacc cacggctccg aggactcc 1368

<210> 133
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-16s21 sequence"

<400> 133
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
85 90 95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
100 105 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
115 120 125

```
Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
```

```
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460

Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495

Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525
```

```
Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540


Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560


Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575


Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
            580                 585                 590


Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
        595                 600                 605


Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
    610                 615                 620


<210> 134
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-16s21 sequence"

<400> 134
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc       60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat      120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg      180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac      240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg      300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt      360
```

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 135
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-16s21 sequence"

<400> 135
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
50 55 60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65 70 75 80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
85 90 95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
100 105 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
115 120 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
130 135 140

```
Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305                 310                 315                 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
                325                 330                 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
```

```
            340                 345                 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
        355                 360                 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
    370                 375                 380

Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385                 390                 395                 400

Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
                405                 410                 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
            420                 425                 430

Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480

Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540
```

```
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560


Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575


Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590


Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
        595                 600                 605


Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
    610                 615                 620


Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625                 630                 635


<210> 136
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-16s21 sequence"

<400> 136
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc       60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg      120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag      180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg      240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag      300

ctccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag      360
```

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 137
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-16s21 sequence"

<400> 137
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
1 5 10 15

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

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

Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
50 55 60

Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
65 70 75 80

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
115 120 125

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

```
Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val
145                 150                 155                 160

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

Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Ser
    210                 215                 220

Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg
225                 230                 235                 240

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
                245                 250                 255

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            260                 265                 270

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        275                 280                 285

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    290                 295                 300

Arg Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp
305                 310                 315                 320

Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe
                325                 330                 335
```

```
Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe
            340                 345                 350

Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn
        355                 360                 365

Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro
    370                 375                 380

Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser
385                 390                 395                 400

Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe
                405                 410                 415

Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr
            420                 425                 430

His Gly Ser Glu Asp Ser
        435
```

<210> 138
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-16s21 sequence"

<400> 138
tccgagctga cccaggaccc tgctgtgtcc gtggctctgg gccagaccgt gaggatcacc 60

tgccagggcg actccctgag gtcctactac gcctcctggt accagcagaa gcccggccag 120

gctcctgtgc tggtgatcta cggcaagaac aacaggccct ccggcatccc tgacaggttc 180

tccggatcct cctccggcaa caccgcctcc ctgaccatca caggcgctca ggccgaggac 240

gaggctgact actactgcaa ctccagggac tcctccggca accatgtggt gttcggcggc 300

ggcaccaagc tgaccgtggg ccatggcggc ggcggctccg gaggcggcgg cagcggcgga 360

ggaggatccg aggtgcagct ggtggagtcc ggaggaggag tggtgaggcc tggaggctcc 420

ctgaggctga gctgtgctgc ctccggcttc accttcgacg actacggcat gtcctgggtg 480

aggcaggctc ctggaaaggg cctggagtgg gtgtccggca tcaactggaa cggcggatcc 540

accggctacg ccgattccgt gaagggcagg ttcaccatca gcagggacaa cgccaagaac 600

tccctgtacc tgcagatgaa ctccctgagg gccgaggaca ccgccgtgta ctactgcgcc 660

aggggcaggt ccctgctgtt cgactactgg ggacagggca ccctggtgac cgtgtccagg 720

attacatgcc cccctcccat gagcgtggag cacgccgaca tctgggtgaa gagctatagc 780

ctctacagcc gggagaggta tatctgtaac agcggcttca agaggaaggc cggcaccagc 840

agcctcaccg agtgcgtgct gaataaggct accaacgtgg ctcactggac aacaccctct 900

ttaaagtgca tccggcaggg ccaggacagg cacatgatcc ggatgaggca gctcatcgac 960

atcgtcgacc agctgaagaa ctacgtgaac gacctggtgc ccgagtttct gcctgccccc 1020

gaggacgtgg agaccaactg cgagtggtcc gccttctcct gctttcagaa ggcccagctg 1080

aagtccgcca acaccggcaa caacgagcgg atcatcaacg tgagcatcaa gaagctgaag 1140

cggaagcctc cctccacaaa cgccggcagg aggcagaagc acaggctgac ctgccccagc 1200

tgtgactcct acgagaagaa gccccccaag gagttcctgg agaggttcaa gtccctgctg 1260

cagaagatga tccatcagca cctgtcctcc aggacccacg gctccgagga ctcc 1314

<210> 139
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-16s21 sequence"

<400> 139
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

```
Tyr Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
            20                  25                  30

Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
        35                  40                  45

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
    50                  55                  60

Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
65                  70                  75                  80

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
                85                  90                  95

Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
            100                 105                 110

His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly
        115                 120                 125

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

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

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser
                165                 170                 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
            180                 185                 190

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg
        195                 200                 205
```

```
Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
    210                 215                 220

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

Arg Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
                245                 250                 255

Ser Arg Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile
            260                 265                 270

Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn
        275                 280                 285

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

Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys
305                 310                 315                 320

Cys Ile Arg Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu
                325                 330                 335

Ile Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro
            340                 345                 350

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

Ala Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly
    370                 375                 380

Asn Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys
385                 390                 395                 400
```

Pro Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys
405 410 415

Pro Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu
420 425 430

Arg Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser
435 440 445

Arg Thr His Gly Ser Glu Asp Ser
450 455

<210> 140
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-16s21 sequence"

<400> 140
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcctccgag 60

ctgacccagg accctgctgt gtccgtggct ctgggccaga ccgtgaggat cacctgccag 120

ggcgactccc tgaggtccta ctacgcctcc tggtaccagc agaagcccgg ccaggctcct 180

gtgctggtga tctacggcaa gaacaacagg ccctccggca tccctgacag gttctccgga 240

tcctcctccg gcaacaccgc ctccctgacc atcacaggcg ctcaggccga ggacgaggct 300

gactactact gcaactccag ggactcctcc ggcaaccatg tggtgttcgg cggcggcacc 360

aagctgaccg tgggccatgg cggcggcggc tccggaggcg gcggcagcgg cggaggagga 420

tccgaggtgc agctggtgga gtccggagga ggagtggtga ggcctggagg ctccctgagg 480

ctgagctgtg ctgcctccgg cttcaccttc gacgactacg gcatgtcctg ggtgaggcag 540

gctcctggaa agggcctgga gtgggtgtcc ggcatcaact ggaacggcgg atccaccggc 600

tacgccgatt ccgtgaaggg caggttcacc atcagcaggg acaacgccaa gaactccctg 660

tacctgcaga tgaactccct gagggccgag gacaccgccg tgtactactg cgccaggggc 720

aggtccctgc tgttcgacta ctggggacag ggcaccctgg tgaccgtgtc caggattaca 780

tgccccctc ccatgagcgt ggagcacgcc gacatctggg tgaagagcta tagcctctac 840

agccgggaga ggtatatctg taacagcggc ttcaagagga aggccggcac cagcagcctc 900

accgagtgcg tgctgaataa ggctaccaac gtggctcact ggacaacacc ctctttaaag 960

tgcatccggc agggccagga caggcacatg atccggatga ggcagctcat cgacatcgtc 1020

gaccagctga agaactacgt gaacgacctg gtgcccgagt ttctgcctgc ccccgaggac 1080

gtggagacca actgcgagtg gtccgccttc tcctgctttc agaaggccca gctgaagtcc 1140

gccaacaccg gcaacaacga gcggatcatc aacgtgagca tcaagaagct gaagcggaag 1200

cctccctcca caaacgccgg caggaggcag aagcacaggc tgacctgccc cagctgtgac 1260

tcctacgaga agaagccccc caaggagttc ctggagaggt tcaagtccct gctgcagaag 1320

atgatccatc agcacctgtc ctccaggacc cacggctccg aggactcc 1368

<210> 141
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 141
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
35 40 45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg

```
    50                  55                  60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140

Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr Val Ala
145                 150                 155                 160

Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
                165                 170                 175

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
            180                 185                 190

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
        195                 200                 205

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
    210                 215                 220

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
225                 230                 235                 240

Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
                245                 250                 255
```

```
Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
            260                 265                 270

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
        275                 280                 285

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
    290                 295                 300

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
305                 310                 315                 320

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
                325                 330                 335

Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
            340                 345                 350

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

Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
    370                 375                 380

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
385                 390                 395                 400

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
                405                 410                 415

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
            420                 425                 430

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
        435                 440                 445
```

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
    450   455   460

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
465   470   475   480

Phe Ile Asn Thr Ser
                485

<210> 142
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-7s sequence"

<400> 142
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc   60

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac   120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc   180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg   240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa   300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag   360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc   420

tgctggaaca agatcctgat gggcaccaag gagcatagcg gcacaaccaa cacagtcgct   480

gcctataacc tcacttggaa gagcaccaac ttcaaaacca tcctcgaatg ggaacccaaa   540

cccgttaacc aagtttacac cgtgcagatc agcaccaagt ccggcgactg gaagtccaaa   600

tgtttctata ccaccgacac cgagtgcgat ctcaccgatg agatcgtgaa agatgtgaaa   660

cagacctacc tcgcccgggt gtttagctac cccgccggca atgtggagag cactggttcc   720

gctggcgagc ctttatacga gaacagcccc gaatttaccc cttacctcga gaccaattta   780

ggacagccca ccatccaaag ctttgagcaa gttggcacaa aggtgaatgt gacagtggag 840

gacgagcgga ctttagtgcg gcggaacaac acctttctca gcctccggga tgtgttcggc 900

aaagatttaa tctacacact gtattactgg aagtcctctt cctccggcaa gaagacagct 960

aaaaccaaca caaacgagtt tttaatcgac gtggataaag gcgaaaacta ctgtttcagc 1020

gtgcaagctg tgatcccctc ccggaccgtg aataggaaaa gcaccgatag ccccgttgag 1080

tgcatgggcc aagaaaaggg cgagttccgg gagaactggg tgaacgtcat cagcgattta 1140

aagaagatcg aagatttaat tcagtccatg catatcgacg ccactttata cacagaatcc 1200

gacgtgcacc cctcttgtaa ggtgaccgcc atgaaatgtt ttttactgga gctgcaagtt 1260

atctctttag agagcggaga cgctagcatc cacgacaccg tggagaattt aatcatttta 1320

gccaataact ctttatccag caacggcaac gtgacagagt ccggctgcaa ggagtgcgaa 1380

gagctggagg agaagaacat caaggagttt ctgcaatcct ttgtgcacat tgtccagatg 1440

ttcatcaata cctcc 1455

<210> 143
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 143
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
20 25 30

Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
35 40 45

```
Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
    50                  55                  60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65                  70                  75                  80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
                85                  90                  95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
            100                 105                 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
        115                 120                 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
    130                 135                 140

Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr
                165                 170                 175

Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile
            180                 185                 190

Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile
        195                 200                 205

Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp
    210                 215                 220

Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr
225                 230                 235                 240

Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr
```

```
                245                 250                 255

Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro
            260                 265                 270

Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
        275                 280                 285

Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val
    290                 295                 300

Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp
305                 310                 315                 320

Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys
                325                 330                 335

Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly
            340                 345                 350

Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val
        355                 360                 365

Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys
    370                 375                 380

Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
385                 390                 395                 400

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                405                 410                 415

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            420                 425                 430

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        435                 440                 445
```

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    450   455   460

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
465   470   475   480

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                485   490   495

Gln Met Phe Ile Asn Thr Ser
            500

<210> 144
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 144
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc   60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag   120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc   180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa   240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg   300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct   360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag   420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg   480

aacaagatcc tgatgggcac caaggagcat agcggcacaa ccaacacagt cgctgcctat   540

aacctcactt ggaagagcac caacttcaaa accatcctcg aatgggaacc caaacccgtt   600

aaccaagttt acaccgtgca gatcagcacc aagtccggcg actggaagtc caaatgtttc 660

tataccaccg acaccgagtg cgatctcacc gatgagatcg tgaaagatgt gaaacagacc 720

tacctcgccc gggtgtttag ctaccccgcc ggcaatgtgg agagcactgg ttccgctggc 780

gagcctttat acgagaacag ccccgaattt acccccttacc tcgagaccaa tttaggacag 840

cccaccatcc aaagctttga gcaagttggc acaaaggtga atgtgacagt ggaggacgag 900

cggactttag tgcggcggaa caacaccttt ctcagcctcc gggatgtgtt cggcaaagat 960

ttaatctaca cactgtatta ctggaagtcc tcttcctccg gcaagaagac agctaaaacc 1020

aacacaaacg agtttttaat cgacgtggat aaaggcgaaa actactgttt cagcgtgcaa 1080

gctgtgatcc cctcccggac cgtgaatagg aaaagcaccg atagccccgt tgagtgcatg 1140

ggccaagaaa agggcgagtt ccgggagaac tgggtgaacg tcatcagcga tttaaagaag 1200

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1260

caccctctt gtaaggtgac cgccatgaaa tgtttttttac tggagctgca agttatctct 1320

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat 1380

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg 1440

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc 1500

aatacctcc 1509

<210> 145
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 145
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser

```
            20                  25                  30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
        35                  40                  45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
    50                  55                  60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140

Ile Leu Met Gly Thr Lys Glu His Ile Thr Cys Pro Pro Pro Met Ser
145                 150                 155                 160

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
                165                 170                 175

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
            180                 185                 190

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
        195                 200                 205

Thr Thr Pro Ser Leu Lys Cys Ile Arg
    210                 215
```

<210> 146
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 146
gattgtgata ttgaaggtaa agatggcaaa caatatgaga gtgttctaat ggtcagcatc 60

gatcaattat tggacagcat gaaagaaatt ggtagcaatt gcctgaataa tgaatttaac 120

ttttttaaaa gacatatctg tgatgctaat aaggaaggta tgtttttatt ccgtgctgct 180

cgcaagttga ggcaatttct taaaatgaat agcactggtg attttgatct ccacttatta 240

aaagtttcag aaggcacaac aatactgttg aactgcactg gccaggttaa aggaagaaaa 300

ccagctgccc tgggtgaagc ccaaccaaca aagagtttgg aagaaaataa atctttaaag 360

gaacagaaaa aactgaatga cttgtgtttc ctaaagagac tattacaaga gataaaaact 420

tgttggaata aaattttgat gggcactaaa gaacacatca cgtgccctcc ccccatgtcc 480

gtggaacacg cagacatctg ggtcaagagc tacagcttgt actccaggga gcggtacatt 540

tgtaactctg gtttcaagcg taaagccggc acgtccagcc tgacggagtg cgtgttgaac 600

aaggccacga atgtcgccca ctggacaacc cccagtctca aatgcattag a 651

<210> 147
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 147
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

```
Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
            20                  25                  30

Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
        35                  40                  45

Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
    50                  55                  60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65                  70                  75                  80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
                85                  90                  95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
            100                 105                 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
        115                 120                 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
    130                 135                 140

Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ile Thr Cys Pro Pro Pro
                165                 170                 175

Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr
            180                 185                 190

Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly
        195                 200                 205
```

Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala
210 215 220

His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
225 230 235

<210> 148
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-7s sequence"

<400> 148
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc 60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag 120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc 180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa 240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg 300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct 360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag 420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg 480

aacaagatcc tgatgggcac caaggagcat attacatgcc cccctcccat gagcgtggag 540

cacgccgaca tctgggtgaa gagctatagc ctctacagcc gggagaggta tatctgtaac 600

agcggcttca agaggaaggc cggcaccagc agcctcaccg agtgcgtgct gaataaggct 660

accaacgtgg ctcactggac aacaccctct ttaaagtgca tccgg 705

<210> 149
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFR sequence"

<400> 149
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
85 90 95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
100 105 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
115 120 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145 150 155 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
165 170 175

```
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365
```

```
Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460

Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495

Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560
```

```
Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575


Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
            580                 585                 590


Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
        595                 600                 605


Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
    610                 615                 620


<210> 150
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-TGFR sequence"

<400> 150
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc       60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat      120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg      180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac      240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg      300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt      360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga      420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg      480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa      540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc      600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac      660
```

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 151
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

TGFRt15-TGFR sequence"

<400> 151
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1   5   10   15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
            20   25   30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35   40   45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50   55   60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65   70   75   80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85   90   95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100   105   110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115   120   125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130   135   140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145   150   155   160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165   170   175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180   185   190

```
Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305                 310                 315                 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
                325                 330                 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
            340                 345                 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
        355                 360                 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
    370                 375                 380
```

```
Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385                 390                 395                 400

Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
                405                 410                 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
            420                 425                 430

Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480

Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575
```

```
Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590


Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
        595                 600                 605


Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
    610                 615                 620


Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625                 630                 635


<210> 152
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-TGFR sequence"

<400> 152
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc       60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg      120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag      180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg      240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag      300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag      360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac      420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga      480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat      540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc      600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc      660
```

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 153
<211> 352
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFR sequence"

<400> 153
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
85 90 95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
100 105 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
115 120 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145 150 155 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
165 170 175

```
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350
```

<210> 154
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFR sequence"

<400> 154
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cattacatgc ccccctccca tgagcgtgga gcacgccgac 900

atctgggtga agagctatag cctctacagc cgggagaggt atatctgtaa cagcggcttc 960

aagaggaagg ccggcaccag cagcctcacc gagtgcgtgc tgaataaggc taccaacgtg 1020

gctcactgga caacaccctc tttaaagtgc atccgg 1056

<210> 155
<211> 370
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFR sequence"

<400> 155
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
50 55 60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65 70 75 80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
85 90 95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
100 105 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
115 120 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
130 135 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145 150 155 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
165 170 175

```
Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365

Ile Arg
```

370

<210> 156
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFR sequence"

<400> 156
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacattac atgccccct cccatgagcg tggagcacgc cgacatctgg 960

gtgaagagct atagcctcta cagccgggag aggtatatct gtaacagcgg cttcaagagg 1020

aaggccggca ccagcagcct caccgagtgc gtgctgaata aggctaccaa cgtggctcac 1080

tggacaacac cctctttaaa gtgcatccgg 1110

<210> 157
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="CD137L"

<400> 157
Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
35 40 45

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
50 55 60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

```
His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145                 150                 155                 160


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


Gly Leu Pro Ser Pro Arg Ser Glu
            180


<210> 158
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="CD137L"

<400> 158
cgcgagggtc ccgagctttc gcccgacgat cccgccggcc tcttggacct gcggcagggc       60

atgtttgcgc agctggtggc ccaaaatgtt ctgctgatcg atgggcccct gagctggtac      120

agtgacccag gcctggcagg cgtgtccctg acgggggccc tgagctacaa agaggacacg      180

aaggagctgg tggtggccaa ggctggagtc tactatgtct tctttcaact agagctgcgg      240

cgcgtggtgg ccggcgaggg ctcaggctcc gtttcacttg cgctgcacct gcagccactg      300

cgctctgctg ctggggccgc cgccctggct ttgaccgtgg acctgccacc cgcctcctcc      360

gaggctcgga actcggcctt cggtttccag ggccgcttgc tgcacctgag tgccggccag      420

cgcctgggcg tccatcttca cactgaggcc agggcacgcc atgcctggca gcttacccag      480

ggcgccacag tcttgggact cttccgggtg acccccgaaa tcccagccgg actcccttca      540

ccgaggtcgg aa                                                          552


<210> 159
<211> 165
<212> PRT
<213> Homo sapiens
```

<220>
<221> source
<223> /note="CD137L"

<400> 159
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
1   5   10   15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
            20   25   30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
        35   40   45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
    50   55   60

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
65   70   75   80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
                85   90   95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
            100   105   110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
        115   120   125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
    130   135   140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145   150   155   160

Val Thr Pro Glu Ile
                165

<210> 160
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="CD137L"

<400> 160
gatcccgccg gcctcttgga cctgcggcag ggcatgtttg cgcagctggt ggcccaaaat 60

gttctgctga tcgatgggcc cctgagctgg tacagtgacc caggcctggc aggcgtgtcc 120

ctgacggggg gcctgagcta caaagaggac acgaaggagc tggtggtggc caaggctgga 180

gtctactatg tcttctttca actagagctg cggcgcgtgg tggccggcga gggctcaggc 240

tccgtttcac ttgcgctgca cctgcagcca ctgcgctctg ctgctggggc cgccgccctg 300

gctttgaccg tggacctgcc acccgcctcc tccgaggctc ggaactcggc cttcggtttc 360

cagggccgct tgctgcacct gagtgccggc cagcgcctgg gcgtccatct tcacactgag 420

gccagggcac gccatgcctg gcagcttacc cagggcgcca cagtcttggg actcttccgg 480

gtgacccccg aaatc 495

<210> 161
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 161
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp

```
        35                  40                  45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
    50                  55                  60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65                  70                  75                  80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
                85                  90                  95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
            100                 105                 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
        115                 120                 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
    130                 135                 140

Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr Val Ala
145                 150                 155                 160

Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
                165                 170                 175

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
            180                 185                 190

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
        195                 200                 205

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
    210                 215                 220

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
225                 230                 235                 240
```

```
Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
                245                 250                 255

Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
            260                 265                 270

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
        275                 280                 285

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
    290                 295                 300

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
305                 310                 315                 320

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
                325                 330                 335

Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
            340                 345                 350

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

Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
    370                 375                 380

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
385                 390                 395                 400

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
                405                 410                 415

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
            420                 425                 430
```

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
        435   440   445

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
    450   455   460

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
465   470   475   480

Phe Ile Asn Thr Ser
                485

<210> 162
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-21s137L sequence"

<400> 162
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc   60

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac   120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc   180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg   240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa   300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag   360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc   420

tgctggaaca agatcctgat gggcaccaag gagcatagcg gcacaaccaa cacagtcgct   480

gcctataacc tcacttggaa gagcaccaac ttcaaaacca tcctcgaatg ggaacccaaa   540

cccgttaacc aagtttacac cgtgcagatc agcaccaagt ccggcgactg gaagtccaaa   600

tgtttctata ccaccgacac cgagtgcgat ctcaccgatg agatcgtgaa agatgtgaaa   660

cagacctacc tcgcccgggt gtttagctac cccgccggca atgtggagag cactggttcc 720

gctggcgagc ctttatacga gaacagcccc gaatttaccc cttacctcga gaccaattta 780

ggacagccca ccatccaaag ctttgagcaa gttggcacaa aggtgaatgt gacagtggag 840

gacgagcgga ctttagtgcg gcggaacaac acctttctca gcctccggga tgtgttcggc 900

aaagatttaa tctacacact gtattactgg aagtcctctt cctccggcaa gaagacagct 960

aaaaccaaca caaacgagtt tttaatcgac gtggataaag gcgaaaacta ctgtttcagc 1020

gtgcaagctg tgatcccctc ccggaccgtg aataggaaaa gcaccgatag ccccgttgag 1080

tgcatgggcc aagaaaaggg cgagttccgg gagaactggg tgaacgtcat cagcgattta 1140

aagaagatcg aagatttaat tcagtccatg catatcgacg ccactttata cacagaatcc 1200

gacgtgcacc cctcttgtaa ggtgaccgcc atgaaatgtt ttttactgga gctgcaagtt 1260

atctctttag agagcggaga cgctagcatc cacgacaccg tggagaattt aatcatttta 1320

gccaataact ctttatccag caacggcaac gtgacagagt ccggctgcaa ggagtgcgaa 1380

gagctggagg agaagaacat caaggagttt ctgcaatcct ttgtgcacat tgtccagatg 1440

ttcatcaata cctcc 1455

<210> 163
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 163
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
20 25 30

```
Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
        35                  40                  45

Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
    50                  55                  60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65                  70                  75                  80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
                85                  90                  95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
            100                 105                 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
        115                 120                 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
    130                 135                 140

Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr
                165                 170                 175

Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile
            180                 185                 190

Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile
        195                 200                 205

Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp
    210                 215                 220

Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr
```

```
225                 230                 235                 240

Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr
                245                 250                 255

Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro
            260                 265                 270

Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
        275                 280                 285

Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val
    290                 295                 300

Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp
305                 310                 315                 320

Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys
                325                 330                 335

Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly
            340                 345                 350

Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val
        355                 360                 365

Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys
    370                 375                 380

Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
385                 390                 395                 400

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                405                 410                 415

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            420                 425                 430
```

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
435 440 445

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
450 455 460

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
465 470 475 480

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
485 490 495

Gln Met Phe Ile Asn Thr Ser
500

<210> 164
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 164
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc 60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag 120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc 180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa 240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg 300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct 360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag 420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg 480

aacaagatcc tgatgggcac caaggagcat agcggcacaa ccaacacagt cgctgcctat 540

aacctcactt ggaagagcac caacttcaaa accatcctcg aatgggaacc caaacccgtt 600

aaccaagttt acaccgtgca gatcagcacc aagtccggcg actggaagtc caaatgtttc 660

tataccaccg acaccgagtg cgatctcacc gatgagatcg tgaaagatgt gaaacagacc 720

tacctcgccc gggtgtttag ctaccccgcc ggcaatgtgg agagcactgg ttccgctggc 780

gagcctttat acgagaacag ccccgaattt acccccttacc tcgagaccaa tttaggacag 840

cccaccatcc aaagctttga gcaagttggc acaaaggtga atgtgacagt ggaggacgag 900

cggactttag tgcggcggaa caacaccttt ctcagcctcc gggatgtgtt cggcaaagat 960

ttaatctaca cactgtatta ctggaagtcc tcttcctccg gcaagaagac agctaaaacc 1020

aacacaaacg agtttttaat cgacgtggat aaaggcgaaa actactgttt cagcgtgcaa 1080

gctgtgatcc cctcccggac cgtgaatagg aaaagcaccg atagccccgt tgagtgcatg 1140

ggccaagaaa agggcgagtt ccgggagaac tgggtgaacg tcatcagcga tttaaagaag 1200

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1260

caccctctt gtaaggtgac cgccatgaaa tgtttttttac tggagctgca agttatctct 1320

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat 1380

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg 1440

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc 1500

aatacctcc 1509

<210> 165
<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 165
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile

```
1               5                   10                  15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
            20                  25                  30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
        35                  40                  45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
    50                  55                  60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65                  70                  75                  80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu His
    130                 135                 140

Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
145                 150                 155                 160

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
                165                 170                 175

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro
            180                 185                 190

Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205
```

```
Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
    210                 215                 220

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
225                 230                 235                 240

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
                245                 250                 255

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
            260                 265                 270

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
        275                 280                 285

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
    290                 295                 300

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
305                 310                 315                 320

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
                325                 330                 335

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
            340                 345                 350

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
        355                 360                 365

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
    370                 375                 380

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
385                 390                 395
```

<210> 166
<211> 1191
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 166
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg 60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc 120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcca ttacatgccc ccctcccatg 420

agcgtggagc acgccgacat ctgggtgaag agctatagcc tctacagccg ggagaggtat 480

atctgtaaca gcggcttcaa gaggaaggcc ggcaccagca gcctcaccga gtgcgtgctg 540

aataaggcta ccaacgtggc tcactggaca acaccctctt taaagtgcat ccggggcggt 600

ggaggatccg gaggaggtgg ctccggcggc ggaggatctc gcgagggtcc cgagctttcg 660

cccgacgatc ccgccggcct cttggacctg cggcagggca tgtttgcgca gctggtggcc 720

caaaatgttc tgctgatcga tgggcccctg agctggtaca gtgacccagg cctggcaggc 780

gtgtccctga cgggggcct gagctacaaa gaggacacga aggagctggt ggtggccaag 840

gctggagtct actatgtctt ctttcaacta gagctgcggc gcgtggtggc cggcgagggc 900

tcaggctccg tttcacttgc gctgcacctg cagccactgc gctctgctgc tggggccgcc 960

gccctggctt tgaccgtgga cctgccaccc gcctcctccg aggctcggaa ctcggccttc 1020

ggtttccagg gccgcttgct gcacctgagt gccggccagc gcctgggcgt ccatcttcac 1080

actgaggcca gggcacgcca tgcctggcag cttacccagg gcgccacagt cttgggactc 1140

ttccgggtga cccccgaaat cccagccgga ctcccttcac cgaggtcgga a 1191

<210> 167
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 167
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
20 25 30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
35 40 45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
50 55 60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65 70 75 80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
85 90 95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
100 105 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
115 120 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
130 135 140

```
Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205

Thr Pro Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
225                 230                 235                 240

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
                245                 250                 255

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

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
        275                 280                 285

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
    290                 295                 300

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
305                 310                 315                 320

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
                325                 330                 335
```

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
340 345 350

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
355 360 365

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
370 375 380

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
385 390 395 400

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
405 410 415

<210> 168
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 168
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc 60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac 120

tacgtgaacg acctggtgcc cgagtttctg cctgccccg aggacgtgga gaccaactgc 180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac 240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac 300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag 360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac 420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccctcc catgagcgtg 480

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt 540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag 600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgggg cggtggagga 660

tccggaggag gtggctccgg cggcggagga tctcgcgagg gtcccgagct ttcgcccgac 720

gatcccgccg gcctcttgga cctgcggcag ggcatgtttg cgcagctggt ggcccaaaat 780

gttctgctga tcgatgggcc cctgagctgg tacagtgacc caggcctggc aggcgtgtcc 840

ctgacggggg gcctgagcta caaagaggac acgaaggagc tggtggtggc caaggctgga 900

gtctactatg tcttctttca actagagctg cggcgcgtgg tggccggcga gggctcaggc 960

tccgtttcac ttgcgctgca cctgcagcca ctgcgctctg ctgctggggc cgccgccctg 1020

gctttgaccg tggacctgcc acccgcctcc tccgaggctc ggaactcggc cttcggtttc 1080

cagggccgct tgctgcacct gagtgccggc cagcgcctgg gcgtccatct tcacactgag 1140

gccagggcac gccatgcctg gcagcttacc cagggcgcca cagtcttggg actcttccgg 1200

gtgacccccg aaatcccagc cggactccct tcaccgaggt cggaa 1245

<210> 169
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 169
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
20 25 30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
35 40 45

```
Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
    50                  55                  60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65                  70                  75                  80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu His
    130                 135                 140

Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
145                 150                 155                 160

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
                165                 170                 175

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro
            180                 185                 190

Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205

Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
    210                 215                 220

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
225                 230                 235                 240

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
```

```
                245                 250                 255

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
            260                 265                 270

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
        275                 280                 285

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
    290                 295                 300

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
305                 310                 315                 320

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
                325                 330                 335

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
            340                 345                 350

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
        355                 360                 365

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
    370                 375


<210> 170
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-21s137L sequence"

<400> 170
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg       60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc      120
```

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcca ttacatgccc ccctcccatg 420

agcgtggagc acgccgacat ctgggtgaag agctatagcc tctacagccg ggagaggtat 480

atctgtaaca gcggcttcaa gaggaaggcc ggcaccagca gcctcaccga gtgcgtgctg 540

aataaggcta ccaacgtggc tcactggaca acaccctctt taaagtgcat ccggggcggt 600

ggaggatccg gaggaggtgg ctccggcggc ggaggatctg atcccgccgg cctcttggac 660

ctgcggcagg gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc 720

ctgagctggt acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac 780

aaagaggaca cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa 840

ctagagctgc ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac 900

ctgcagccac tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca 960

cccgcctcct ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg 1020

agtgccggcc agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg 1080

cagcttaccc agggcgccac agtcttggga ctcttccggg tgacccccga aatc 1134

<210> 171
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 171
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

```
Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
            20                  25                  30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
        35                  40                  45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
    50                  55                  60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65                  70                  75                  80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
                85                  90                  95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
            100                 105                 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
        115                 120                 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205
```

```
Thr Pro Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp Leu Arg
225                 230                 235                 240

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
                245                 250                 255

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
            260                 265                 270

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
        275                 280                 285

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
    290                 295                 300

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
305                 310                 315                 320

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
                325                 330                 335

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
            340                 345                 350

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
        355                 360                 365

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
    370                 375                 380

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
385                 390                 395
```

<210> 172
<211> 1188
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-21s137L sequence"

<400> 172
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc 60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac 120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc 180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac 240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac 300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag 360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac 420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccccctcc catgagcgtg 480

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt 540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag 600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgggg cggtggagga 660

tccggaggag gtggctccgg cggcggagga tctgatcccg ccggcctctt ggacctgcgg 720

cagggcatgt ttgcgcagct ggtggcccaa aatgttctgc tgatcgatgg gcccctgagc 780

tggtacagtg acccaggcct ggcaggcgtg tccctgacgg ggggcctgag ctacaaagag 840

gacacgaagg agctggtggt ggccaaggct ggagtctact atgtcttctt tcaactagag 900

ctgcggcgcg tggtggccgg cgagggctca ggctccgttt cacttgcgct gcacctgcag 960

ccactgcgct ctgctgctgg ggccgccgcc ctggctttga ccgtggacct gccacccgcc 1020

tcctccgagg ctcggaactc ggccttcggt ttccagggcc gcttgctgca cctgagtgcc 1080

ggccagcgcc tgggcgtcca tcttcacact gaggccaggg cacgccatgc ctggcagctt 1140

acccagggcg ccacagtctt gggactcttc cgggtgaccc ccgaaatc 1188

<210> 173
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-TGFRs sequence"

<400> 173
Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
35 40 45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
50 55 60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65 70 75 80

Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val
85 90 95

Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
100 105 110

Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
115 120 125

Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
130 135 140

```
Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr Val Ala
145                 150                 155                 160

Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
                165                 170                 175

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
            180                 185                 190

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
        195                 200                 205

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
    210                 215                 220

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
225                 230                 235                 240

Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
                245                 250                 255

Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
            260                 265                 270

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
        275                 280                 285

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
    290                 295                 300

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
305                 310                 315                 320

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
                325                 330                 335
```

```
Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
            340                 345                 350

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

Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
    370                 375                 380

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
385                 390                 395                 400

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
                405                 410                 415

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
            420                 425                 430

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
        435                 440                 445

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
    450                 455                 460

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
465                 470                 475                 480

Phe Ile Asn Thr Ser
                485
```

<210> 174
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic 7t15-TGFRs sequence"

<400> 174
gattgcgaca tcgagggcaa ggacggcaag cagtacgaga gcgtgctgat ggtgtccatc 60

gaccagctgc tggacagcat gaaggagatc ggctccaact gcctcaacaa cgagttcaac 120

ttcttcaagc ggcacatctg cgacgccaac aaggagggca tgttcctgtt cagggccgcc 180

aggaaactgc ggcagttcct gaagatgaac tccaccggcg acttcgacct gcacctgctg 240

aaggtgtccg agggcaccac catcctgctg aactgcaccg gacaggtgaa gggccggaaa 300

cctgctgctc tgggagaggc ccaacccacc aagagcctgg aggagaacaa gtccctgaag 360

gagcagaaga agctgaacga cctgtgcttc ctgaagaggc tgctgcagga gatcaagacc 420

tgctggaaca agatcctgat gggcaccaag gagcatagcg gcacaaccaa cacagtcgct 480

gcctataacc tcacttggaa gagcaccaac ttcaaaacca tcctcgaatg ggaacccaaa 540

cccgttaacc aagtttacac cgtgcagatc agcaccaagt ccggcgactg gaagtccaaa 600

tgtttctata ccaccgacac cgagtgcgat ctcaccgatg agatcgtgaa agatgtgaaa 660

cagacctacc tcgcccgggt gtttagctac cccgccggca atgtggagag cactggttcc 720

gctggcgagc ctttatacga gaacagcccc gaatttaccc cttacctcga gaccaattta 780

ggacagccca ccatccaaag ctttgagcaa gttggcacaa aggtgaatgt gacagtggag 840

gacgagcgga ctttagtgcg gcggaacaac acctttctca gcctccggga tgtgttcggc 900

aaagatttaa tctacacact gtattactgg aagtcctctt cctccggcaa gaagacagct 960

aaaaccaaca caaacgagtt tttaatcgac gtggataaag gcgaaaacta ctgtttcagc 1020

gtgcaagctg tgatcccctc ccggaccgtg aataggaaaa gcaccgatag ccccgttgag 1080

tgcatgggcc aagaaaaggg cgagttccgg gagaactggg tgaacgtcat cagcgattta 1140

aagaagatcg aagatttaat tcagtccatg catatcgacg ccactttata cacagaatcc 1200

gacgtgcacc cctcttgtaa ggtgaccgcc atgaaatgtt ttttactgga gctgcaagtt 1260

atctctttag agagcggaga cgctagcatc cacgacaccg tggagaattt aatcatttta 1320

gccaataact ctttatccag caacggcaac gtgacagagt ccggctgcaa ggagtgcgaa 1380

gagctggagg agaagaacat caaggagttt ctgcaatcct ttgtgcacat tgtccagatg 1440

ttcatcaata cctcc 1455

<210> 175
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-TGFRs sequence"

<400> 175
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser
20 25 30

Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile
35 40 45

Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile
50 55 60

Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys
65 70 75 80

Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His
85 90 95

Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly
100 105 110

Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr
115 120 125

Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn
130 135 140

```
Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp
145                 150                 155                 160

Asn Lys Ile Leu Met Gly Thr Lys Glu His Ser Gly Thr Thr Asn Thr
                165                 170                 175

Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile
            180                 185                 190

Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile
        195                 200                 205

Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp
    210                 215                 220

Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr
225                 230                 235                 240

Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr
                245                 250                 255

Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro
            260                 265                 270

Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
        275                 280                 285

Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val
    290                 295                 300

Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp
305                 310                 315                 320

Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys
                325                 330                 335
```

```
Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly
            340                 345                 350

Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val
        355                 360                 365

Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys
    370                 375                 380

Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
385                 390                 395                 400

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                405                 410                 415

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            420                 425                 430

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        435                 440                 445

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    450                 455                 460

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
465                 470                 475                 480

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                485                 490                 495

Gln Met Phe Ile Asn Thr
            500
```

<210> 176
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-TGFRs sequence"

<400> 176
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccgattgc 60

gacatcgagg gcaaggacgg caagcagtac gagagcgtgc tgatggtgtc catcgaccag 120

ctgctggaca gcatgaagga gatcggctcc aactgcctca acaacgagtt caacttcttc 180

aagcggcaca tctgcgacgc caacaaggag ggcatgttcc tgttcagggc cgccaggaaa 240

ctgcggcagt tcctgaagat gaactccacc ggcgacttcg acctgcacct gctgaaggtg 300

tccgagggca ccaccatcct gctgaactgc accggacagg tgaagggccg gaaacctgct 360

gctctgggag aggcccaacc caccaagagc ctggaggaga acaagtccct gaaggagcag 420

aagaagctga acgacctgtg cttcctgaag aggctgctgc aggagatcaa gacctgctgg 480

aacaagatcc tgatgggcac caaggagcat agcggcacaa ccaacacagt cgctgcctat 540

aacctcactt ggaagagcac caacttcaaa accatcctcg aatgggaacc caaacccgtt 600

aaccaagttt acaccgtgca gatcagcacc aagtccggcg actggaagtc caaatgtttc 660

tataccaccg acaccgagtg cgatctcacc gatgagatcg tgaaagatgt gaaacagacc 720

tacctcgccc gggtgtttag ctaccccgcc ggcaatgtgg agagcactgg ttccgctggc 780

gagcctttat acgagaacag ccccgaattt acccccttacc tcgagaccaa tttaggacag 840

cccaccatcc aaagctttga gcaagttggc acaaaggtga atgtgacagt ggaggacgag 900

cggactttag tgcggcggaa caacaccttt ctcagcctcc gggatgtgtt cggcaaagat 960

ttaatctaca cactgtatta ctggaagtcc tcttcctccg gcaagaagac agctaaaacc 1020

aacacaaacg agtttttaat cgacgtggat aaaggcgaaa actactgttt cagcgtgcaa 1080

gctgtgatcc cctcccggac cgtgaatagg aaaagcaccg atagccccgt tgagtgcatg 1140

ggccaagaaa agggcgagtt ccgggagaac tgggtgaacg tcatcagcga tttaaagaag 1200

atcgaagatt taattcagtc catgcatatc gacgccactt tatacacaga atccgacgtg 1260

```
cacccctctt gtaaggtgac cgccatgaaa tgtttttac tggagctgca agttatctct     1320

ttagagagcg gagacgctag catccacgac accgtggaga atttaatcat tttagccaat     1380

aactctttat ccagcaacgg caacgtgaca gagtccggct gcaaggagtg cgaagagctg     1440

gaggagaaga acatcaagga gtttctgcaa tcctttgtgc acattgtcca gatgttcatc     1500

aatacctcc                                                             1509


<210> 177
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-TGFRs sequence"

<400> 177
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1               5                   10                  15


Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20                  25                  30


Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35                  40                  45


Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60


Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80


Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95


Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110
```

```
Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300
```

```
Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320


Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335


Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350


<210> 178
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-TGFRs sequence"

<400> 178
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc       60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat      120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg      180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac      240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg      300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt      360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga      420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg      480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa      540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc      600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac      660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc      720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc      780
```

```
tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa      840

tacaatacca gcaaccccga cattacatgc ccccctccca tgagcgtgga gcacgccgac      900

atctgggtga agagctatag cctctacagc cgggagaggt atatctgtaa cagcggcttc      960

aagaggaagg ccggcaccag cagcctcacc gagtgcgtgc tgaataaggc taccaacgtg     1020

gctcactgga caacaccctc tttaaagtgc atccgg                               1056


<210> 179
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      7t15-TGFRs sequence"

<400> 179
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1               5                  10                  15


Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
            20                  25                  30


Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35                  40                  45


Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50                  55                  60


Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80


Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95


His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110
```

```
Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300
```

```
Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320


Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335


Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350


Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365


Ile Arg
    370
```

<210> 180
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
7t15-TGFRs sequence"

<400> 180

```
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc       60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg      120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag      180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg      240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag      300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag      360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac      420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga      480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat      540
```

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacattac atgcccccct cccatgagcg tggagcacgc cgacatctgg 960

gtgaagagct atagcctcta cagccgggag aggtatatct gtaacagcgg cttcaagagg 1020

aaggccggca ccagcagcct caccgagtgc gtgctgaata aggctaccaa cgtggctcac 1080

tggacaacac cctctttaaa gtgcatccgg 1110

<210> 181
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 181
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp

```
65                  70                  75                  80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270
```

```
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460
```

```
Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480


Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495


Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510


Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525


Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540


Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560


Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575


Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
            580                 585                 590


Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
        595                 600                 605


Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
    610                 615                 620


<210> 182
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

TGFRt15-21s137L sequence"

<400> 182
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 183
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 183
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
50 55 60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65 70 75 80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys

```
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285
```

```
Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305                 310                 315                 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
                325                 330                 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
            340                 345                 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
        355                 360                 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
    370                 375                 380

Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385                 390                 395                 400

Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
                405                 410                 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
            420                 425                 430

Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480
```

```
Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
        595                 600                 605

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
    610                 615                 620

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625                 630                 635
```

<210> 184
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

TGFRt15-21s137L sequence"

<400> 184
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 185
<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 185
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
20 25 30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
35 40 45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
50 55 60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65 70 75 80

```
Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
                85                  90                  95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
            100                 105                 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
        115                 120                 125

Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu His
    130                 135                 140

Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
145                 150                 155                 160

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
                165                 170                 175

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro
            180                 185                 190

Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205

Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
    210                 215                 220

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
225                 230                 235                 240

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
                245                 250                 255

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
            260                 265                 270
```

```
Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
        275                 280                 285


Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
    290                 295                 300


Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
305                 310                 315                 320


Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
                325                 330                 335


Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
            340                 345                 350


Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
        355                 360                 365


Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
    370                 375                 380


Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
385                 390                 395


<210> 186
<211> 1191
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-21s137L sequence"

<400> 186
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg       60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc      120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc      180
```

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcca ttacatgccc ccctcccatg 420

agcgtggagc acgccgacat ctgggtgaag agctatagcc tctacagccg ggagaggtat 480

atctgtaaca gcggcttcaa gaggaaggcc ggcaccagca gcctcaccga gtgcgtgctg 540

aataaggcta ccaacgtggc tcactggaca acaccctctt taaagtgcat ccggggcggt 600

ggaggatccg gaggaggtgg ctccggcggc ggaggatctc gcgagggtcc cgagctttcg 660

cccgacgatc ccgccggcct cttggacctg cggcagggca tgtttgcgca gctggtggcc 720

caaaatgttc tgctgatcga tgggcccctg agctggtaca gtgacccagg cctggcaggc 780

gtgtccctga cgggggggcct gagctacaaa gaggacacga aggagctggt ggtggccaag 840

gctggagtct actatgtctt ctttcaacta gagctgcggc gcgtggtggc cggcgagggc 900

tcaggctccg tttcacttgc gctgcacctg cagccactgc gctctgctgc tggggccgcc 960

gccctggctt tgaccgtgga cctgccaccc gcctcctccg aggctcggaa ctcggccttc 1020

ggtttccagg gccgcttgct gcacctgagt gccggccagc gcctgggcgt ccatcttcac 1080

actgaggcca gggcacgcca tgcctggcag cttacccagg gcgccacagt cttgggactc 1140

ttccgggtga cccccgaaat cccagccgga ctcccttcac cgaggtcgga a 1191

<210> 187
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 187
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

```
Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
            20                  25                  30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
        35                  40                  45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
    50                  55                  60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65                  70                  75                  80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
                85                  90                  95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
            100                 105                 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
        115                 120                 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205
```

```
Thr Pro Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
225                 230                 235                 240

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
                245                 250                 255

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

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
        275                 280                 285

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
    290                 295                 300

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
305                 310                 315                 320

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
                325                 330                 335

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
            340                 345                 350

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
        355                 360                 365

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
    370                 375                 380

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
385                 390                 395                 400

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
```

405 410 415

<210> 188
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 188
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc 60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac 120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc 180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac 240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac 300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag 360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac 420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccccctcc catgagcgtg 480

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt 540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag 600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgggg cggtggagga 660

tccggaggag gtggctccgg cggcggagga tctcgcgagg gtcccgagct ttcgcccgac 720

gatcccgccg gcctcttgga cctgcggcag ggcatgtttg cgcagctggt ggcccaaaat 780

gttctgctga tcgatgggcc cctgagctgg tacagtgacc caggcctggc aggcgtgtcc 840

ctgacggggg gcctgagcta caaagaggac acgaaggagc tggtggtggc caaggctgga 900

gtctactatg tcttctttca actagagctg cggcgcgtgg tggccggcga gggctcaggc 960

tccgtttcac ttgcgctgca cctgcagcca ctgcgctctg ctgctggggc cgccgccctg 1020

gctttgaccg tggacctgcc acccgcctcc tccgaggctc ggaactcggc cttcggtttc 1080

cagggccgct tgctgcacct gagtgccggc cagcgcctgg gcgtccatct tcacactgag 1140

gccagggcac gccatgcctg gcagcttacc cagggcgcca cagtcttggg actcttccgg 1200

gtgacccccg aaatcccagc cggactccct tcaccgaggt cggaa 1245

<210> 189
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 189
Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
20 25 30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
35 40 45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
50 55 60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65 70 75 80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
85 90 95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
100 105 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
115 120 125

```
Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val Glu His
    130                 135                 140

Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
145                 150                 155                 160

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
                165                 170                 175

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro
            180                 185                 190

Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205

Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
    210                 215                 220

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
225                 230                 235                 240

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
                245                 250                 255

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
            260                 265                 270

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
        275                 280                 285

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
    290                 295                 300

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
305                 310                 315                 320
```

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
325 330 335

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
340 345 350

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
355 360 365

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
370 375

<210> 190
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-21s137L sequence"

<400> 190
cagggccagg acaggcacat gatccggatg aggcagctca tcgacatcgt cgaccagctg 60

aagaactacg tgaacgacct ggtgcccgag tttctgcctg cccccgagga cgtggagacc 120

aactgcgagt ggtccgcctt ctcctgcttt cagaaggccc agctgaagtc cgccaacacc 180

ggcaacaacg agcggatcat caacgtgagc atcaagaagc tgaagcggaa gcctccctcc 240

acaaacgccg gcaggaggca gaagcacagg ctgacctgcc ccagctgtga ctcctacgag 300

aagaagcccc ccaaggagtt cctggagagg ttcaagtccc tgctgcagaa gatgatccat 360

cagcacctgt cctccaggac ccacggctcc gaggactcca ttacatgccc ccctcccatg 420

agcgtggagc acgccgacat ctgggtgaag agctatagcc tctacagccg ggagaggtat 480

atctgtaaca gcggcttcaa gaggaaggcc ggcaccagca gcctcaccga gtgcgtgctg 540

aataaggcta ccaacgtggc tcactggaca acaccctctt taaagtgcat ccggggcggt 600

ggaggatccg gaggaggtgg ctccggcggc ggaggatctg atcccgccgg cctcttggac 660

ctgcggcagg gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc 720

ctgagctggt acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac 780

aaagaggaca cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa 840

ctagagctgc ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac 900

ctgcagccac tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca 960

cccgcctcct ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg 1020

agtgccggcc agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg 1080

cagcttaccc agggcgccac agtcttggga ctcttccggg tgacccccga aatc 1134

<210> 191
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-21s137L sequence"

<400> 191
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
20 25 30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
35 40 45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
50 55 60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65 70 75 80

```
Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
                85                  90                  95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
            100                 105                 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
        115                 120                 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205

Thr Pro Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp Leu Arg
225                 230                 235                 240

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
                245                 250                 255

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
            260                 265                 270

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
```

```
        275                 280                 285

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
    290                 295                 300

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
305                 310                 315                 320

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
                325                 330                 335

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
            340                 345                 350

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
        355                 360                 365

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
    370                 375                 380

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
385                 390                 395


<210> 192
<211> 1188
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-21s137L sequence"

<400> 192
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc       60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac      120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc      180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac      240
```

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac 300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag 360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac 420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccctcc catgagcgtg 480

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt 540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag 600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgggg cggtggagga 660

tccggaggag gtggctccgg cggcggagga tctgatcccg ccggcctctt ggacctgcgg 720

cagggcatgt ttgcgcagct ggtggcccaa aatgttctgc tgatcgatgg gcccctgagc 780

tggtacagtg acccaggcct ggcaggcgtg tccctgacgg ggggcctgag ctacaaagag 840

gacacgaagg agctggtggt ggccaaggct ggagtctact atgtcttctt tcaactagag 900

ctgcggcgcg tggtggccgg cgagggctca ggctccgttt cacttgcgct gcacctgcag 960

ccactgcgct ctgctgctgg ggccgccgcc ctggctttga ccgtggacct gccacccgcc 1020

tcctccgagg ctcggaactc ggccttcggt ttccagggcc gcttgctgca cctgagtgcc 1080

ggccagcgcc tgggcgtcca tcttcacact gaggccaggg cacgccatgc ctggcagctt 1140

acccagggcg ccacagtctt gggactcttc cgggtgaccc ccgaaatc 1188

<210> 193
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs21 sequence"

<400> 193
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

```
Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20                  25                  30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35                  40                  45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
```

```
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415
```

```
Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460

Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495

Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
            580                 585                 590

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
        595                 600                 605
```

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
610 615 620

<210> 194
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs21 sequence"

<400> 194
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 195
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs21 sequence"

<400> 195
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

```
Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35                  40                  45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50                  55                  60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
```

225 230 235 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
245 250 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
260 265 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
275 280 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
290 295 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305 310 315 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
325 330 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
340 345 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
355 360 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
370 375 380

Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385 390 395 400

Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
405 410 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
420 425 430

```
Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480

Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
        595                 600                 605

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
    610                 615                 620
```

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625 630 635

<210> 196
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs21 sequence"

<400> 196
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 197
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs21 sequence"

<400> 197
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

```
Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35                  40                  45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220
```

```
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350

Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
        355                 360                 365

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
    370                 375                 380

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
385                 390                 395                 400

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
                405                 410                 415
```

```
Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
            420                 425                 430

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
        435                 440                 445

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
    450                 455                 460

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
465                 470                 475                 480

Gly Ser Glu Asp Ser
                485
```

<210> 198
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs21 sequence"

<400> 198

```
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc       60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat      120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg      180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac      240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg      300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt      360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga      420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg      480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa      540
```

ttctgcgatg tgaggtttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cattacatgc ccccctccca tgagcgtgga gcacgccgac 900

atctgggtga agagctatag cctctacagc cgggagaggt atatctgtaa cagcggcttc 960

aagaggaagg ccggcaccag cagcctcacc gagtgcgtgc tgaataaggc taccaacgtg 1020

gctcactgga caacaccctc tttaaagtgc atccggcagg gccaggacag gcacatgatc 1080

cggatgaggc agctcatcga catcgtcgac cagctgaaga actacgtgaa cgacctggtg 1140

cccgagtttc tgcctgcccc cgaggacgtg gagaccaact gcgagtggtc cgccttctcc 1200

tgctttcaga aggcccagct gaagtccgcc aacaccggca acaacgagcg gatcatcaac 1260

gtgagcatca agaagctgaa gcggaagcct ccctccacaa acgccggcag gaggcagaag 1320

cacaggctga cctgccccag ctgtgactcc tacgagaaga agccccccaa ggagttcctg 1380

gagaggttca agtccctgct gcagaagatg atccatcagc acctgtcctc caggacccac 1440

ggctccgagg actcc 1455

<210> 199
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs21 sequence"

<400> 199
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile

```
            20                  25                  30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35                  40                  45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50                  55                  60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220
```

```
Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365

Ile Arg Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
    370                 375                 380

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
385                 390                 395                 400

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
                405                 410                 415
```

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
420 425 430

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
435 440 445

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
450 455 460

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
465 470 475 480

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
485 490 495

Thr His Gly Ser Glu Asp Ser
500

<210> 200
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs21 sequence"

<400> 200
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacattac atgccccccc cccatgagcg tggagcacgc cgacatctgg 960

gtgaagagct atagcctcta cagccgggag aggtatatct gtaacagcgg cttcaagagg 1020

aaggccggca ccagcagcct caccgagtgc gtgctgaata aggctaccaa cgtggctcac 1080

tggacaacac cctctttaaa gtgcatccgg cagggccagg acaggcacat gatccggatg 1140

aggcagctca tcgacatcgt cgaccagctg aagaactacg tgaacgacct ggtgcccgag 1200

tttctgcctg cccccgagga cgtggagacc aactgcgagt ggtccgcctt ctcctgcttt 1260

cagaaggccc agctgaagtc cgccaacacc ggcaacaacg agcggatcat caacgtgagc 1320

atcaagaagc tgaagcggaa gcctccctcc acaaacgccg gcaggaggca gaagcacagg 1380

ctgacctgcc ccagctgtga ctcctacgag aagaagcccc ccaaggagtt cctggagagg 1440

ttcaagtccc tgctgcagaa gatgatccat cagcacctgt cctccaggac ccacggctcc 1500

gaggactcc 1509

<210> 201
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 201
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1   5   10   15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20   25   30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35   40   45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50   55   60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65   70   75   80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85   90   95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100   105   110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115   120   125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130   135   140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145   150   155   160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165   170   175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180   185   190

```
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380
```

```
Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460

Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480

Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495

Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
```

580 585 590

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
595 600 605

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
610 615 620

<210> 202
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs16 sequence"

<400> 202
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 203
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 203
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

```
Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
            20                  25                  30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35                  40                  45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50                  55                  60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205
```

```
Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305                 310                 315                 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
                325                 330                 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
            340                 345                 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
        355                 360                 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
    370                 375                 380

Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385                 390                 395                 400
```

```
Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
                405                 410                 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
            420                 425                 430

Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480

Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
```

595 600 605

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
610 615 620

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625 630 635

<210> 204
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs16 sequence"

<400> 204
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 205
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 205

```
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1               5                   10                  15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
            20                  25                  30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
        35                  40                  45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
    50                  55                  60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65                  70                  75                  80

Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
```

```
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350

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

Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
    370                 375                 380

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
385                 390                 395                 400
```

```
Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
               405                 410                 415

Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
            420                 425                 430

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val
        435                 440                 445

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
465                 470                 475                 480

Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu Arg Leu Ser
               485                 490                 495

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val
            500                 505                 510

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp
        515                 520                 525

Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
    530                 535                 540

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
545                 550                 555                 560

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Ser
               565                 570                 575

Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg
            580                 585                 590
```

<210> 206
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 206
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cattacatgc ccccctccca tgagcgtgga gcacgccgac 900

atctgggtga agagctatag cctctacagc cgggagaggt atatctgtaa cagcggcttc 960

aagaggaagg ccggcaccag cagcctcacc gagtgcgtgc tgaataaggc taccaacgtg 1020

gctcactgga caacaccctc tttaaagtgc atccggtccg agctgaccca ggaccctgct 1080

gtgtccgtgg ctctgggcca gaccgtgagg atcacctgcc agggcgactc cctgaggtcc 1140

tactacgcct cctggtacca gcagaagccc ggccaggctc ctgtgctggt gatctacggc 1200

aagaacaaca ggccctccgg catccctgac aggttctccg gatcctcctc cggcaacacc 1260

gcctccctga ccatcacagg cgctcaggcc gaggacgagg ctgactacta ctgcaactcc 1320

agggactcct ccggcaacca tgtggtgttc ggcggcggca ccaagctgac cgtgggccat 1380

ggcggcggcg gctccggagg cggcggcagc ggcggaggag gatccgaggt gcagctggtg 1440

gagtccggag gaggagtggt gaggcctgga ggctccctga ggctgagctg tgctgcctcc 1500

ggcttcacct tcgacgacta cggcatgtcc tgggtgaggc aggctcctgg aaagggcctg 1560

gagtgggtgt ccggcatcaa ctggaacggc ggatccaccg gctacgccga ttccgtgaag 1620

ggcaggttca ccatcagcag ggacaacgcc aagaactccc tgtacctgca gatgaactcc 1680

ctgagggccg aggacaccgc cgtgtactac tgcgccaggg gcaggtccct gctgttcgac 1740

tactggggac agggcaccct ggtgaccgtg tccagg 1776

<210> 207
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 207
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
50 55 60

```
Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65                  70                  75                  80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85                  90                  95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255
```

```
Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365

Ile Arg Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
    370                 375                 380

Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
385                 390                 395                 400

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

Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
            420                 425                 430

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
        435                 440                 445
```

```
Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
    450                 455                 460

His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Gly His Gly Gly
465                 470                 475                 480

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
                485                 490                 495

Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly Ser Leu Arg
            500                 505                 510

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser
        515                 520                 525

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
    530                 535                 540

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg
545                 550                 555                 560

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
                565                 570                 575

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
            580                 585                 590

Arg Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
        595                 600                 605

Ser Arg
    610
```

<210> 208
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs16 sequence"

<400> 208
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacattac atgccccct cccatgagcg tggagcacgc cgacatctgg 960

gtgaagagct atagcctcta cagccgggag aggtatatct gtaacagcgg cttcaagagg 1020

aaggccggca ccagcagcct caccgagtgc gtgctgaata aggctaccaa cgtggctcac 1080

tggacaacac cctctttaaa gtgcatccgg tccgagctga cccaggaccc tgctgtgtcc 1140

gtggctctgg gccagaccgt gaggatcacc tgccagggcg actccctgag gtcctactac 1200

gcctcctggt accagcagaa gcccggccag gctcctgtgc tggtgatcta cggcaagaac 1260

aacaggccct ccggcatccc tgacaggttc tccggatcct cctccggcaa caccgcctcc 1320

ctgaccatca caggcgctca ggccgaggac gaggctgact actactgcaa ctccagggac 1380

tcctccggca accatgtggt gttcggcggc ggcaccaagc tgaccgtggg ccatggcggc 1440

ggcggctccg gaggcggcgg cagcggcgga ggaggatccg aggtgcagct ggtggagtcc 1500

ggaggaggag tggtgaggcc tggaggctcc ctgaggctga gctgtgctgc ctccggcttc 1560

accttcgacg actacggcat gtcctgggtg aggcaggctc ctggaaaggg cctggagtgg 1620

gtgtccggca tcaactggaa cggcggatcc accggctacg ccgattccgt gaagggcagg 1680

ttcaccatca gcagggacaa cgccaagaac tccctgtacc tgcagatgaa ctccctgagg 1740

gccgaggaca ccgccgtgta ctactgcgcc aggggcaggt ccctgctgtt cgactactgg 1800

ggacagggca ccctggtgac cgtgtccagg 1830

<210> 209
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs137 sequence"

<400> 209
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

```
Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270
```

```
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
        275                 280                 285

Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr
    290                 295                 300

Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val
305                 310                 315                 320

Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys
                325                 330                 335

Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys
            340                 345                 350

Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly
        355                 360                 365

Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser
    370                 375                 380

Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile
385                 390                 395                 400

Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp
                405                 410                 415

Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp
            420                 425                 430

Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser
        435                 440                 445

Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile
    450                 455                 460
```

```
Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
465                 470                 475                 480


Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys
                485                 490                 495


Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn Val Ile
            500                 505                 510


Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        515                 520                 525


Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    530                 535                 540


Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
545                 550                 555                 560


Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
                565                 570                 575


Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
            580                 585                 590


Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
        595                 600                 605


Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
    610                 615                 620


<210> 210
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-TGFRs137 sequence"
```

<400> 210
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc 60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat 120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg 180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac 240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg 300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt 360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga 420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg 480

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggttttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cagcggcaca accaacacag tcgctgccta taacctcact 900

tggaagagca ccaacttcaa aaccatcctc gaatgggaac ccaaacccgt taaccaagtt 960

tacaccgtgc agatcagcac caagtccggc gactggaagt ccaaatgttt ctataccacc 1020

gacaccgagt gcgatctcac cgatgagatc gtgaaagatg tgaaacagac ctacctcgcc 1080

cgggtgttta gctaccccgc cggcaatgtg gagagcactg gttccgctgg cgagccttta 1140

tacgagaaca gccccgaatt taccccttac ctcgagacca atttaggaca gcccaccatc 1200

caaagctttg agcaagttgg cacaaaggtg aatgtgacag tggaggacga gcggacttta 1260

gtgcggcgga acaacacctt tctcagcctc cgggatgtgt tcggcaaaga tttaatctac 1320

acactgtatt actggaagtc ctcttcctcc ggcaagaaga cagctaaaac caacacaaac 1380

gagtttttaa tcgacgtgga taaaggcgaa aactactgtt tcagcgtgca agctgtgatc 1440

ccctcccgga ccgtgaatag gaaaagcacc gatagccccg ttgagtgcat gggccaagaa 1500

aagggcgagt tccgggagaa ctgggtgaac gtcatcagcg atttaaagaa gatcgaagat 1560

ttaattcagt ccatgcatat cgacgccact ttatacacag aatccgacgt gcacccctct 1620

tgtaaggtga ccgccatgaa atgtttttta ctggagctgc aagttatctc tttagagagc 1680

ggagacgcta gcatccacga caccgtggag aatttaatca ttttagccaa taactcttta 1740

tccagcaacg gcaacgtgac agagtccggc tgcaaggagt gcgaagagct ggaggagaag 1800

aacatcaagg agtttctgca atcctttgtg cacattgtcc agatgttcat caatacctcc 1860

<210> 211
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs137 sequence"

<400> 211
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
20 25 30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
35 40 45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
50 55 60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65 70 75 80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
85 90 95

```
His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100                 105                 110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115                 120                 125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130                 135                 140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165                 170                 175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180                 185                 190

Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285
```

```
Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys
305                 310                 315                 320

Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn
                325                 330                 335

Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser
            340                 345                 350

Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile
        355                 360                 365

Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro
    370                 375                 380

Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu
385                 390                 395                 400

Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro
                405                 410                 415

Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val
            420                 425                 430

Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
        435                 440                 445

Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys
    450                 455                 460

Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe
465                 470                 475                 480
```

```
Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala
                485                 490                 495

Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val
            500                 505                 510

Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asn Trp Val Asn
        515                 520                 525

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
    530                 535                 540

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
545                 550                 555                 560

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
                565                 570                 575

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
            580                 585                 590

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
        595                 600                 605

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
    610                 615                 620

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
625                 630                 635
```

<210> 212
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic TGFRt15-TGFRs137 sequence"

<400> 212
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacagcgg cacaaccaac acagtcgctg cctataacct cacttggaag 960

agcaccaact tcaaaaccat cctcgaatgg gaacccaaac ccgttaacca agtttacacc 1020

gtgcagatca gcaccaagtc cggcgactgg aagtccaaat gtttctatac caccgacacc 1080

gagtgcgatc tcaccgatga gatcgtgaaa gatgtgaaac agacctacct cgcccgggtg 1140

tttagctacc ccgccggcaa tgtggagagc actggttccg ctggcgagcc tttatacgag 1200

aacagccccg aatttacccc ttacctcgag accaatttag gacagcccac catccaaagc 1260

tttgagcaag ttggcacaaa ggtgaatgtg acagtggagg acgagcggac tttagtgcgg 1320

cggaacaaca cctttctcag cctccgggat gtgttcggca aagatttaat ctacacactg 1380

tattactgga agtcctcttc ctccggcaag aagacagcta aaaccaacac aaacgagttt 1440

ttaatcgacg tggataaagg cgaaaactac tgtttcagcg tgcaagctgt gatcccctcc 1500

cggaccgtga ataggaaaag caccgatagc cccgttgagt gcatgggcca agaaaagggc 1560

gagttccggg agaactgggt gaacgtcatc agcgatttaa agaagatcga agatttaatt 1620

cagtccatgc atatcgacgc cactttatac acagaatccg acgtgcaccc ctcttgtaag 1680

gtgaccgcca tgaaatgttt tttactggag ctgcaagtta tctctttaga gagcggagac 1740

gctagcatcc acgacaccgt ggagaattta atcattttag ccaataactc tttatccagc 1800

aacggcaacg tgacagagtc cggctgcaag gagtgcgaag agctggagga gaagaacatc 1860

aaggagtttc tgcaatcctt tgtgcacatt gtccagatgt tcatcaatac ctcc 1914

<210> 213
<211> 551
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs137 sequence"

<400> 213
Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val Thr
1 5 10 15

Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp
20 25 30

Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys
35 40 45

Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val
50 55 60

Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp
65 70 75 80

```
Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro
                85                  90                  95

Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
            100                 105                 110

Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser Glu
        115                 120                 125

Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys Ser Val
145                 150                 155                 160

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
                165                 170                 175

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
            180                 185                 190

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
        195                 200                 205

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
    210                 215                 220

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
225                 230                 235                 240

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
                245                 250                 255

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
            260                 265                 270

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ile
```

```
        275                 280                 285

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    290                 295                 300

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
305                 310                 315                 320

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
                325                 330                 335

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            340                 345                 350

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
        355                 360                 365

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
    370                 375                 380

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
385                 390                 395                 400

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
                405                 410                 415

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
            420                 425                 430

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
        435                 440                 445

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
    450                 455                 460

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
465                 470                 475                 480
```

```
Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
                485                 490                 495


Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
            500                 505                 510


Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
        515                 520                 525


Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
    530                 535                 540


Leu Pro Ser Pro Arg Ser Glu
545                 550


<210> 214
<211> 1653
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      TGFRt15-TGFRs137 sequence"

<400> 214
atccccccc atgtgcaaaa gagcgtgaac aacgatatga tcgtgaccga caacaacggc       60

gccgtgaagt ttccccagct ctgcaagttc tgcgatgtca ggttcagcac ctgcgataat      120

cagaagtcct gcatgtccaa ctgcagcatc acctccatct gcgagaagcc ccaagaagtg      180

tgcgtggccg tgtggcggaa aaatgacgag aacatcaccc tggagaccgt gtgtcacgac      240

cccaagctcc cttatcacga cttcattctg gaggacgctg cctcccccaa atgcatcatg      300

aaggagaaga agaagcccgg agagaccttc tttatgtgtt cctgtagcag cgacgagtgt      360

aacgacaaca tcatcttcag cgaagagtac aacaccagca accctgatgg aggtggcgga      420

tccggaggtg gaggttctgg tggaggtggg agtattcctc cccacgtgca gaagagcgtg      480
```

aataatgaca tgatcgtgac cgataacaat ggcgccgtga aatttcccca gctgtgcaaa 540

ttctgcgatg tgaggtttc cacctgcgac aaccagaagt cctgtatgag caactgctcc 600

atcacctcca tctgtgagaa gcctcaggag gtgtgcgtgg ctgtctggcg gaagaatgac 660

gagaatatca ccctggaaac cgtctgccac gatcccaagc tgccctacca cgatttcatc 720

ctggaagacg ccgccagccc taagtgcatc atgaaagaga aaaagaagcc tggcgagacc 780

tttttcatgt gctcctgcag cagcgacgaa tgcaacgaca atatcatctt tagcgaggaa 840

tacaatacca gcaaccccga cattacatgc ccccctccca tgagcgtgga gcacgccgac 900

atctgggtga agagctatag cctctacagc cgggagaggt atatctgtaa cagcggcttc 960

aagaggaagg ccggcaccag cagcctcacc gagtgcgtgc tgaataaggc taccaacgtg 1020

gctcactgga caacaccctc tttaaagtgc atccggggcg gtggaggatc cggaggaggt 1080

ggctccggcg gcggaggatc tcgcgagggt cccgagcttt cgcccgacga tcccgccggc 1140

ctcttggacc tgcggcaggg catgtttgcg cagctggtgg cccaaaatgt tctgctgatc 1200

gatgggcccc tgagctggta cagtgaccca ggcctggcag gcgtgtccct gacgggggggc 1260

ctgagctaca aagaggacac gaaggagctg gtggtggcca aggctggagt ctactatgtc 1320

ttctttcaac tagagctgcg gcgcgtggtg gccggcgagg gctcaggctc cgtttcactt 1380

gcgctgcacc tgcagccact gcgctctgct gctggggccg ccgccctggc tttgaccgtg 1440

gacctgccac ccgcctcctc cgaggctcgg aactcggcct tcggtttcca gggccgcttg 1500

ctgcacctga gtgccggcca gcgcctgggc gtccatcttc acactgaggc cagggcacgc 1560

catgcctggc agcttaccca gggcgccaca gtcttgggac tcttccgggt gacccccgaa 1620

atcccagccg gactcccttc accgaggtcg gaa 1653

<210> 215
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

TGFRt15-TGFRs137 sequence"

<400> 215
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1   5   10   15

Tyr Ser Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile
            20   25   30

Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe
        35   40   45

Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser
    50   55   60

Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val
65   70   75   80

Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys
                85   90   95

His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala
            100   105   110

Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
        115   120   125

Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
    130   135   140

Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Gly Gly Gly Gly Ser Gly
145   150   155   160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Pro Pro His Val Gln Lys
                165   170   175

Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys
            180   185   190

```
Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp
        195                 200                 205

Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu
    210                 215                 220

Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn
225                 230                 235                 240

Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp
                245                 250                 255

Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys
            260                 265                 270

Lys Lys Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu
        275                 280                 285

Cys Asn Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro
    290                 295                 300

Asp Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
305                 310                 315                 320

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
                325                 330                 335

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
            340                 345                 350

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
        355                 360                 365

Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380
```

```
Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
385                 390                 395                 400

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
                405                 410                 415

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
            420                 425                 430

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
        435                 440                 445

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
    450                 455                 460

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
465                 470                 475                 480

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
                485                 490                 495

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
            500                 505                 510

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
        515                 520                 525

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
    530                 535                 540

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
545                 550                 555                 560

Ala Gly Leu Pro Ser Pro Arg Ser Glu
                565
```

<210> 216
<211> 1707
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
TGFRt15-TGFRs137 sequence"

<400> 216
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctccatcccc 60

ccccatgtgc aaaagagcgt gaacaacgat atgatcgtga ccgacaacaa cggcgccgtg 120

aagtttcccc agctctgcaa gttctgcgat gtcaggttca gcacctgcga taatcagaag 180

tcctgcatgt ccaactgcag catcacctcc atctgcgaga agccccaaga agtgtgcgtg 240

gccgtgtggc ggaaaaatga cgagaacatc accctggaga ccgtgtgtca cgaccccaag 300

ctcccttatc acgacttcat tctggaggac gctgcctccc ccaaatgcat catgaaggag 360

aagaagaagc ccggagagac cttctttatg tgttcctgta gcagcgacga gtgtaacgac 420

aacatcatct tcagcgaaga gtacaacacc agcaaccctg atggaggtgg cggatccgga 480

ggtggaggtt ctggtggagg tgggagtatt cctccccacg tgcagaagag cgtgaataat 540

gacatgatcg tgaccgataa caatggcgcc gtgaaatttc cccagctgtg caaattctgc 600

gatgtgaggt tttccacctg cgacaaccag aagtcctgta tgagcaactg ctccatcacc 660

tccatctgtg agaagcctca ggaggtgtgc gtggctgtct ggcggaagaa tgacgagaat 720

atcaccctgg aaaccgtctg ccacgatccc aagctgccct accacgattt catcctggaa 780

gacgccgcca gccctaagtg catcatgaaa gagaaaaaga agcctggcga gacctttttc 840

atgtgctcct gcagcagcga cgaatgcaac gacaatatca tctttagcga ggaatacaat 900

accagcaacc ccgacattac atgccccct cccatgagcg tggagcacgc cgacatctgg 960

gtgaagagct atagcctcta cagccgggag aggtatatct gtaacagcgg cttcaagagg 1020

aaggccggca ccagcagcct caccgagtgc gtgctgaata aggctaccaa cgtggctcac 1080

tggacaacac cctctttaaa gtgcatccgg ggcggtggag gatccggagg aggtggctcc 1140

ggcggcggag gatctcgcga gggtcccgag ctttcgcccg acgatcccgc cggcctcttg 1200

gacctgcggc agggcatgtt tgcgcagctg gtggcccaaa atgttctgct gatcgatggg 1260

cccctgagct ggtacagtga cccaggcctg gcaggcgtgt ccctgacggg gggcctgagc 1320

tacaaagagg acacgaagga gctggtggtg gccaaggctg gagtctacta tgtcttcttt 1380

caactagagc tgcggcgcgt ggtggccggc gagggctcag gctccgtttc acttgcgctg 1440

cacctgcagc cactgcgctc tgctgctggg gccgccgccc tggctttgac cgtggacctg 1500

ccacccgcct cctccgaggc tcggaactcg gccttcggtt tccagggccg cttgctgcac 1560

ctgagtgccg gccagcgcct gggcgtccat cttcacactg aggccagggc acgccatgcc 1620

tggcagctta cccagggcgc cacagtcttg ggactcttcc gggtgacccc cgaaatccca 1680

gccggactcc cttcaccgag gtcggaa 1707

<210> 217
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-18/IL-15RalphaSu sequence"

<400> 217
atgaagtggg tcacatttat ctctttactg ttcctcttct ccagcgccta cagctacttc 60

ggcaaactgg aatccaagct gagcgtgatc cggaatttaa acgaccaagt tctgtttatc 120

gatcaaggta accggcctct gttcgaggac atgaccgact ccgattgccg ggacaatgcc 180

ccccggacca tcttcattat ctccatgtac aaggacagcc agccccgggg catggctgtg 240

acaattagcg tgaagtgtga gaaaatcagc actttatctt gtgagaacaa gatcatctcc 300

tttaaggaaa tgaacccccc cgataacatc aaggacacca agtccgatat catcttcttc 360

cagcggtccg tgcccggtca cgataacaag atgcagttcg aatcctcctc ctacgagggc 420

tacttttag cttgtgaaaa ggagagggat ttattcaagc tgatcctcaa gaaggaggac 480

gagctgggcg atcgttccat catgttcacc gtccaaaacg aggatattac atgccccct 540

cccatgagcg tggagcacgc cgacatctgg gtgaagagct atagcctcta cagccgggag 600

aggtatatct gtaacagcgg cttcaagagg aaggccggca ccagcagcct caccgagtgc 660

gtgctgaata aggctaccaa cgtggctcac tggacaacac cctctttaaa gtgcatccgg 720

<210> 218
<211> 2607
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-12/TF/IL-15 sequence"

<400> 218
atgaaatggg tgacctttat ttctttactg ttcctcttta gcagcgccta ctccatttgg 60

gaactgaaga aggacgtcta cgtggtcgaa ctggactggt atcccgatgc tcccggcgaa 120

atggtggtgc tcacttgtga cacccccgaa gaagacggca tcacttggac cctcgatcag 180

agcagcgagg tgctgggctc cggaaagacc ctcacaatcc aagttaagga gttcggagac 240

gctggccaat acacatgcca caagggaggc gaggtgctca gccattcctt attattatta 300

cacaagaagg aagacggaat ctggtccacc gacattttaa aagatcagaa ggagcccaag 360

aataagacct ttttaaggtg tgaggccaaa aactacagcg gtcgtttcac ttgttggtgg 420

ctgaccacca tttccaccga tttaaccttc tccgtgaaaa gcagccgggg aagctccgac 480

cctcaaggtg tgacatgtgg agccgctacc ctcagcgctg agagggttcg tggcgataac 540

aaggaatacg agtacagcgt ggagtgccaa gaagatagcg cttgtcccgc tgccgaagaa 600

tctttaccca ttgaggtgat ggtggacgcc gtgcacaaac tcaagtacga gaactacacc 660

tcctccttct ttatccggga catcattaag cccgatcctc ctaagaattt acagctgaag 720

cctctcaaaa atagccggca agttgaggtc tcttgggaat atcccgacac ttggagcaca 780

ccccacagct acttctcttt aacctttttgt gtgcaagttc aaggtaaaag caagcgggag 840

aagaaagacc gggtgtttac cgacaaaacc agcgccaccg tcatctgtcg gaagaacgcc 900

tccatcagcg tgagggctca agatcgttat tactccagca gctggtccga gtgggccagc 960

gtgccttgtt ccggcggtgg aggatccgga ggaggtggct ccggcggcgg aggatctcgt 1020

aacctccccg tggctacccc cgatcccgga atgttccctt gtttacacca cagccagaat 1080

ttactgaggg ccgtgagcaa catgctgcag aaagctaggc agactttaga attttaccct 1140

tgcaccagcg aggagatcga ccatgaagat atcaccaagg acaagacatc caccgtggag 1200

gcttgtttac ctctggagct gacaaagaac gagtcttgtc tcaactctcg tgaaaccagc 1260

ttcatcacaa atggctcttg tttagcttcc cggaagacct cctttatgat ggctttatgc 1320

ctcagctcca tctacgagga tttaaagatg taccaagtgg agttcaagac catgaacgcc 1380

aagctgctca tggaccctaa acggcagatc tttttagacc agaacatgct ggctgtgatt 1440

gatgagctga tgcaagcttt aaacttcaac tccgagaccg tccctcagaa gtcctccctc 1500

gaggagcccg atttttacaa gacaaagatc aaactgtgca ttttactcca cgcctttagg 1560

atccgggccg tgaccattga ccgggtcatg agctatttaa acgccagcag cggcacaacc 1620

aacacagtcg ctgcctataa cctcacttgg aagagcacca acttcaaaac catcctcgaa 1680

tgggaaccca aacccgttaa ccaagtttac accgtgcaga tcagcaccaa gtccggcgac 1740

tggaagtcca aatgtttcta taccaccgac accgagtgcg atctcaccga tgagatcgtg 1800

aaagatgtga aacagaccta cctcgcccgg gtgtttagct accccgccgg caatgtggag 1860

agcactggtt ccgctggcga gcctttatac gagaacagcc ccgaatttac cccttacctc 1920

gagaccaatt taggacagcc caccatccaa agctttgagc aagttggcac aaaggtgaat 1980

gtgacagtgg aggacgagcg gactttagtg cggcggaaca acacctttct cagcctccgg 2040

gatgtgttcg gcaaagattt aatctacaca ctgtattact ggaagtcctc ttcctccggc 2100

aagaagacag ctaaaaccaa cacaaacgag tttttaatcg acgtggataa aggcgaaaac 2160

tactgtttca gcgtgcaagc tgtgatcccc tcccggaccg tgaataggaa aagcaccgat 2220

agccccgttg agtgcatggg ccaagaaaag ggcgagttcc gggagaactg ggtgaacgtc 2280

atcagcgatt taaagaagat cgaagattta attcagtcca tgcatatcga cgccacttta 2340

tacacagaat ccgacgtgca cccctcttgt aaggtgaccg ccatgaaatg ttttttactg 2400

gagctgcaag ttatctcttt agagagcgga gacgctagca tccacgacac cgtggagaat 2460

ttaatcattt tagccaataa ctctttatcc agcaacggca acgtgacaga gtccggctgc 2520

aaggagtgcg aagagctgga ggagaagaac atcaaggagt ttctgcaatc ctttgtgcac 2580

attgtccaga tgttcatcaa tacctcc 2607

<210> 219
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-18/IL-15RalphaSu sequence"

<400> 219
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn
20 25 30

Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe
35 40 45

Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile
50 55 60

Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val
65 70 75 80

Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn
85 90 95

Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp
100 105 110

```
Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp
        115                 120                 125


Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala
    130                 135                 140


Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp
145                 150                 155                 160


Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp Ile
                165                 170                 175


Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
            180                 185                 190


Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
        195                 200                 205


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


Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
225                 230                 235                 240


<210> 220
<211> 869
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      IL-12/TF/IL-15 sequence"

<400> 220
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1               5                   10                  15


Tyr Ser Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp
            20                  25                  30
```

```
Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr
        35                  40                  45

Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val
    50                  55                  60

Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp
65                  70                  75                  80

Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
                85                  90                  95

Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile
            100                 105                 110

Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu
        115                 120                 125

Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile
    130                 135                 140

Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp
145                 150                 155                 160

Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
                165                 170                 175

Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp
            180                 185                 190

Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val
        195                 200                 205

Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe
    210                 215                 220
```

```
Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys
225                 230                 235                 240

Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp
                245                 250                 255

Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln
            260                 265                 270

Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp
        275                 280                 285

Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val
    290                 295                 300

Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser
305                 310                 315                 320

Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                325                 330                 335

Gly Gly Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe
            340                 345                 350

Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met
        355                 360                 365

Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu
    370                 375                 380

Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu
385                 390                 395                 400

Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser
                405                 410                 415
```

```
Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys
            420                 425                 430

Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu
        435                 440                 445

Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met
    450                 455                 460

Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile
465                 470                 475                 480

Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln
                485                 490                 495

Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu
            500                 505                 510

Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg
        515                 520                 525

Val Met Ser Tyr Leu Asn Ala Ser Ser Gly Thr Thr Asn Thr Val Ala
    530                 535                 540

Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu
545                 550                 555                 560

Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr
                565                 570                 575

Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu
            580                 585                 590

Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu
        595                 600                 605

Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser
```

```
    610                 615                 620

Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu
625                 630                 635                 640

Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly
                645                 650                 655

Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg
            660                 665                 670

Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile
        675                 680                 685

Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala
    690                 695                 700

Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn
705                 710                 715                 720

Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg
                725                 730                 735

Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu
            740                 745                 750

Phe Arg Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
        755                 760                 765

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
    770                 775                 780

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
785                 790                 795                 800

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
                805                 810                 815
```

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
            820   825   830

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
        835   840   845

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
    850   855   860

Phe Ile Asn Thr Ser
865

<210> 221
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      IL-21/TF mutant/IL-15 sequence"

<400> 221
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc   60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac   120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc   180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac   240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac   300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag   360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac   420

ctgtcctcca ggacccacgg ctccgaggac tcctccggca ccaccaatac cgtggccgct   480

tataacctca catggaagag caccaacttc gcgacagctc tggaatggga acccaagccc   540

gtcaatcaag tttacaccgt gcagatctcc accaaatccg gagactggaa gagcaagtgc   600

ttctacacaa cagacaccga gtgtgcttta accgacgaaa tcgtcaagga cgtcaagcaa 660

acctatctgg ctcgggtctt ttcctacccc gctggcaatg tcgagtccac cggctccgct 720

ggcgagcctc tctacgagaa ttcccccgaa ttcacccctt atttagagac caatttaggc 780

cagcctacca tccagagctt cgagcaagtt ggcaccaagg tgaacgtcac cgtcgaggat 840

gaaaggactt tagtggcgcg gaataacaca gctttatccc tccgggatgt gttcggcaaa 900

gacctcatct acacactgta ctattggaag tccagctcct ccggcaaaaa gaccgctaag 960

accaacacca acgagttttt aattgacgtg gacaaaggcg agaactactg cttcagcgtg 1020

caagccgtga tcccttctcg taccgtcaac cggaagagca cagattcccc cgttgagtgc 1080

atgggccaag aaaagggcga gttccgggag aactgggtga acgtcatcag cgatttaaag 1140

aagatcgaag atttaattca gtccatgcat atcgacgcca ctttatacac agaatccgac 1200

gtgcacccct cttgtaaggt gaccgccatg aaatgttttt tactggagct gcaagttatc 1260

tctttagaga gcggagacgc tagcatccac gacaccgtgg agaatttaat cattttagcc 1320

aataactctt tatccagcaa cggcaacgtg acagagtccg gctgcaagga gtgcgaagag 1380

ctggaggaga agaacatcaa ggagtttctg caatcctttg tgcacattgt ccagatgttc 1440

atcaatacct cc 1452

<210> 222
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
IL-21/TF mutant/IL-15 sequence"

<400> 222
Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala Tyr
1 5 10 15

Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp
20 25 30

```
Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe
        35                  40                  45

Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe
    50                  55                  60

Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn
65                  70                  75                  80

Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro
                85                  90                  95

Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser
            100                 105                 110

Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe
        115                 120                 125

Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr
    130                 135                 140

His Gly Ser Glu Asp Ser Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr
145                 150                 155                 160

Asn Leu Thr Trp Lys Ser Thr Asn Phe Ala Thr Ala Leu Glu Trp Glu
                165                 170                 175

Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser
            180                 185                 190

Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Ala
        195                 200                 205

Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg
    210                 215                 220
```

```
Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly
225                 230                 235                 240

Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr
                245                 250                 255

Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr Lys
            260                 265                 270

Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Ala Arg Asn Asn
        275                 280                 285

Thr Ala Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr
    290                 295                 300

Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr
305                 310                 315                 320

Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys
                325                 330                 335

Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys Ser
            340                 345                 350

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

Glu Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
    370                 375                 380

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
385                 390                 395                 400

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
                405                 410                 415

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
```

```
            420                 425                 430

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
        435                 440                 445

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
    450                 455                 460

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
465                 470                 475                 480

Asn Thr Ser
```

<210> 223
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Signal sequence"

<400> 223

```
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

Ala
```

<210> 224
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
Linker sequence"

<400> 224

Gly Gly Gly Ser Gly Gly Gly Ser
1   5

<210> 225
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      21s137L sequence"

<400> 225
atgaagtggg tgaccttcat cagcctgctg ttcctgttct ccagcgccta ctcccagggc   60

caggacaggc acatgatccg gatgaggcag ctcatcgaca tcgtcgacca gctgaagaac   120

tacgtgaacg acctggtgcc cgagtttctg cctgcccccg aggacgtgga gaccaactgc   180

gagtggtccg ccttctcctg ctttcagaag gcccagctga agtccgccaa caccggcaac   240

aacgagcgga tcatcaacgt gagcatcaag aagctgaagc ggaagcctcc ctccacaaac   300

gccggcagga ggcagaagca caggctgacc tgccccagct gtgactccta cgagaagaag   360

ccccccaagg agttcctgga gaggttcaag tccctgctgc agaagatgat ccatcagcac   420

ctgtcctcca ggacccacgg ctccgaggac tccattacat gccccccctcc catgagcgtg   480

gagcacgccg acatctgggt gaagagctat agcctctaca gccgggagag gtatatctgt   540

aacagcggct tcaagaggaa ggccggcacc agcagcctca ccgagtgcgt gctgaataag   600

gctaccaacg tggctcactg gacaacaccc tctttaaagt gcatccgggg cggtggagga   660

tccggaggag gtggctccgg cggcggagga tctcgcgagg gtcccgagct ttcgcccgac   720

gatcccgccg gcctcttgga cctgcggcag ggcatgtttg cgcagctggt ggcccaaaat   780

gttctgctga tcgatgggcc cctgagctgg tacagtgacc caggcctggc aggcgtgtcc   840

ctgacggggg gcctgagcta caaagaggac acgaaggagc tggtggtggc caaggctgga   900

gtctactatg tcttctttca actagagctg cggcgcgtgg tggccggcga gggctcaggc   960

tccgtttcac ttgcgctgca cctgcagcca ctgcgctctg ctgctggggc cgccgccctg   1020

gctttgaccg tggacctgcc acccgcctcc tccgaggctc ggaactcggc cttcggtttc 1080

cagggccgct tgctgcacct gagtgccggc cagcgcctgg gcgtccatct tcacactgag 1140

gccagggcac gccatgcctg gcagcttacc cagggcgcca cagtcttggg actcttccgg 1200

gtgacccccg aaatcccagc cggactccct tcaccgaggt cggaa 1245

<210> 226
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
21s137L sequence"

<400> 226
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
20 25 30

Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
35 40 45

Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
50 55 60

Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
65 70 75 80

Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
85 90 95

Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
100 105 110

Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg

```
        115                 120                 125

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
    130                 135                 140

Thr His Gly Ser Glu Asp Ser Ile Thr Cys Pro Pro Pro Met Ser Val
145                 150                 155                 160

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
                165                 170                 175

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
            180                 185                 190

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
        195                 200                 205

Thr Pro Ser Leu Lys Cys Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
225                 230                 235                 240

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
                245                 250                 255

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

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
        275                 280                 285

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
    290                 295                 300

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
305                 310                 315                 320
```

```
Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
                325                 330                 335

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
            340                 345                 350

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
        355                 360                 365

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
    370                 375                 380

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
385                 390                 395                 400

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
                405                 410                 415
```