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<120> RECOMBINANT BINDING PROTEINS AND THEIR USE

<130> MD41211

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<151> 2015-04-02

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<220>
<223> His-tag

<400> 1
Met Arg Gly Ser His His His His His His Gly Ser
1 5 10

<210> 2
<211> 5
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<220>
<223> GS-linker

<400> 2
Gly Gly Gly Gly Ser
1 5

<210> 3
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<213> Artificial Sequence

<220>

<223> GS-linker

<400> 3
Gly Gly Gly Gly Ser Gly Ser
1   5

<210> 4
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker

<400> 4
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser
1   5   10

<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> GS-linker

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

<210> 6
<211> 22
<212> PRT
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<220>
<223> GS-linker

<400> 6
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15
Gly Gly Gly Ser Gly Ser
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<210> 7
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> PT-linker

<400> 7
Gly Ser Pro Thr Pro Thr Pro Thr Gly Ser
1 5 10

<210> 8
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> PT-linker

<400> 8
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly
1 5 10 15
Ser

<210> 9
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> PT-linker

<400> 9
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
1 5 10 15
Pro Thr Pro Thr Pro Thr Gly Ser
20

<210> 10
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 10
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp

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1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Thr Asp
            20                  25                  30
Asn Asp Gly Tyr Thr Pro Leu His Leu Ala Ala Ser Asn Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ser
    50                  55                  60
Asp Leu Thr Gly Ile Thr Pro Leu His Leu Ala Ala Ala Thr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Tyr Asp Asn Asp Gly His Thr Pro Leu His Leu Ala Ala Lys Tyr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 11
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 11

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala Arg Glu Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala Arg Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
        115                 120
```

<210> 12
<211> 157

<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 12
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Phe Asp
            20 25 30
Trp Met Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His Leu
        35 40 45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Thr
    50 55 60
Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Thr
                85 90 95
Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly
            100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn
        115 120 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130 135 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145 150 155

<210> 13
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 13
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20 25 30
Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His Leu
        35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50 55 60
Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala

85 90 95
Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly
100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130 135 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145 150 155

<210> 14
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 14
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Thr Ala Asp
20 25 30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala His
50 55 60
Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Thr Leu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 15
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 15
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Thr Ala Asp

```
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Val Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ile Gly His
65                  70                  75                  80
Gln Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
        115                 120
```

<210> 16
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 16

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Tyr Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115                 120
```

<210> 17
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 17
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Arg Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ala
    50   55   60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100   105   110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
        115   120

<210> 18
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 18
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 19
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 19
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 20
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 20
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 21
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 21
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 22
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 22
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly

100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 23
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 23
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Arg Phe Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Glu
50 55 60
Asp Trp Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Met Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
85 90 95
Met Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130 135 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145 150 155

<210> 24
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 24
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Arg Phe Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu

```
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Trp Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Phe Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155

<210> 25
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 25
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50                  55                  60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130                 135                 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
145                 150                 155

<210> 26
<211> 157
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<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 26
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20 25 30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
        35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50 55 60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85 90 95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115 120 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130 135 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
145 150 155

<210> 27
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 27
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20 25 30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala Gly His Leu
        35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50 55 60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala

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85 90 95
Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
100 105 110
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
130 135 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
145 150 155

<210> 28
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 28
Asp Leu Gly Met Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala His Asp
20 25 30
Thr Trp Gly Leu Thr Pro Leu His Leu Ala Ala Phe His Gly His Gln
35 40 45
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln
50 55 60
Asp Phe Tyr Gly Lys Thr Pro Leu His Leu Ala Ala Leu Arg Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Gln Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 29
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 29
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Tyr

```
            20                  25                  30
Glu Asp Gly Leu Thr Pro Leu His Leu Ala Ala Phe Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Thr
    50                  55                  60
Asp Ala Trp Gly His Thr Pro Leu His Leu Ala Ala Tyr Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Thr
                85                  90                  95
His Asp Lys Glu Gly Met Thr Ala Leu His Leu Ala Ala Leu Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155

<210> 30
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 30
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Thr His Asp
            20                  25                  30
Asn Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ile Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Phe
    50                  55                  60
Asp Ser Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
                85                  90                  95
Leu Asp Tyr Asn Gly Asn Thr Pro Leu His Leu Ala Ala Asn Ser Gly
            100                 105                 110
Arg Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 31
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 31
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Val Asp
            20   25   30
Ala Trp Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ile Gly His Leu
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ala
    50   55   60
Asp Tyr Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ala Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Asp Asn Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100   105   110
Arg Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
        115   120   125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130   135   140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145   150   155

<210> 32
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 32
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ile Asp
            20   25   30
Thr Trp Gly Asn Thr Pro Leu His Leu Ala Ala Asp Tyr Gly His Leu
        35   40   45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Leu
    50   55   60
Asp Trp Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Leu Gly His

65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala
85 90 95
Val Asp Thr Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
100 105 110
Arg Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130 135 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145 150 155

<210> 33
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 33
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Gln Asp
20 25 30
Arg Trp Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Asp
50 55 60
Asp Val Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Leu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
85 90 95
Asp Asp Tyr Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
130 135 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145 150 155

<210> 34
<211> 157
<212> PRT
<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 34

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Gln Asp
            20                  25                  30
Arg Trp Gly Asp Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Asp
    50                  55                  60
Asp Val Phe Gly Asp Thr Pro Leu His Leu Ala Ala Ser Leu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
                85                  90                  95
Asp Asp Tyr Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 35
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 35

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Asn Asp
            20                  25                  30
Phe Leu Gly Leu Thr Pro Leu His Leu Ala Ala Ser Thr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Ile
    50                  55                  60
Asp Ala Tyr Gly His Thr Pro Leu His Leu Ala Ala Asn Asn Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
                85                  90                  95
Ile Asp His Phe Gly Tyr Thr Pro Leu His Leu Ala Ala Met Phe Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn
```

```
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 36
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 36

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Asn Asp
            20                  25                  30
Ser Ser Gly Leu Thr Pro Leu His Leu Ala Ala Phe Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Asp
    50                  55                  60
Asp Asp Trp Gly His Thr Pro Leu His Leu Ala Ala His Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Ile Asp Thr Arg Gly Leu Thr Pro Leu His Leu Ala Ala Ile Ala Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 37
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 37

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ser Asp
```

```
            20                  25                  30
Asp Thr Gly Leu Thr Pro Leu His Leu Ala Ala Asn Arg Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Asn
    50                  55                  60
Asp Phe Ala Gly Met Thr Pro Leu His Leu Ala Ala Asn Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala
                85                  90                  95
His Asp Asp Tyr Gly Leu Thr Pro Leu His Leu Ala Ala Asn Trp Arg
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155

<210> 38
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 38
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
        35                  40                  45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
145                 150                 155
```

<210> 39
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 39
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Leu Asp
            20 25 30
Gln Ile Gly Trp Thr Pro Leu His Leu Ala Ala Asn Tyr Gly His Leu
        35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50 55 60
Asp Leu Trp Gly Gln Thr Pro Leu His Leu Ala Ala Trp Lys Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85 90 95
Lys Asp Thr Asp Gly Leu Thr Pro Leu His Leu Ala Ala Ile Arg Gly
            100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115 120 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130 135 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
145 150 155

<210> 40
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 40
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Ser Gly Ala Asp Val Asn Ala Ala Asp
            20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asp Gly His Leu
        35 40 45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asp Ala Ser
    50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His

65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Asp Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 41
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 41
Asp Leu Gly Lys Glu Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ala Asp
20 25 30
Tyr Phe Gly His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Ser
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Ala Phe Glu Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 42
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 42
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ala Asp
20 25 30
Tyr Phe Gly His Thr Pro Leu His Leu Ala Ala Arg Asp Gly His Leu

```
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Ser
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
        115                 120
```

<210> 43
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 43

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ala Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asp Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Ser
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
        115                 120
```

<210> 44
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 44

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
```

1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
115 120

<210> 45
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 45
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
115 120

<210> 46
<211> 124
<212> PRT
<213> Artificial Sequence

<220>

<223> Designed ankyrin repeat domain

<400> 46
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Ala Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 47
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 47
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 48
<211> 124

<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 48
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115   120

<210> 49
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 49
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala

115 120

<210> 50
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 50
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
115 120

<210> 51
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 51
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala

```
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115                 120
```

<210> 52
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 52

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115                 120
```

<210> 53
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 53

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Phe Leu Met Ala Asn Gly Ala Asp Val Asn Ala Ala Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Gln
```

50 55 60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
115 120

<210> 54
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 54
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
115 120

<210> 55
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 55
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp

```
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115                 120
```

<210> 56
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain

<400> 56

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        115                 120
```

<210> 57
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed ankyrin repeat domain with a C-terminal polypeptide linker

<400> 57
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115   120   125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130   135   140
Thr Gly Ser Arg Ser Asp Leu Asp Ile Thr Gly Leu Lys Leu Asn
145   150   155

<210> 58
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 58
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115   120   125

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His
            180                 185                 190
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195                 200                 205
Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly
    210                 215                 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225                 230                 235                 240
Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr
                245                 250                 255
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
            260                 265                 270
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
        275                 280                 285
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
    290                 295                 300
```

<210> 59
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 59

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115                 120                 125
```

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His
            180                 185                 190
Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195                 200                 205
Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly
    210                 215                 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225                 230                 235                 240
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
                245                 250                 255
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
            260                 265
```

<210> 60
<211> 305
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 60

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
```

```
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala
305
```

<210> 61
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 61

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
```

```
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
```

<210> 62
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 62

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
```

```
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
                245                 250                 255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
            260                 265                 270
Asn
```

<210> 63
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 63

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
```

Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His
            180   185   190
Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195   200   205
Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly
    210   215   220
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
225   230   235   240
Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala
                245   250   255
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
            260   265

<210> 64
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 64
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115   120   125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130   135   140
Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
145   150   155   160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165   170   175
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
            180   185   190
Pro Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195   200   205

Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
210 215 220
Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225 230 235 240
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
245 250 255
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu
260 265 270
Asn

<210> 65
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 65
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115 120 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130 135 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145 150 155 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
165 170 175
Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala
180 185 190
Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195 200 205
Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala
210 215 220

Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225 230 235 240
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
245 250 255
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu
260 265 270
Asn

<210> 66
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 66
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
180 185 190
Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
210 215 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240

Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
245 250 255
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
260 265 270

<210> 67
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising two designed ankyrin repeat domains

<400> 67
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
100 105 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
180 185 190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
210 215 220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
245 250 255

Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260 265 270

<210> 68
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 68
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115 120 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130 135 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145 150 155 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
165 170 175
Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala
180 185 190
Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195 200 205
Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala
210 215 220
Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225 230 235 240
Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu
245 250 255
Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
260 265 270

```
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
        275                 280                 285
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
    290                 295                 300
Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
Ala Glu Ile Leu Gln Lys Leu Asn
                485
```

<210> 69
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 69

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
```

```
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala
            180                 185                 190
His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu
                245                 250                 255
Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
            260                 265                 270
Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp
        275                 280                 285
Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys
    290                 295                 300
Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly
            420                 425                 430
Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser
    450                 455                 460
```

Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile
465 470 475 480
Ala Glu Val Leu Gln Lys Leu Asn
485

<210> 70
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 70
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
130 135 140
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145 150 155 160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
165 170 175
Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala Gly His
180 185 190
Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
195 200 205
Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly
210 215 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225 230 235 240
Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr
245 250 255
Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
260 265 270

```
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
        275                 280                 285
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
                325                 330                 335
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
            340                 345                 350
Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu
        355                 360                 365
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    370                 375                 380
Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala
385                 390                 395                 400
Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
                405                 410                 415
Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala
            420                 425                 430
Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        435                 440                 445
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
    450                 455                 460
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Asn
465                 470                 475                 480
```

<210> 71
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 71

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
```

```
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His
            180                 185                 190
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195                 200                 205
Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly
    210                 215                 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225                 230                 235                 240
Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu
                245                 250                 255
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
            260                 265                 270
Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp
        275                 280                 285
Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
                325                 330                 335
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
            340                 345                 350
Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala
        355                 360                 365
Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    370                 375                 380
Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser
385                 390                 395                 400
Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
                405                 410                 415
Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala
            420                 425                 430
Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        435                 440                 445
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
    450                 455                 460
```

Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
465 470 475 480

<210> 72
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 72
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115 120 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130 135 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145 150 155 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
165 170 175
Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala
180 185 190
Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195 200 205
Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala
210 215 220
Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225 230 235 240
Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu
245 250 255
Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
260 265 270

```
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
        275                 280                 285
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
    290                 295                 300
Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Tyr Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Leu Asn
    450                 455

<210> 73
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 73
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
```

```
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Pro Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
                245                 250                 255
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305                 310                 315                 320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
385                 390                 395                 400
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
                405                 410                 415
Val Leu Gln Lys Leu Asn
            420
```

<210> 74
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 74
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115   120   125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130   135   140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145   150   155   160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165   170   175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
            180   185   190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195   200   205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
    210   215   220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225   230   235   240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
                245   250   255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
            260   265   270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275   280   285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu
    290   295   300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305   310   315   320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro
                325   330   335
Leu His Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val Leu
            340   345   350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr
        355   360   365

Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val
370 375 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys
385 390 395 400
Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu
405 410 415
Ile Leu Gln Lys Leu Asn
420

<210> 75
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 75
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
115 120 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
130 135 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145 150 155 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
165 170 175
Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala
180 185 190
Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
195 200 205
Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala
210 215 220
Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225 230 235 240

```
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
                245                 250                 255
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305                 310                 315                 320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
385                 390                 395                 400
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
                405                 410                 415
Val Leu Gln Lys Leu Asn
            420
```

<210> 76
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 76

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
```

```
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
                245                 250                 255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305                 310                 315                 320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys
385                 390                 395                 400
Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu
                405                 410                 415
Ile Leu Gln Lys Leu Asn
            420
```

<210> 77
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 77
```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
            180                 185                 190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
    210                 215                 220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu
        355                 360                 365
```

```
His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala
385                 390                 395                 400
Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu
                405                 410                 415
Gln Lys Ala Ala
            420
```

<210> 78
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 78

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
```

```
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
                245                 250                 255
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu
        355                 360                 365
His Leu Ala Asp Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro
385                 390                 395                 400
Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
                405                 410                 415
Gln Lys Ala Ala
            420
```

<210> 79
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 79

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
```

```
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
            180                 185                 190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro
385                 390                 395                 400
Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
                405                 410                 415
Gln Lys Ala Ala
            420
```

<210> 80
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 80
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180   185   190
Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210   215   220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
                245   250   255
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
            260   265   270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275   280   285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290   295   300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala
305   310   315   320
Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His
                325   330   335
Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro
385                 390                 395                 400
Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
                405                 410                 415
Gln Lys Ala Ala
            420
```

<210> 81
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 81

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
            180                 185                 190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
```

```
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala
385                 390                 395                 400
Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu
                405                 410                 415
Gln Lys Ala Ala
            420
```

<210> 82
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 82

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
```

```
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
                245                 250                 255
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305                 310                 315                 320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys
385                 390                 395                 400
Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu
                405                 410                 415
Ile Leu Gln Lys Leu Asn
            420
```

<210> 83
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 83
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg
            180                 185                 190
Phe Gly His Leu Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ile Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Lys Leu Arg His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
        275                 280                 285
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu
        355                 360                 365
```

```
His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr
            420                 425                 430
Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val
        435                 440                 445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys
    450                 455                 460
Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                 470                 475                 480
Val Leu Gln Lys Ala Ala
                485
```

<210> 84
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 84

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
        35                  40                  45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
```

```
Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr Pro Leu His Leu
        275                 280                 285
Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
    290                 295                 300
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
305                 310                 315                 320
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
                325                 330                 335
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
            340                 345                 350
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
        355                 360                 365
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
            420                 425                 430
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
        435                 440                 445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
    450                 455                 460
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                 470                 475                 480
Val Leu Gln Lys Ala Ala
                485
```

<210> 85
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 85
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
```

```
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala
    450
```

<210> 86
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 86

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
145                 150                 155                 160
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                165                 170                 175
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
            180                 185                 190
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        195                 200                 205
```

```
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
    210                 215                 220
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
225                 230                 235                 240
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
                245                 250                 255
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
            260                 265                 270
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
        275                 280                 285
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
    290                 295                 300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
305                 310                 315                 320
Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
                325                 330                 335
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
            340                 345                 350
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
        355                 360                 365
Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
    370                 375                 380
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
385                 390                 395                 400
Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
                405                 410                 415
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
            420                 425                 430
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
        435                 440                 445
Ala
```

<210> 87
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 87

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
        35                  40                  45
```

```
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50                  55                  60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130                 135                 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
```

Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435   440   445
Leu Gln Lys Ala Ala
    450

<210> 88
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 88
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130   135   140
Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145   150   155   160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                165   170   175
Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His
            180   185   190
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195   200   205
Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly
    210   215   220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225   230   235   240
Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu
                245   250   255
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
            260   265   270

```
Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp
        275                 280                 285
Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
                325                 330                 335
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
            340                 345                 350
Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala
        355                 360                 365
Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    370                 375                 380
Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser
385                 390                 395                 400
Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
                405                 410                 415
Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala
            420                 425                 430
Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        435                 440                 445
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
    450                 455                 460
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
465                 470                 475                 480
```

<210> 89
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 89

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
```

```
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala
    450
```

<210> 90
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 90
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
```

```
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala
    450
```

<210> 91
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 91

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140
```

```
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
145                 150                 155                 160
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                165                 170                 175
Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly
            180                 185                 190
His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        195                 200                 205
Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val
    210                 215                 220
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
225                 230                 235                 240
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
                245                 250                 255
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
            260                 265                 270
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        275                 280                 285
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
    290                 295                 300
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
305                 310                 315                 320
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
                325                 330                 335
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
            340                 345                 350
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
        355                 360                 365
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
    370                 375                 380
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
385                 390                 395                 400
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
                405                 410                 415
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
            420                 425                 430
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
        435                 440                 445
Ala
```

<210> 92
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 92
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180   185   190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210   215   220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
                245   250   255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260   265   270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275   280   285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290   295   300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305   310   315   320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325   330   335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala
    450
```

<210> 93
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 93

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
```

```
Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala
    450
```

<210> 94
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising three designed ankyrin repeat domains

<400> 94

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
```

```
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala
            340                 345                 350
Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro
385                 390                 395                 400
Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
```

Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435   440   445
Leu Gln Lys Ala Ala
    450

<210> 95
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 95
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180   185   190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210   215   220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245   250   255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260   265   270

```
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 96
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 96

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
```

```
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 97
<211> 637
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 97

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
```

```
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu
                245                 250                 255
Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
            260                 265                 270
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
        275                 280                 285
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
    290                 295                 300
Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
```

```
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
Ala Glu Ile Leu Gln Lys Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr
                485                 490                 495
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg
            500                 505                 510
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
        515                 520                 525
Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys
    530                 535                 540
Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His
545                 550                 555                 560
Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                565                 570                 575
Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly
            580                 585                 590
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
        595                 600                 605
Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala
    610                 615                 620
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
625                 630                 635
```

<210> 98
<211> 637
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 98

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
```

```
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala
            180                 185                 190
His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu
                245                 250                 255
Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
            260                 265                 270
Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp
        275                 280                 285
Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys
    290                 295                 300
Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly
            420                 425                 430
Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser
    450                 455                 460
Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile
465                 470                 475                 480
```

```
Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr
                485                 490                 495
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg
            500                 505                 510
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
        515                 520                 525
Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys
    530                 535                 540
Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His
545                 550                 555                 560
Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                565                 570                 575
Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly
            580                 585                 590
His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn
        595                 600                 605
Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala
    610                 615                 620
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
625                 630                 635
```

<210> 99
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 99

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
```

```
Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala Gly His
            180                 185                 190
Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195                 200                 205
Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly
    210                 215                 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225                 230                 235                 240
Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr
                245                 250                 255
Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
            260                 265                 270
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
        275                 280                 285
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
Ser Arg Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
                325                 330                 335
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
            340                 345                 350
Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu
        355                 360                 365
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    370                 375                 380
Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala
385                 390                 395                 400
Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
                405                 410                 415
Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala
            420                 425                 430
Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        435                 440                 445
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
    450                 455                 460
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Gly
465                 470                 475                 480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495
Gly Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
            500                 505                 510
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
        515                 520                 525
```

```
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
    530                 535                 540
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
545                 550                 555                 560
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
                565                 570                 575
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
            580                 585                 590
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
        595                 600                 605
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
    610                 615                 620
Asn
625
```

<210> 100
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 100

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
    130                 135                 140
Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp
145                 150                 155                 160
Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                165                 170                 175
Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His
            180                 185                 190
```

```
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        195                 200                 205
Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly
    210                 215                 220
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
225                 230                 235                 240
Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu
                245                 250                 255
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
            260                 265                 270
Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp
        275                 280                 285
Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305                 310                 315                 320
Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
                325                 330                 335
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
            340                 345                 350
Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ala
        355                 360                 365
Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
    370                 375                 380
Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser
385                 390                 395                 400
Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
                405                 410                 415
Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala Ala
            420                 425                 430
Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        435                 440                 445
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
    450                 455                 460
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly
465                 470                 475                 480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495
Gly Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
            500                 505                 510
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
        515                 520                 525
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
    530                 535                 540
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
545                 550                 555                 560
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
                565                 570                 575
```

Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
580 585 590
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
595 600 605
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
610 615 620
Asn
625

<210> 101
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 101
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
115 120 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
145 150 155 160
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
165 170 175
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
180 185 190
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
195 200 205
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
210 215 220
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
225 230 235 240

```
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
                245                 250                 255
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
            260                 265                 270
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
        275                 280                 285
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
    290                 295                 300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
305                 310                 315                 320
Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
                325                 330                 335
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
            340                 345                 350
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
        355                 360                 365
Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
    370                 375                 380
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
385                 390                 395                 400
Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
                405                 410                 415
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
            420                 425                 430
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
        435                 440                 445
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460
Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala
465                 470                 475                 480
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly
                485                 490                 495
Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu
            500                 505                 510
Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
        515                 520                 525
Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His
    530                 535                 540
Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
545                 550                 555                 560
Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala
                565                 570                 575
Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
            580                 585                 590
Lys Ala Ala
        595
```

<210> 102

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

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 102
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180 185 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210 215 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
245 250 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260 265 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
275 280 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
290 295 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305 310 315 320

```
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 103
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 103
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
```

```
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
```

```
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 104
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 104

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
```

```
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
```

Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
485 490 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
500 505 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
515 520 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
530 535 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545 550 555 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
565 570 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
580 585 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 105
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 105
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
115 120 125
Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
145 150 155 160
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
165 170 175

```
Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly
            180                 185                 190
His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        195                 200                 205
Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val
    210                 215                 220
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
225                 230                 235                 240
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
                245                 250                 255
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
            260                 265                 270
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        275                 280                 285
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
    290                 295                 300
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
305                 310                 315                 320
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
                325                 330                 335
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
            340                 345                 350
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
        355                 360                 365
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
    370                 375                 380
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
385                 390                 395                 400
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
                405                 410                 415
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
            420                 425                 430
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
        435                 440                 445
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460
Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala
465                 470                 475                 480
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly
                485                 490                 495
Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu
            500                 505                 510
Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
        515                 520                 525
Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His
    530                 535                 540
Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
545                 550                 555                 560
```

Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala
565 570 575
Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
580 585 590
Lys Ala Ala
595

<210> 106
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 106
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
180 185 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
210 215 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
245 250 255

```
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 107
<211> 601
<212> PRT

<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 107
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
```

```
Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 108
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 108
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
```

```
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
```

```
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 109
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 109

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
```

```
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
                245                 250                 255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
305                 310                 315                 320
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Lys Asp Gly Tyr Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys
385                 390                 395                 400
Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu
                405                 410                 415
Ile Leu Gln Lys Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
            420                 425                 430
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp
        435                 440                 445
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
    450                 455                 460
Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Lys
465                 470                 475                 480
Asp Gly Tyr Thr Pro Leu His Leu Ala Ala Arg Glu Gly His Leu Glu
                485                 490                 495
```

Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            500   505   510
Lys Asp Gly Tyr Thr Pro Leu His Leu Ala Ala Arg Glu Gly His Leu
        515   520   525
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
    530   535   540
Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn
545   550   555   560
Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Asn
                565   570

<210> 110
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 110
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg
            180   185   190
Phe Gly His Leu Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Lys Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala
    210   215   220

```
Ile Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Lys Leu Arg His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
        275                 280                 285
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr
            420                 425                 430
Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val
        435                 440                 445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys
    450                 455                 460
Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                 470                 475                 480
Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
                485                 490                 495
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu
            500                 505                 510
Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
        515                 520                 525
Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe
    530                 535                 540
Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe
                565                 570                 575
Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
```

Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu
610 615 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625 630

<210> 111
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 111
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg
180 185 190
Phe Gly His Leu Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala
210 215 220
Ile Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala
245 250 255
Ala Lys Leu Arg His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260 265 270

```
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
        275                 280                 285
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp
    530                 535                 540
Gly Gln Thr Pro Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr
                565                 570                 575
Asp Gly Leu Thr Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu
    610                 615                 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630
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<210> 112

<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 112
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
35 40 45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
100 105 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
115 120 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
130 135 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
180 185 190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
210 215 220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
245 250 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
260 265 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
275 280 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
290 295 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala
305 310 315 320

```
Gly Ala Asp Val Asn Ala Lys Asp Lys Ser Gly Asn Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Arg Phe Gly His Leu Glu Ile Val Glu Phe Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Glu Thr Gly Lys Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ile Trp Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Tyr Gly Arg Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Lys Leu Arg His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr
            420                 425                 430
Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp
    530                 535                 540
Gly Gln Thr Pro Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr
                565                 570                 575
Asp Gly Leu Thr Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu
    610                 615                 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630
```

<210> 113
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 113
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
        35   40   45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
            100   105   110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115   120   125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130   135   140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145   150   155   160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165   170   175
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
            180   185   190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
    210   215   220
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
                245   250   255
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260   265   270
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
        275   280   285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290   295   300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305   310   315   320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325   330   335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr
            420                 425                 430
Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val
        435                 440                 445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys
    450                 455                 460
Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                 470                 475                 480
Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
                485                 490                 495
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu
            500                 505                 510
Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
        515                 520                 525
Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe
    530                 535                 540
Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe
                565                 570                 575
Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu
    610                 615                 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630
```

<210> 114
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 114

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
```

```
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
        35                  40                  45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Leu Asp Gln Ile Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Asn Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Leu Trp Gly Gln Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Trp Lys Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Lys Asp Thr Asp Gly Leu Thr Pro Leu His Leu
        275                 280                 285
Ala Ala Ile Arg Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
    290                 295                 300
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
305                 310                 315                 320
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
                325                 330                 335
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
            340                 345                 350
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
        355                 360                 365
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
```

```
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
            420                 425                 430
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
        435                 440                 445
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
    450                 455                 460
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
465                 470                 475                 480
Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
                485                 490                 495
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu
            500                 505                 510
Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
        515                 520                 525
Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe
    530                 535                 540
Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe
                565                 570                 575
Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu
    610                 615                 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630
```

<210> 115
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 115

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Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Lys Ser Gly Asn Thr Pro Leu His Leu Ala Ala Arg Phe Gly His Leu
        35                  40                  45
Glu Ile Val Glu Phe Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Glu Thr Gly Lys Thr Pro Leu His Leu Ala Ala Ile Trp Gly His
65                  70                  75                  80
```

```
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Leu Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Lys Leu Arg
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    130                 135                 140
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
```

```
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Leu Asp Gln Ile Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Asn Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Leu Trp
    530                 535                 540
Gly Gln Thr Pro Leu His Leu Ala Ala Trp Lys Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Thr
                565                 570                 575
Asp Gly Leu Thr Pro Leu His Leu Ala Ala Ile Arg Gly His Leu Glu
            580                 585                 590
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp
        595                 600                 605
Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu
    610                 615                 620
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630

<210> 116
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 116
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
        115                 120                 125
```

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
145                 150                 155                 160
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                165                 170                 175
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
            180                 185                 190
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        195                 200                 205
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
    210                 215                 220
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
225                 230                 235                 240
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
                245                 250                 255
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
            260                 265                 270
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
        275                 280                 285
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
    290                 295                 300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
305                 310                 315                 320
Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
                325                 330                 335
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
            340                 345                 350
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
        355                 360                 365
Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
    370                 375                 380
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
385                 390                 395                 400
Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
                405                 410                 415
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
            420                 425                 430
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
        435                 440                 445
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460
Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala
465                 470                 475                 480
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly
                485                 490                 495
Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu
            500                 505                 510
```

```
Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
        515                 520                 525
Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His
    530                 535                 540
Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
545                 550                 555                 560
Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala
                565                 570                 575
Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
            580                 585                 590
Lys Ala Ala
        595

<210> 117
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 117
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50                  55                  60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130                 135                 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
```

```
Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
```

Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 118
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 118
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
50 55 60
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65 70 75 80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
85 90 95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
100 105 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
115 120 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
130 135 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro
145 150 155 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
165 170 175
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
180 185 190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
210 215 220
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
245 250 255
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
260 265 270
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
275 280 285

```
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 119
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 119
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
            180   185   190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
    210   215   220
Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
                245   250   255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260   265   270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275   280   285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290   295   300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305   310   315   320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325   330   335
Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 120
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 120

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu
    50                  55                  60
```

```
Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly
            100                 105                 110
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        115                 120                 125
Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala
    130                 135                 140
Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro
145                 150                 155                 160
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
                165                 170                 175
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
            180                 185                 190
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
```

```
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 121
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 121
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
```

```
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
            420                 425                 430
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
```

```
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 122
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 122

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
```

```
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
                245                 250                 255
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly
            500                 505                 510
Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr
    530                 535                 540
Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 123
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 123
```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
```

```
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala
            340                 345                 350
Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro
385                 390                 395                 400
Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly
            500                 505                 510
Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr
    530                 535                 540
Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 124
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 124

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
            180                 185                 190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
    210                 215                 220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Pro Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
```

Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala
385 390 395 400
Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu
405 410 415
Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
420 425 430
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys
435 440 445
Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile
450 455 460
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp
465 470 475 480
Thr Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu
485 490 495
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly
500 505 510
Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val
515 520 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala
530 535 540
Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile
545 550 555 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
565 570 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
580 585 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 125
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 125
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1 5 10 15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
20 25 30
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
35 40 45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
50 55 60
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
65 70 75 80

```
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser
                245                 250                 255
Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu
        355                 360                 365
His Leu Ala Asp Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro
385                 390                 395                 400
Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
                405                 410                 415
Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
            420                 425                 430
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys
        435                 440                 445
Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile
    450                 455                 460
```

```
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp
465                 470                 475                 480
Thr Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu
                485                 490                 495
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly
            500                 505                 510
Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala
    530                 535                 540
Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 126
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 126
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
```

```
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
            180                 185                 190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
    210                 215                 220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu
        355                 360                 365
His Leu Ala Asp Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro
385                 390                 395                 400
Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
                405                 410                 415
Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro
            420                 425                 430
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys
        435                 440                 445
Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile
    450                 455                 460
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp
465                 470                 475                 480
Thr Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu
                485                 490                 495
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly
            500                 505                 510
Asn Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala
    530                 535                 540
```

```
Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 127
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 127

```
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Leu
        35                  40                  45
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly
            100                 105                 110
Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
            180                 185                 190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
    210                 215                 220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225                 230                 235                 240
```

```
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly
            500                 505                 510
Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr
    530                 535                 540
Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 128

<211> 637
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 128
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro
        115                 120                 125
Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
    130                 135                 140
Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
145                 150                 155                 160
Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp
                165                 170                 175
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
            180                 185                 190
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
        195                 200                 205
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
    210                 215                 220
Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly
225                 230                 235                 240
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
                245                 250                 255
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
```

```
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Leu Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
    450                 455                 460
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Arg Ser
465                 470                 475                 480
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
                485                 490                 495
Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            500                 505                 510
Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His Glu Gly His Leu
        515                 520                 525
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    530                 535                 540
Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala Ala Asp Gly His
545                 550                 555                 560
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                565                 570                 575
Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly
            580                 585                 590
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
        595                 600                 605
Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn
    610                 615                 620
Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Leu Asn
625                 630                 635
```

<210> 129
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 129
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1   5   10   15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20   25   30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35   40   45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50   55   60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65   70   75   80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85   90   95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100   105   110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115   120   125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130   135   140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145   150   155   160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165   170   175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180   185   190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195   200   205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210   215   220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225   230   235   240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245   250   255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260   265   270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275   280   285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290   295   300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305   310   315   320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325   330   335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly
            500                 505                 510
Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr
    530                 535                 540
Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 130
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 130

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
```

```
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
```

```
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 131
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 131

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
```

```
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg Gly
            500                 505                 510
Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile Val
        515                 520                 525
```

```
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu Thr
    530                 535                 540
Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 132
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 132

```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                   10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg
            180                 185                 190
Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala
    210                 215                 220
```

```
Asn Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 133
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 133
```
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
1               5                  10                  15
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
            20                  25                  30
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
        35                  40                  45
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
    50                  55                  60
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
65                  70                  75                  80
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
                85                  90                  95
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
            100                 105                 110
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
        115                 120                 125
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
    130                 135                 140
Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val
            180                 185                 190
Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp
    210                 215                 220
Ser Ser Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr
        275                 280                 285
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    290                 295                 300
```

```
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
305                 310                 315                 320
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                325                 330                 335
Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            500                 505                 510
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    530                 535                 540
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                565                 570                 575
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 134
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 134

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
```

Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385 390 395 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
405 410 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
420 425 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
435 440 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
450 455 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465 470 475 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
485 490 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
500 505 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
515 520 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
530 535 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545 550 555 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
565 570 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
580 585 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 135
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 135
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80

```
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
                245                 250                 255
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
            260                 265                 270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
        275                 280                 285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
```

```
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 136
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 136

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
```

```
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
```

Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545 550 555 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
565 570 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
580 585 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 137
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 137
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145 150 155 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165 170 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
180 185 190
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
195 200 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
210 215 220
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225 230 235 240

```
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 138

<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 138
```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
```

```
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 139
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 139

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
```

```
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
```

```
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 140
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 140

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
```

```
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
```

```
Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr
                485                 490                 495
Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser
            500                 505                 510
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
        515                 520                 525
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
545                 550                 555                 560
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                565                 570                 575
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His
            580                 585                 590
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
        595                 600                 605
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
    610                 615                 620
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630                 635

<210> 141
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 141
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
```

```
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
```

```
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 142
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 142

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Phe Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Lys Ile Val Glu Val Leu Leu Lys His Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Trp Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
```

```
Ala Ala Ser Met Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Met Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
His Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe
        275                 280                 285
Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 143
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 143
```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
```

```
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 144
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 144

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
```

```
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 145
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 145

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
```

```
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp
                245                 250                 255
Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
            260                 265                 270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
        275                 280                 285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
```

Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465 470 475 480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
485 490 495
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser
500 505 510
Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu
515 520 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
530 535 540
Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu
545 550 555 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
565 570 575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
580 585 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 146
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 146
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145 150 155 160

```
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
            420                 425                 430
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser
            500                 505                 510
Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
```

```
Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 147
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 147

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
        35                  40                  45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
            100                 105                 110
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        115                 120                 125
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
    130                 135                 140
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
145                 150                 155                 160
Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro
                165                 170                 175
Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala
            180                 185                 190
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
```

```
Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala
        275                 280                 285
Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 148

<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 148
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly
35 40 45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn
100 105 110
Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
115 120 125
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
130 135 140
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
145 150 155 160
Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro
165 170 175
Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala
180 185 190
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
195 200 205
Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu
210 215 220
Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala
225 230 235 240
Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His
245 250 255
Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
260 265 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
275 280 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
290 295 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305 310 315 320

```
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
            420                 425                 430
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 149
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 149

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
```

```
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305                 310                 315                 320
Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala
                325                 330                 335
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu
        355                 360                 365
Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His
385                 390                 395                 400
```

```
Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
            420                 425                 430
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
        435                 440                 445
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu
465                 470                 475                 480
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
                485                 490                 495
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
            500                 505                 510
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
        515                 520                 525
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
545                 550                 555                 560
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
                565                 570                 575
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
            580                 585                 590
Leu Gln Lys Ala Ala
        595
```

<210> 150
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 150

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
                85                  90                  95
```

```
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
```

```
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 151
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 151
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly
        35                  40                  45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
```

```
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu
            500                 505                 510
Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn
    530                 535                 540
Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu
545                 550                 555                 560
```

Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln
565 570 575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
580 585 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 152
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 152
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145 150 155 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
165 170 175
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
180 185 190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
195 200 205
Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala
210 215 220
Ala Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225 230 235 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
245 250 255

```
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        275                 280                 285
Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
    290                 295                 300
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
305                 310                 315                 320
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
                325                 330                 335
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
        355                 360                 365
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
385                 390                 395                 400
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
            420                 425                 430
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
        435                 440                 445
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu
465                 470                 475                 480
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
                485                 490                 495
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
            500                 505                 510
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
        515                 520                 525
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
545                 550                 555                 560
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
                565                 570                 575
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
            580                 585                 590
Leu Gln Lys Ala Ala
        595
```

<210> 153
<211> 582
<212> PRT

<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 153
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1   5   10   15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20   25   30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35   40   45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50   55   60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65   70   75   80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85   90   95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100   105   110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115   120   125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
    130   135   140
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
145   150   155   160
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg
                165   170   175
Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu Glu
            180   185   190
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp
        195   200   205
Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu
    210   215   220
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
225   230   235   240
Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His
                245   250   255
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            260   265   270
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
        275   280   285
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr
    290   295   300
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp
305   310   315   320
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                325   330   335

```
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            340                 345                 350
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        355                 360                 365
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    370                 375                 380
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
385                 390                 395                 400
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                405                 410                 415
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            420                 425                 430
Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro
        435                 440                 445
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
    450                 455                 460
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu
465                 470                 475                 480
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
                485                 490                 495
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
            500                 505                 510
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
        515                 520                 525
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
    530                 535                 540
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
545                 550                 555                 560
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
                565                 570                 575
Val Leu Gln Lys Ala Ala
            580
```

<210> 154
<211> 561
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 154

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
```

```
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu
    130                 135                 140
Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala
145                 150                 155                 160
Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His
                165                 170                 175
Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            180                 185                 190
Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu
        195                 200                 205
His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu
    210                 215                 220
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro
225                 230                 235                 240
Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu
                245                 250                 255
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            260                 265                 270
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        275                 280                 285
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Gly Ser Asp
    290                 295                 300
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
305                 310                 315                 320
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser
                325                 330                 335
Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu
            340                 345                 350
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
        355                 360                 365
Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu
    370                 375                 380
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
385                 390                 395                 400
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
                405                 410                 415
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro
            420                 425                 430
```

```
Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg
        435                 440                 445
Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp
    450                 455                 460
Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala
465                 470                 475                 480
Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala
                485                 490                 495
Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala
            500                 505                 510
Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        515                 520                 525
Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile
    530                 535                 540
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
545                 550                 555                 560
Ala
```

<210> 155
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 155

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp
    130                 135                 140
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
145                 150                 155                 160
```

```
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg
                165                 170                 175
Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu Glu
            180                 185                 190
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp
        195                 200                 205
Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu
    210                 215                 220
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
225                 230                 235                 240
Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His
                245                 250                 255
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            260                 265                 270
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
        275                 280                 285
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
    290                 295                 300
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp
305                 310                 315                 320
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                325                 330                 335
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            340                 345                 350
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        355                 360                 365
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    370                 375                 380
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile
385                 390                 395                 400
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                405                 410                 415
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            420                 425                 430
Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly
        435                 440                 445
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
    450                 455                 460
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu
465                 470                 475                 480
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
                485                 490                 495
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
            500                 505                 510
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
        515                 520                 525
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
    530                 535                 540
```

Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
545 550 555 560
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
565 570 575
Val Leu Gln Lys Ala Ala
580

<210> 156
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 156
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
130 135 140
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
145 150 155 160
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
165 170 175
Leu His Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu
180 185 190
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
195 200 205
Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val
210 215 220
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn
225 230 235 240
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu
245 250 255

```
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            260                 265                 270
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        275                 280                 285
Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
    290                 295                 300
Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
305                 310                 315                 320
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
                325                 330                 335
Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp
            340                 345                 350
Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
        355                 360                 365
Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala
    370                 375                 380
Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
385                 390                 395                 400
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
                405                 410                 415
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
            420                 425                 430
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys
        435                 440                 445
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
    450                 455                 460
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
465                 470                 475                 480
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
                485                 490                 495
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
            500                 505                 510
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
        515                 520                 525
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
    530                 535                 540
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
545                 550                 555                 560
Glu Val Leu Gln Lys Ala Ala
                565
```

<210> 157
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 157
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1   5   10   15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20   25   30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35   40   45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50   55   60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65   70   75   80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85   90   95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100   105   110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115   120   125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130   135   140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145   150   155   160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165   170   175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180   185   190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195   200   205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210   215   220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225   230   235   240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245   250   255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260   265   270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275   280   285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290   295   300
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
305   310   315   320
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325   330   335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340   345   350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355   360   365

```
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 158
<211> 599
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 158

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
```

```
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
```

```
Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys
465                 470                 475                 480
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
                485                 490                 495
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
            500                 505                 510
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
        515                 520                 525
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
    530                 535                 540
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
545                 550                 555                 560
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
                565                 570                 575
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
            580                 585                 590
Glu Val Leu Gln Lys Ala Ala
        595
```

<210> 159
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 159

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
```

```
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305                 310                 315                 320
Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala
                325                 330                 335
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu
        355                 360                 365
Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His
385                 390                 395                 400
Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
            420                 425                 430
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
        435                 440                 445
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu
465                 470                 475                 480
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
                485                 490                 495
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
            500                 505                 510
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
        515                 520                 525
```

```
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val Leu
545                 550                 555                 560
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
                565                 570                 575
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
            580                 585                 590
Leu Gln Lys Ala Ala
        595
```

<210> 160
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 160

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp
    130                 135                 140
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
145                 150                 155                 160
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg
                165                 170                 175
Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp Ile Gly His Leu Glu
            180                 185                 190
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp
        195                 200                 205
Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu
    210                 215                 220
```

```
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
225                 230                 235                 240
Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His
                245                 250                 255
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            260                 265                 270
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
        275                 280                 285
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly
    290                 295                 300
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp
305                 310                 315                 320
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                325                 330                 335
Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly
            340                 345                 350
Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val
        355                 360                 365
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln
    370                 375                 380
Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile
385                 390                 395                 400
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys
                405                 410                 415
Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp
            420                 425                 430
Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly
        435                 440                 445
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
    450                 455                 460
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu
465                 470                 475                 480
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
                485                 490                 495
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
            500                 505                 510
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
        515                 520                 525
Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu Val
    530                 535                 540
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
545                 550                 555                 560
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
                565                 570                 575
Val Leu Gln Lys Ala Ala
            580
```

<210> 161

<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 161
```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
    130                 135                 140
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
145                 150                 155                 160
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
                165                 170                 175
Leu His Leu Ala Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu
            180                 185                 190
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
        195                 200                 205
Pro Leu His Leu Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val
    210                 215                 220
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn
225                 230                 235                 240
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu
                245                 250                 255
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            260                 265                 270
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        275                 280                 285
Glu Val Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
    290                 295                 300
Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly
305                 310                 315                 320
```

```
Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn
                325                 330                 335
Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp
            340                 345                 350
Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
        355                 360                 365
Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala
    370                 375                 380
Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
385                 390                 395                 400
Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala
                405                 410                 415
Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly
            420                 425                 430
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys
        435                 440                 445
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
    450                 455                 460
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
465                 470                 475                 480
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
                485                 490                 495
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
            500                 505                 510
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
        515                 520                 525
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
    530                 535                 540
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
545                 550                 555                 560
Glu Val Leu Gln Lys Ala Ala
                565
```

<210> 162
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 162

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
```

```
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
305                 310                 315                 320
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
```

```
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr
    450                 455                 460
Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly
465                 470                 475                 480
Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
                485                 490                 495
Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser
            500                 505                 510
His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val
        515                 520                 525
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala
    530                 535                 540
Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile
545                 550                 555                 560
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile
                565                 570                 575
Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp
            580                 585                 590
Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 163
<211> 599
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 163

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr
305                 310                 315                 320
Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu
                325                 330                 335
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys
            340                 345                 350
Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu
        355                 360                 365
His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu
    370                 375                 380
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr Pro
385                 390                 395                 400
Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu
                405                 410                 415
Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr
            420                 425                 430
Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
        435                 440                 445
Leu Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys
465                 470                 475                 480
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
                485                 490                 495
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
            500                 505                 510
```

```
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
        515                 520                 525
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
    530                 535                 540
Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu Glu Ile Val Glu
545                 550                 555                 560
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
                565                 570                 575
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
            580                 585                 590
Glu Val Leu Gln Lys Ala Ala
        595
```

<210> 164
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 164

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
```

```
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Glu Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
```

Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 165
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 165
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145 150 155 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165 170 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
180 185 190
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
195 200 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
210 215 220
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225 230 235 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
245 250 255
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
260 265 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
275 280 285

```
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr
                485                 490                 495
Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser
            500                 505                 510
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
        515                 520                 525
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
545                 550                 555                 560
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                565                 570                 575
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
            580                 585                 590
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
        595                 600                 605
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
    610                 615                 620
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
625                 630                 635

<210> 166
<211> 636
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 166
```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His
                245                 250                 255
Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe
        275                 280                 285
Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
```

```
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly
            420                 425                 430
Asn Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser
    450                 455                 460
Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile
465                 470                 475                 480
Ala Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr
                485                 490                 495
Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser
            500                 505                 510
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
        515                 520                 525
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
545                 550                 555                 560
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                565                 570                 575
Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
            580                 585                 590
Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala
        595                 600                 605
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
    610                 615                 620
His Glu Asp Ile Ala Glu Val Leu Gln Lys Leu Asn
625                 630                 635

<210> 167
<211> 630
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 167
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```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala Ala Asp
            180                 185                 190
Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His Leu Ala
                245                 250                 255
Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu
        275                 280                 285
Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala
    290                 295                 300
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305                 310                 315                 320
Gly Gly Gly Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala
                325                 330                 335
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu
        355                 360                 365
Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
```

```
Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His
385                 390                 395                 400
Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu
            420                 425                 430
His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu
        435                 440                 445
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala
    450                 455                 460
Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu
465                 470                 475                 480
Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
            500                 505                 510
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
        515                 520                 525
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
545                 550                 555                 560
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
                565                 570                 575
Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val
            580                 585                 590
Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
        595                 600                 605
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
    610                 615                 620
Val Leu Gln Lys Leu Asn
625                 630

<210> 168
<211> 630
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 168
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
```

```
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala Ala His
            180                 185                 190
Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His Leu Ser
                245                 250                 255
Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
            260                 265                 270
Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe Asp Ile
        275                 280                 285
Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys Ala
    290                 295                 300
Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305                 310                 315                 320
Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala
                325                 330                 335
Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu
        355                 360                 365
Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His
385                 390                 395                 400
Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu
            420                 425                 430
```

```
His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu
        435                 440                 445
Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro
    450                 455                 460
Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu
465                 470                 475                 480
Gln Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495
Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu
            500                 505                 510
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met
        515                 520                 525
Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu
545                 550                 555                 560
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr
                565                 570                 575
Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val
            580                 585                 590
Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys
        595                 600                 605
Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
    610                 615                 620
Val Leu Gln Lys Leu Asn
625                 630

<210> 169
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 169
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
```

```
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
```

```
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600

<210> 170
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 170
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala
145                 150                 155                 160
Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val
                165                 170                 175
```

```
Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro
            180                 185                 190
Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp
        195                 200                 205
Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu Ala Ala
    210                 215                 220
Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala
225                 230                 235                 240
Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala
                245                 250                 255
Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
            260                 265                 270
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        275                 280                 285
Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
    290                 295                 300
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
305                 310                 315                 320
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
                325                 330                 335
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
            340                 345                 350
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
        355                 360                 365
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
    370                 375                 380
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
385                 390                 395                 400
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
                405                 410                 415
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
            420                 425                 430
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
        435                 440                 445
Lys Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460
Gly Ser Gly Gly Gly Gly Ser Gly Ser Asp Leu Gly Lys Lys Leu Leu
465                 470                 475                 480
Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu Leu Lys
                485                 490                 495
Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr Pro Leu
            500                 505                 510
His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val Leu Leu
        515                 520                 525
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys Thr Pro
    530                 535                 540
Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu Val Leu
545                 550                 555                 560
```

Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly Lys Thr
565 570 575
Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val
580 585 590
Leu Gln Lys Ala Ala
595

<210> 171
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 171
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
35 40 45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
85 90 95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145 150 155 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
165 170 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
180 185 190
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
195 200 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
210 215 220
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225 230 235 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
245 250 255

```
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 172
<211> 603
<212> PRT

<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 172
```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Tyr Gln Gly Trp Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ala Val Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp
                245                 250                 255
Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys
            260                 265                 270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
        275                 280                 285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro
                325                 330                 335
```

```
Leu His Leu Ala Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly
            420                 425                 430
Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr
            500                 505                 510
Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 173
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 173

```
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20                  25                  30
```

```
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35                  40                  45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
```

Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
            420   425   430
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435   440   445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450   455   460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465   470   475   480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485   490   495
Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser
            500   505   510
Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu
        515   520   525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530   535   540
Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu
545   550   555   560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565   570   575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
            580   585   590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595   600

<210> 174
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 174
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1   5   10   15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20   25   30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35   40   45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50   55   60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65   70   75   80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85   90   95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100   105   110

```
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Glu Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Phe Ser His Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Lys Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Ala Gly Lys
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Asn Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Ile Phe Gly
            420                 425                 430
Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly His Glu Asp Ile Ala
        435                 440                 445
Glu Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
```

Val Arg Ile Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser
            500   505   510
Thr Gly Trp Thr Pro Leu His Leu Ala Ala Pro Trp Gly His Pro Glu
        515   520   525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530   535   540
Phe Gln Gly Trp Thr Pro Leu His Leu Ala Ala Ala Val Gly His Leu
545   550   555   560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln
                565   570   575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
            580   585   590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595   600

<210> 175
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 175
Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1   5   10   15
Asp Asp Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
            20   25   30
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
        35   40   45
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50   55   60
Ala Lys Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp
65   70   75   80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val
                85   90   95
Asn Ala Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp
            100   105   110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115   120   125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130   135   140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145   150   155   160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165   170   175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180   185   190

```
Ala Asp Ala Gly His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Ala Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Ala Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Lys Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr
                485                 490                 495
Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser
            500                 505                 510
Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
        515                 520                 525
Glu Val Arg Glu Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu
545                 550                 555                 560
Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                565                 570                 575
```

Asp Phe Ala Gly Lys Thr Pro Leu His Leu Ala Ala Asn Asp Gly His
580 585 590
Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala
595 600 605
Gln Asp Ile Phe Gly Lys Thr Pro Ala Asp Ile Ala Ala Asp Ala Gly
610 615 620
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625 630 635

<210> 176
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 176
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1 5 10 15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
20 25 30
Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly
35 40 45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
50 55 60
Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser
65 70 75 80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val
85 90 95
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
100 105 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
115 120 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
130 135 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Met Lys Leu Leu Glu Ala Ala
145 150 155 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
165 170 175
Asp Val Asn Ala His Asp Thr Trp Gly Leu Thr Pro Leu His Leu Ala
180 185 190
Ala Phe His Gly His Gln Glu Ile Val Glu Val Leu Leu Lys His Gly
195 200 205
Ala Asp Val Asn Ala Gln Asp Phe Tyr Gly Lys Thr Pro Leu His Leu
210 215 220
Ala Ala Leu Arg Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr
225 230 235 240

```
Gly Ala Asp Val Asn Ala Gln Asp Gln Phe Gly Lys Thr Ala Phe Asp
                245                 250                 255
Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys
            260                 265                 270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
        275                 280                 285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Ser Thr Gly Trp Thr Pro
                325                 330                 335
Leu His Leu Ala Ala Pro Trp Gly His Pro Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Phe Gln Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ala Ala Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys
385                 390                 395                 400
Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu
                405                 410                 415
Val Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro
            420                 425                 430
Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu
        435                 440                 445
Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val
    450                 455                 460
Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu Arg
465                 470                 475                 480
Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu Ile
                485                 490                 495
Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn Glu
            500                 505                 510
Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu Glu
        515                 520                 525
Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln Asp
    530                 535                 540
Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His Glu
545                 550                 555                 560
Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
                565                 570
```

<210> 177
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 177
```
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                  10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly
        35                  40                  45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Arg Tyr Gly Asp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Asp Ile Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Glu Asp Tyr Phe Gly Asn Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ser Tyr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asp Tyr Gly Asn Thr Pro Leu His
                245                 250                 255
Leu Ala Ala Asn Thr Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala
        275                 280                 285
Asp Leu Ala Ala Asp Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
```

```
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr
        355                 360                 365
Pro Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly
            420                 425                 430
Trp Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val
        435                 440                 445
Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe
    450                 455                 460
Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu
465                 470                 475                 480
Ala Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr
                485                 490                 495
Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser
            500                 505                 510
Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp
        515                 520                 525
Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp
    530                 535                 540
Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys
                565                 570                 575
Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His
            580                 585                 590
Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala
        595                 600                 605
Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly
    610                 615                 620
His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
625                 630                 635

<210> 178
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 178
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
```

```
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly
        35                  40                  45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val
                85                  90                  95
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Gly Met Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala
                165                 170                 175
Asp Val Asn Ala His Asp Thr Trp Gly Leu Thr Pro Leu His Leu Ala
            180                 185                 190
Ala Phe His Gly His Gln Glu Ile Val Glu Val Leu Leu Lys His Gly
        195                 200                 205
Ala Asp Val Asn Ala Gln Asp Phe Tyr Gly Lys Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Leu Arg Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Tyr
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Gln Asp Gln Phe Gly Lys Thr Ala Phe Asp
                245                 250                 255
Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln Lys
            260                 265                 270
Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro
        275                 280                 285
Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu
    290                 295                 300
Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu
305                 310                 315                 320
Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro
                325                 330                 335
Leu His Leu Ala Ala His Glu Gly His Leu Glu Ile Val Glu Val Leu
            340                 345                 350
Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp
385                 390                 395                 400
```

```
Thr Pro Leu His Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly
            420                 425                 430
Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala
        435                 440                 445
Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
                485                 490                 495
Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu
            500                 505                 510
Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu
        515                 520                 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn
    530                 535                 540
Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu
545                 550                 555                 560
Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln
                565                 570                 575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
            580                 585                 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
        595                 600
```

<210> 179
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein comprising four designed ankyrin repeat domains

<400> 179

```
Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln
1               5                   10                  15
Asp Asp Glu Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala
            20                  25                  30
Lys Asp Glu Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly
        35                  40                  45
His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
    50                  55                  60
Ala Lys Asn Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser
65                  70                  75                  80
Gly His Leu Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val
                85                  90                  95
```

```
Asn Ala Gln Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp
            100                 105                 110
Ala Gly His Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala Gly Ser
        115                 120                 125
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Thr Pro Thr
    130                 135                 140
Pro Thr Pro Thr Gly Ser Asp Leu Asp Lys Lys Leu Leu Glu Ala Ala
145                 150                 155                 160
Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu Leu Lys Ala Gly Ala
                165                 170                 175
Asp Val Asn Ala Lys Asp Tyr Leu Gly Trp Thr Pro Leu His Leu Ala
            180                 185                 190
Ala His Glu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala Gly
        195                 200                 205
Ala Asp Val Asn Ala Lys Asp Val Ser Gly Tyr Thr Pro Leu His Leu
    210                 215                 220
Ala Ala Ala Asp Gly His Leu Glu Ile Val Glu Val Leu Leu Lys Ala
225                 230                 235                 240
Gly Ala Asp Val Asn Ala Lys Asp Asn Thr Gly Trp Thr Pro Leu His
                245                 250                 255
Leu Ser Ala Asp Leu Gly His Leu Glu Ile Val Glu Val Leu Leu Lys
            260                 265                 270
Ala Gly Ala Asp Val Asn Ala Gln Asp Lys Phe Gly Lys Thr Ala Phe
        275                 280                 285
Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala Glu Ile Leu Gln
    290                 295                 300
Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr
305                 310                 315                 320
Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp Leu Gly Met Lys
                325                 330                 335
Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg Ile Leu
            340                 345                 350
Met Ala Asn Gly Ala Asp Val Asn Ala His Asp Thr Trp Gly Leu Thr
        355                 360                 365
Pro Leu His Leu Ala Ala Phe His Gly His Gln Glu Ile Val Glu Val
    370                 375                 380
Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Phe Tyr Gly Lys
385                 390                 395                 400
Thr Pro Leu His Leu Ala Ala Leu Arg Gly His Leu Glu Ile Val Glu
                405                 410                 415
Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Gln Asp Gln Phe Gly
            420                 425                 430
Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp Leu Ala
        435                 440                 445
Glu Ile Leu Gln Lys Ala Ala Gly Ser Pro Thr Pro Thr Pro Thr Thr
    450                 455                 460
Pro Thr Pro Thr Pro Thr Thr Pro Thr Pro Thr Pro Thr Gly Ser Asp
465                 470                 475                 480
```

Leu Asp Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu
485 490 495
Val Arg Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Glu
500 505 510
Arg Gly Thr Thr Pro Leu His Leu Ala Ala Val Tyr Gly His Leu Glu
515 520 525
Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn Ala Lys Asn
530 535 540
Glu Thr Gly Tyr Thr Pro Leu His Leu Ala Asp Ser Ser Gly His Leu
545 550 555 560
Glu Ile Val Glu Val Leu Leu Lys His Ser Ala Asp Val Asn Ala Gln
565 570 575
Asp Lys Ser Gly Lys Thr Pro Ala Asp Leu Ala Ala Asp Ala Gly His
580 585 590
Glu Asp Ile Ala Glu Val Leu Gln Lys Ala Ala
595 600

<210> 180
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Ankyrin repeat module of designed ankyrin repeat domains with binding specificity for serum albumin.

<400> 180
Lys Asp Tyr Phe Ser His Thr Pro Leu His Leu Ala Ala Arg Asn Gly
1 5 10 15
His Leu Lys Ile Val Glu Val Leu Leu Lys Ala Gly Ala Asp Val Asn
20 25 30
Ala

<210> 181
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Ankyrin repeat module of designed ankyrin repeat domains with binding specificity for serum albumin.

<220>
<221> VARIANT
<222> 1
<223> Xaa represents an amino acid residue selected from the group consisting of D, K and A

<220>
<221> VARIANT
<222> 1..33
<223> Optionally up to 5, 4, 3, 2, 1, 0 amino acids in other than the
positions denoted with Xaa can be exchanged by any amino acid

<220>
<221> VARIANT
<222> 5
<223> Xaa represents an amino acid residue selected from the group
consisting of D, G and S
<220>
<221> VARIANT
<222> 15
<223> Xaa represents an amino acid residue selected from the group
consisting of E, N, D, H, S, A, Q, T and G

<220>
<221> VARIANT
<222> 16
<223> Xaa represents an amino acid residue selected from the group
consisting of G and D

<220>
<221> VARIANT
<222> 19
<223> Xaa represents an amino acid residue selected from the group
consisting of E, K and G

<220>
<221> VARIANT
<222> 27
<223> Xaa represents an amino acid residue selected from the group
consisting of H, Y, A and N

<400> 181
Xaa Asp Tyr Phe Xaa His Thr Pro Leu His Leu Ala Ala Arg Xaa Xaa
1 5 10 15
His Leu Xaa Ile Val Glu Val Leu Leu Lys Xaa Gly Ala Asp Val Asn
20 25 30
Ala