SEQUENCE LISTING

<110> ImmunoGen, Inc.

<120> CD37-BINDING MOLECULES AND IMMUNOCONJUGATES THEREOF

<130> 2921.017PC01/EKS/CLD

<140> PCT/US2012/031648
<141> 2012-03-30

<150> 61/470,863
<151> 2011-04-01

<160> 194

<170> PatentIn version 3.5

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Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
        115                 120                 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
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Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145                 150                 155                 160
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Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
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Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
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Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
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Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
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Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

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

Phe Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val
        35                  40                  45

Gly Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile
    50                  55                  60

Ser Gly Val Phe Thr Met Gly Leu Ala Leu Leu Gly Cys Val Gly Ala
65                  70                  75                  80

Leu Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu
                85                  90                  95
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Leu Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln
            100                 105                 110

Arg Ala Gln Leu Glu Arg Ser Leu Gln Asp Ile Val Glu Lys Thr Ile
        115                 120                 125

Gln Arg Tyr His Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp
    130                 135                 140

Asp Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Ser Pro Gln
145                 150                 155                 160

Asp Trp Phe Gln Val Leu Thr Leu Arg Gly Asn Gly Ser Glu Ala His
                165                 170                 175

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

Ile Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly Gln Leu
        195                 200                 205

Ala Arg Ser Arg His Ser Thr Asp Ile Cys Ala Val Pro Ala Asn Ser
    210                 215                 220

His Ile Tyr Arg Glu Gly Cys Ala Arg Ser Leu Gln Lys Trp Leu His
225                 230                 235                 240

Asn Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu
                245                 250                 255

Glu Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp
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His Val Tyr Asn Arg Leu Arg Tyr Arg
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Val Phe Asn Leu Phe Phe Phe Val Leu Gly Gly Leu Ile Phe Cys Phe
            20                  25                  30
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Gly Thr Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
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Gly Val Leu Thr Met Ala Leu Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val Leu Arg Thr Ile Gln
        115                 120                 125

Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

Tyr Ala Gln Phe Gln Leu Arg Cys Cys Gly Trp Gln Ser Pro Arg Asp
145                 150                 155                 160

Trp Asn Lys Ala Gln Met Leu Lys Ala Asn Glu Ser Glu Glu Pro Phe
                165                 170                 175

Val Pro Cys Ser Cys Tyr Asn Ser Thr Ala Thr Asn Asp Ser Thr Val
            180                 185                 190

Phe Asp Lys Leu Phe Phe Ser Gln Leu Ser Arg Leu Gly Pro Arg Ala
        195                 200                 205

Lys Leu Arg Gln Thr Ala Asp Ile Cys Ala Leu Pro Ala Lys Ala His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Gln Ser Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Ile Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

Val Tyr Asp Arg Leu Ala Arg Tyr Arg
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Gly Thr Val Val Ala Asp
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Ser Gly Phe Gly Trp His
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Tyr Ile Leu Tyr Ser Gly Gly Thr Asp
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Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr

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Ser Gly Phe Ala Trp His
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Tyr Ile Leu Tyr Ser Gly Ser Thr Val
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Tyr Ile His Tyr Ser Gly Ser Thr Asn
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Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Val Tyr
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Ser Gly Phe Ala Trp His
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Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr

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Arg Ala Ser Glu Asn Ile Arg Ser Asn Leu Ala
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Val Ala Thr Asn Leu Ala Asp
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Gln His Tyr Trp Gly Thr Thr Trp Thr
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Tyr Ala Ser Asn Leu Ala Ser
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Gln His Ser Trp Glu Ile Pro Tyr Thr
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Ser Ala Ser Ser Ser Val Thr Tyr Met His
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Gln Gln Trp Ile Ser Asn Pro Pro Thr
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Ser Ala Thr Ser Ser Val Thr Tyr Met His
1 5 10

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<400> 38

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Gln Gln Trp Ser Asp Asn Pro Pro Thr
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Ser Ala Thr Ser Ser Val Thr Tyr Met His
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Gln Gln Trp Ser Ser Asn Pro Pro Thr
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Ser Ala Ser Ser Ser Val Thr Tyr Met His
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Ser Ala Thr Ser Ser Val Thr Tyr Met His
1 5 10

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1 5

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Ser Ala Xaa Ser Ser Val Thr Tyr Met His
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Asp Thr Ser Xaa Leu Xaa Xaa
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Gln Gln Trp Xaa Xaa Xaa Pro Pro Thr
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Gln Val Gln Val Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala

85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

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Gln Val Gln Val Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

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Gln Val Gln Val Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
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Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Pro Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
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Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys Ala

85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
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Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Gln Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Ser Arg Asn Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Gly Arg Gly Thr Val Val Ala Asp Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
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1               5                   10                  15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
            20                  25                  30

Gly Met Asn Trp Val Lys Gln Ala Gln Gly Lys Gly Leu Lys Trp Met
        35                  40                  45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Ser Arg Asn Ala Glu Glu Phe
    50                  55                  60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

Gly Arg Gly Thr Val Val Ala Asp Trp Gly Gln Gly Thr Thr Leu Thr
            100                 105                 110

Val Ser Ser
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1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
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85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
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Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 64
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 64

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
```

85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 65
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 65

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg Gln His Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 66
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 66

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Ser Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Ser Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Val Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ala
        115                 120
```

<210> 67
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 67

```
Glu Val Gln Leu Val Glu Ser Gly Pro Glu Val Leu Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Gly
            20                  25                  30

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

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
    50                  55                  60

Gln Gly Arg Ile Ser Ile Thr Arg Asp Ser Ser Ile Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Ala Ser Asp Thr Ala Thr Tyr Tyr Cys
```

85 90 95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 68
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-56

<400> 68

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Pro Val Ser Ala
115 120

<210> 69
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 69

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

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

Met Gly Tyr Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Pro Val Ser Ala
        115                 120


<210>  70
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  muCD37-57

<400>  70

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
```

85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 71
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 71

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 72
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 72

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 73
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 73

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
```

100 105

<210> 74
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3 (1.0 and 1.1)

<400> 74

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

Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Val
35 40 45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 75
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 75

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

<210> 76
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 76

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 77

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
                85                  90                  95

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


<210>  78
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  chCD37-38

<400>  78

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
                85                  90                  95
```

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

<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 79

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

Glu Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
85 90 95

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

<210> 80
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 80

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

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

<210> 81
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 81

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 82
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 82

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Asn Met Glu Ala Glu
65 70 75 80

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

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

<210> 83
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 83

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 84
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-56

<400> 84

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

Asp Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
65 70 75 80

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

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

<210> 85
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 85

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Arg Trp Ile Tyr
35 40 45

```
Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Gly
    50                  55                  60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 86
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-57

<400> 86

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

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

<210> 87
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 87

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

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

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 88
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 88

Gln Val Gln Val Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

```
Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
        115                 120                 125

Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val
    130                 135                 140

Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser
145                 150                 155                 160

Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
                165                 170                 175

Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser
            180                 185                 190

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

Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro
    210                 215                 220

Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile
225                 230                 235                 240

Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln
            260                 265                 270

Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln
        275                 280                 285

Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu
    290                 295                 300

Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys
305                 310                 315                 320

Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys
                325                 330                 335

Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro
```

340 345 350

Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr
355 360 365

Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys
370 375 380

Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val
405 410 415

Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn
420 425 430

His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 89
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 89

Gln Val Gln Val Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

```
Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
```

355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 90
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3v1.0

<400> 90

Gln Val Gln Val Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Pro Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

```
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
```

370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440

<210> 91
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 91

Gln Val Gln Val Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Ser
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Gly Tyr Ser Leu Ala His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

```
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
```

385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440

<210> 92
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 92

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Gln Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Ser Arg Asn Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Gly Arg Gly Thr Val Val Ala Asp Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
115 120 125

Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val
130 135 140

Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser
145 150 155 160

```
Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
                165                 170                 175

Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser
            180                 185                 190

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

Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro
    210                 215                 220

Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile
225                 230                 235                 240

Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln
            260                 265                 270

Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln
        275                 280                 285

Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu
    290                 295                 300

Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys
305                 310                 315                 320

Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys
                325                 330                 335

Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro
            340                 345                 350

Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr
        355                 360                 365

Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys
    370                 375                 380

Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val
```

405 410 415

Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn
420 425 430

His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 93
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 93

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Gln Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Ser Arg Asn Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Gly Arg Gly Thr Val Val Ala Asp Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

```
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
```

420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 94
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 94

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val
115 120 125

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

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145 150 155 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Glu Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
180 185 190

```
Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
            260                 265                 270

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser
385                 390                 395                 400

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
```

435 440

<210> 95
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 95

Gln Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

```
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 96
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 96

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Val Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
```

```
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 97
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 97

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val
        115                 120                 125

Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
    130                 135                 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr
145                 150                 155                 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
            180                 185                 190

Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205
```

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Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile
    210                 215                 220

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
                245                 250                 255

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp
            260                 265                 270

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His
        275                 280                 285

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg
    290                 295                 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305                 310                 315                 320

Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu
                325                 330                 335

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
            340                 345                 350

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
        355                 360                 365

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
    370                 375                 380

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
                405                 410                 415

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
            420                 425                 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
        435                 440                 445

Gly Lys
```

450

<210> 98
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 98

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg Gln His Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

```
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 99
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 99

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Ser Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Ser Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Val Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val
        115                 120                 125

Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
    130                 135                 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr
145                 150                 155                 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
            180                 185                 190

Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205
```

```
Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile
    210                 215                 220

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
                245                 250                 255

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp
            260                 265                 270

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His
        275                 280                 285

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg
    290                 295                 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305                 310                 315                 320

Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu
                325                 330                 335

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
            340                 345                 350

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
        355                 360                 365

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
    370                 375                 380

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
                405                 410                 415

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
            420                 425                 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
        435                 440                 445

Gly Lys
```

450

<210> 100
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 100

Glu Val Gln Leu Val Glu Ser Gly Pro Glu Val Leu Lys Pro Gly Glu
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

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

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
50 55 60

Gln Gly Arg Ile Ser Ile Thr Arg Asp Ser Ser Ile Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Ala Ser Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

```
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 101
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-56

<400> 101

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Pro Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125

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

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Glu Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190

Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205
```

```
Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
            260                 265                 270

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser
385                 390                 395                 400

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440
```

<210> 102

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

<220>
<223> huCD37-56

<400> 102

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

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

Met Gly Tyr Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Pro Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 103

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-57

<400> 103

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gln
1               5                   10                  15


Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30


Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45


Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
    50                  55                  60


Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80


Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val
        115                 120                 125


Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
    130                 135                 140


Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr
145                 150                 155                 160


Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175


Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
            180                 185                 190


Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205


Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile
    210                 215                 220
```

```
Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
                245                 250                 255

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp
            260                 265                 270

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His
        275                 280                 285

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg
    290                 295                 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305                 310                 315                 320

Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu
                325                 330                 335

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
            340                 345                 350

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
        355                 360                 365

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
    370                 375                 380

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
                405                 410                 415

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
            420                 425                 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
        435                 440                 445

Gly Lys
    450
```

<210> 104

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

<220>
<223> huCD37-57

<400> 104

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

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

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 105

<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 105

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
            100                 105                 110

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

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
    130                 135                 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145                 150                 155                 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 106
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 106

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
```

Phe Asn Arg Gly Glu Cys
210

<210> 107
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3 (1.0 and 1.1)

<400> 107

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

Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Val
35 40 45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 108
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 108

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg

180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 109
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 109

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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

Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

```
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


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

<220>
<223>  muCD37-38

<400>  110

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


Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30


His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45


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


Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80


Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
                85                  90                  95


Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro
            100                 105                 110


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


Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140


Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145                 150                 155                 160
```

```
Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

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

<220>
<223> chCD37-38

<400> 111

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
                85                  90                  95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
```

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 112
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 112

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

Glu Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

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

<220>
<223> muCD37-50

<400> 113

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

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

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

```
Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145                 150                 155                 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

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

<220>
<223> huCD37-50

<400> 114

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
```

```
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210


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

<220>
<223>  muCD37-51

<400>  115

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Asn Met Glu Ala Glu
65                  70                  75                  80

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

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

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145                 150                 155                 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

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

<220>
<223> huCD37-51

<400> 116

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr
```

85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

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

<220>
<223> muCD37-56

<400> 117

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

Asp Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
65 70 75 80

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

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro
            100                 105                 110

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145                 150                 155                 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

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

<220>
<223> huCD37-56

<400> 118

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Gly
    50                  55                  60
```

```
Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

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

<220>
<223> muCD37-57

<400> 119

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45
```

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80

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

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

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145                 150                 155                 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210


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

<220>
<223>  huCD37-57

<400>  120

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

Glu Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Trp Ile Tyr
```

35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 121
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 121
caggtgcagg tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatt 60

acatgcactg tctcagggtt ctcattaacc acctctggtg taagctgggt tcgccagcct 120

ccaggaaagg gtctggagtg gctgggagta atatggggtg acgggagcac aaactatcat 180

tcagctctca aatccagact gagcatcaag aaggatcact ccaagagcca agttttctta 240

aaactgaaca gtctgcaaac tgatgacaca gccacgtact actgtgccaa aggaggctac 300

tcgttggctc actggggcca agggactctg gtcacagtct ctgca 345

<210> 122
<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 122
aagcttgcca ccatggctgt cctggcactg ctcctctgcc tggtgacata cccaagctgt 60

gtcctatcac aggtgcaggt gaaggagtca ggacctggcc tggtggcgcc ctcacagagc 120

ctgtccatta catgcactgt ctcagggttc tcattaacca cctctggtgt aagctgggtt 180

cgccagcctc caggaaaggg tctggagtgg ctgggagtaa tatggggtga cgggagcaca 240

aactatcatt cagctctcaa atccagactg agcatcaaga aggatcactc caagagccaa 300

gttttcttaa aactgaacag tctgcaaact gatgacacag ccacgtacta ctgtgccaaa 360

ggaggctact cgttggctca ctggggccaa gggactctgg tcacagtctc tgcagcctct 420

acgaagggcc c 431

<210> 123
<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3v1.0

<400> 123
aagcttgcca ccatgggttg gagctgcatt attctgtttc tggtggccac cgccaccggt 60

gtgcactcac aagtccaagt ccaagaatct ggtccaggtc tggtggcccc ttcccaaact 120

ctgagcatca cctgtaccgt ttctggtttt agccttacca cctctggtgt gagttgggta 180

cgccaaccac ccggtaaggg tctcgaatgg ctgggtgtaa tctggggtga tggttccaca 240

aattaccatc cttccctcaa gtcccgcctt agcatcaaaa aggatcacag caaaagtcaa 300

gttttcctga aactgaatag tctgacagca gccgatacag ccacctacta ttgcgccaag 360

ggtggttata gtcttgcaca ctggggtcaa ggtaccctcg ttaccgtctc ctcagctagt 420

accaagggcc c 431

<210> 124
<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 124
aagcttgcca ccatgggctg gagctgtatc attctgtttc tggtggcgac agctactggg 60

gtccactccc aagtgcaggt acaagagtcc gggcctggat tggtcgcacc aagccagacc 120

ctctctatca cttgtaccgt tagcgggttc tctctgacaa ccagtggagt gagttgggtg 180

aggcagccac caggaaaggg actggagtgg ctgggggtga tttggggcga cggcagcaca 240

aactatcatt ccagtcttaa atctcggttg tccattaaaa aagaccatag taaatctcaa 300

gttttcctga aactcaatag cctgacagcc gcagacactg ctacgtatta ctgcgccaaa 360

ggaggataca gtctggctca ctggggacag gggaccctgg tgaccgtgtc atccgcatca 420

acaaagggcc c 431

<210> 125
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 125
cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttctgggta taccttcaca aagtatggaa tgaactgggt gaagcaggct 120

caaggaaagg gtttaaagtg gatgggctgg ataaacacca acactggaga gtcaagaaat 180

gctgaagaat tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat 240

ttgcagatca acaacctcaa atatgaggac acggctacat atttctgtgg aaggggcacg 300

gtagtagcgg actggggcca aggcaccact ctcacagtct cctca 345

<210> 126
<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 126
aagcttgcca ccatggggtg gtcatgcata atcctctttc tggtcgctac tgctaccggt 60

gtgcactcac agattcagct ggttcaaagt ggcccagagc tgaaaaagcc aggggaaaca 120

gtgaaaataa gttgcaaggc atccggttac actttcacaa agtacggcat gaactgggtc 180

aagcaggccc agggcaaggg gctcaaatgg atgggttgga tcaataccaa cactggcgag 240

tctaggaatg ctgaggagtt taagggccgg tttgccttca gcctggagac aagtgccagc 300

acagcttacc tgcaaatcaa caatctgaag tatgaggata cagcaaccta tttctgcggc 360

cgcggcactg tcgttgcaga ctggggacaa ggtaccacct tgactgtatc cagtgccagc 420

actaagggcc c 431

<210> 127
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 127
gatgtgcagc ttcaggagtc aggacctgac ctggtgaaac cttctcagtc actttcactc 60

acctgcactg tcactggcta ctccatcacc agtggttttg gctggcactg gatccggcag 120

tttccaggaa acaagctgga atggatggcc tacatactct acagtggtgg cactgactac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca cttccaagaa ccagttcttc 240

ctgcggttga gttctgtgac tactgaggac acagccacat attactgtgc aagaggctac 300

tatggttacg gggcctggtt tgtttactgg ggccaaggga ctctggtcac tgtctctgca 360

<210> 128
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 128
aagcttgcca ccatgggctg gagttgtatc attctgtttt tggtggccac cgccactgga 60

gtccattccc aagtgcaact ccaggaatct ggccctgacc tggttaagcc atctcagagc 120

ctctccctga cctgcactgt tacaggatac tcaatcacat caggctttgg ctggcactgg 180

atcagacaat ttcccgggaa caagttggaa tggatggctt acattctgta tagcgggggt 240

accgattaca atccttccct caagagccga atctctatca ccagggatac aagcaagaac 300

caatttttc tccgcctcag ctctgtgact accgaagata ccgctactta ctattgtgcc 360

aggggctact atggatatgg tgcatggttc gtctattggg gccagggaac cctggtgact 420

gtgagcgctg cctctaccaa gggccc 446

<210> 129
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 129

aagcttgcca ccatgggttg gagctgcatc attcttttcc tggtcgctac tgcaactgga 60

gtccactcac aggtccagct gcaagagtcc ggtcctgggc ttgtgaaacc cagccagtcc 120

ctcagtctca cctgtactgt ctctggctac tctattacca gtgggttcgg ctggcattgg 180

attaggcagt ttcccggtaa ggggctggag tggatggcat atatcctgta cagcggagga 240

accgattaca acccaagtct gaagagcagg atcagcatta cccgggacac aagcaaaaac 300

cagtttttcc ttcggctgtc tagtgttaca gctgcagaca ccgctactta ctattgtgct 360

cggggttact atggctatgg ggcttggttt gtgtattggg gacaaggcac tcttgtgacc 420

gtgagcagcg cctcaacaaa gggccc 446

<210> 130
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 130
gatgtgcagc ttcaggagtc aggacctgac ctgttgaaac cttctcagtc actttcactc 60

acctgcactg tcactggcta ctccatcacc agtggttttg cctggcactg gatccggcag 120

tttccaggaa acaaactgga atggatgggc tacatactct acagtggtag cactgtctac 180

agcccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccacttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagagggtac 300

tatggttacg gcgcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 360

<210> 131
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 131
gatgtgcagc ttcaggagtc aggacctgac ctgttgaaac cttctcagtc actttcactc 60

acctgcactg tcactggcta ctccatctcc agtggttttg cctggcactg gatccggcag 120

tttccaggaa acaaactgga atggatgggc tacatacact acagtggtag cactaactac 180

agcccatctc tcaaaagtcg aatctctatc actcgagact catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagaggatac 300

tatggtttcg gcgcctggtt tgtttactgg ggccaaggga ctctggtcac tgtctctgca 360

<210> 132
<211> 360

<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-56

<400> 132
gatgtgcagc ttcaggagtc aggacctgac ctggtgaaac cttctcagtc actttcactc 60

acctgcactg tcactggcta ctccatcacc agtggttttg cctggcactg gatccggcag 120

tttccaggaa acaaactgga atggatgggc tacatacact acagtggtgg cactaactac 180

aacccatctc tcaaaagtcg agtctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagaggctac 300

tatggtttcg gggcctggtt tgcttactgg ggccaaggga ctctggtccc tgtctctgca 360

<210> 133
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 133
aagcttgcca ccatggggtg gagctgcatt atcctgttcc tcgtcgccac cgcaaccggc 60

gtccactccc aggtgcagct gcaagaaagc gggccaggat tggtaaaacc ttcccagtct 120

ctgagtctta cttgtaccgt atctggatac agtatcacat ctggcttcgc ctggcattgg 180

attcgccagt ttcccggcaa ggggcttgag tggatggggt atattcatta ttctggaggt 240

accaactaca acccttccct gaagagtcga gtctcaatta ccagggacac ttccaagaac 300

caattctttt tgcagcttaa ttcagtgacc gctgccgaca ccgctactta ctactgcgcc 360

cggggctact atgggtttgg tgcctggttc gcctactggg gccaggggac cctggtgccc 420

gtgtctgctg cctccacaaa gggccc 446

<210> 134
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-57

<400> 134
gatgtgcagc ttcaggagtc aggacctgac ctgttgaaac cttctcagtc actttcactc 60

acctgcactg tcactggcta ctccatcacc agtggttttg cctggcactg gatccggcag 120

tttccaggaa acaaactgga atggatgggc tacatactct acagtggtag cactgtctac 180

agcccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagagggtac 300

tatggttacg gcgcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 360

<210> 135
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 135
aagcttgcca ccatgggctg gagctgcatc attctgtttc tggtggccac agcaactggc 60

gttcacagtc aagtccaact gcaggagagc ggccccggac tcctgaaacc atctcagtca 120

ctcagtctga catgtactgt gagcggctac agcattacct caggcttcgc ttggcattgg 180

atcaggcagt tccccggaaa aggtctggag tggatggggt acattctgta cagcggcagt 240

acagtgtatt caccctcctt gaaatctagg atatcaatca cacgtgatac aagcaaaaat 300

cagttcttcc tccagctgaa ctccgtcacc gccgcagaca cagcaaccta ttattgtgct 360

cgcggatact acggatatgg cgcatggttc gcctattggg gccaggggac actcgtgacc 420

gtttccgccg cctccacaaa gggccc 446

<210> 136
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 136
gacatccaga tgactcagtc tccagcctcc ctttctgtat ctgtgggaga aactgtcacc 60

atcacatgtc gagcaagtga gaatattcgc agtaatttag catggtatca gcagaaacag 120

ggaaaatctc ctcagctcct ggtcaatgtt gcaacaaact tagcagatgg tgtgccatca 180

aggttcagtg gcagtggatc aggcacacag tattccctca agatcaacag cctgcagtct 240

gaagattttg ggacttatta ctgtcaacat tattggggta ctacgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgt 324

<210> 137
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 137
gaattcgcca ccatgagtgt gcccactcag gtcctggggt tgctgctgct gtggcttaca 60

gatgccagat gtgacatcca gatgactcag tctccagcct ccctttctgt atctgtggga 120

gaaactgtca ccatcacatg tcgagcaagt gagaatattc gcagtaattt agcatggtat 180

cagcagaaac agggaaaatc tcctcagctc ctggtcaatg ttgcaacaaa cttagcagat 240

ggtgtgccat caaggttcag tggcagtgga tcaggcacac agtattccct caagatcaac 300

agcctgcagt ctgaagattt tgggacttat tactgtcaac attattgggg tactacgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgtacg 399

<210> 138
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3 (1.0 and 1.1)

<400> 138
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gttcactctg atatacaaat gactcaaagc ccttccagtt tgagcgtaag tgtgggtgaa 120

cgcgtaacaa tcacctgtag agctagtgaa aacatccgca gtaatctcgc atggtaccaa 180

caaaagccag gtaagtcacc taagctcctc gtgaatgttg ctaccaacct cgctgatggt 240

gtgccttcac gattctctgg ttcaggttcc ggtaccgatt attcacttaa gatcaactca 300

ctccaaccag aagatttcgg tacatattac tgtcaacact actggggtac gacctggaca 360

ttcggtcaag gtactaagct ggaaatcaag cgtacg 396

<210> 139
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 139
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atctcatgca gggccagcca aagtgtcagt acatctagct atagttattt gtactggttc 120

cagcagaaac caggacagcc acccaaactc ctcatcaagt atgcatccaa cctagcatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacatat tactgtcaac acagttggga gattccgtac 300

acgttcggag gggggaccaa actggaaata aaacgg 336

<210> 140
<211> 408
<212> DNA

<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 140
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gttcatagtg atattgtact cactcagtca ccagccagtc tggcagtgtc cctgggccag 120

cgtgccacca tctcctgccg ggcctcacag tccgtgagca ctagctctta ttcctatctc 180

tactggtttc aacagaagcc aggacagccc cctaagctgc tgatcaagta cgcctccaac 240

ctcgccagcg gcgttcccgc tagattctct ggttccggta gcggaactga tttcactttg 300

aacatccacc ccgttgagga agaggatacc gccacttact attgtcaaca ctcttgggag 360

attccttaca cctttggagg aggaacaaag ctcgaaatta agcgtacg 408

<210> 141
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 141
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atgacctgca gtgccagctc aagtgtaact tacatgcact ggtaccagca gaagtcaggc 120

acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180

ttcagtggcg gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg attagtaacc cacccacgtt cggaggggg 300

accaagctgg aaattaaacg g 321

<210> 142
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 142
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gttcattctc agattgtgct gacccaatca ccagctatta tgtccgctag ccccggcgag 120

aaagtgacaa tgacatgtag cgctagctct tctgtgactt acatgcattg gtatcaacag 180

aagtcaggta ccagtcccaa gcgttggatc tacgacacat ccaaactggc ctccggagtc 240

cctgccaggt tcagcggagg tgggtccggc accagttatt cactgaccat atcctctatg 300

gaagctgaag atgctgctac ttattattgt caacaatgga tttctaaccc ccccaccttt 360

ggtggcggaa caaagctgga gatcaagcgt acg 393

<210> 143
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 143
gaattcgcca ccatgggatg gtcctgcatt attctgttct tggtcgccac tgctactggc 60

gttcactctg acattgtgct cacacagtct ccagcctcaa tgtctgcttc ccccggtgag 120

cgggtgacca tgacatgctc tgccagttcc tccgtgacat atatgcattg gtatcagcaa 180

aaacccggta cctctccaaa aagatggatc tacgacactt caaagcttgc atcaggcgtt 240

cctgccagat tttccgggtc tgggtctggc acttcataca gtctgaccat tagttccatg 300

gaagctgaag atgcagccac ctattactgt cagcagtgga tttcaaatcc tcctaccttc 360

ggcggcggaa ccaaactgga gataaagcgt acg 393

<210> 144
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 144
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atgacctgca gtgccacctc aagtgtgact tacatgcact ggtaccagca gaagtcaggc 120

acctccccca aaagatggat ttatgacaca tccaaactgc cttatggagt ccctggtcgt 180

ttcagtggta gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg agtgataacc cacccacgtt cggctcgggg 300

acaaagttgg aaataaagcg g 321

<210> 145
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 145
gaattcgcca ccatgggttg gtcatgcatt attctgttcc tggttgctac cgcaacagga 60

gtacatagtg agatagtcct cacccaaagt cctgctacta tgtctgccag cccaggagag 120

cgtgtgacca tgacttgctc tgcaacctca agtgtgacat acatgcattg gtatcagcaa 180

aagcctggcc aatcccctaa aaggtggatc tacgatactt ctaatctgcc atacggtgtg 240

cccgcaaggt tctccgggag tggcagtggc accagttata gtctgaccat cagttcaatg 300

gaagcagagg atgcagcaac ctattattgt cagcagtggt ccgataatcc ccctactttt 360

ggtcagggta caaagctgga gattaagcgt acg 393

<210> 146
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 146
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atgacctgca gtgccacctc aagtgtgact tacatgcact ggtaccagca gaagtcaggc 120

acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcaacat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg agtagtaacc cacccacgtt cggctcgggg 300

acaaagttgg aaataaagcg g 321

<210> 147
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 147
gaattcgcca ccatgggatg gagctgtatt attctgttcc tggttgctac tgctactggc 60

gtccattccg agatagtcct cacccagagc cccgcaacca tgagtgcctc ccctggggag 120

cgagtgacta tgacttgttc cgccacttct tcagttacct atatgcattg gtatcagcag 180

aaacctggac agtctccaaa gcgttggatt tacgacacct ccaacctggc ttcaggagtt 240

cctgctaggt tcagcggatc tgggtctggc acaagttatt cactcaccat tagttccatg 300

gaggccgaag atgccgctac ttactactgt cagcagtgga gcagcaaccc ccctacattc 360

gggcagggaa ctaagctgga gatcaaacgt acg 393

<210> 148
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> muCD37-56

<400> 148
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atgacctgca gtgccagttc aagtgttact tacatgcact ggtatcagca gaagtcaggc 120

acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180

ttcagtggcg gtgggtctgg gacctcttac tctctcacaa tcagcaccat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg attagtgacc cacccacgtt cggaggggg 300

accaagctgg aaataaaacg g 321

<210> 149
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 149
gaattcgcca ccatgggctg gtcctgtatc atcctgtttc tggtggcaac cgctactggg 60

gttcactctg atattgtcct gacacagagt ccagccttca tgagtgcttc tcccggagaa 120

aaggtcacaa tgacttgttc agcttcctcc tccgtcacat acatgcattg gtaccagcag 180

aagcctgacc agagtcctaa gaggtggatc tatgatacaa gcaatctggc ttccggtgtc 240

ccctcccgct tttcaggcgg cggaagcgga actgactata gccttaccat ctcctcaatg 300

gaagccgagg acgctgctac atattactgc cagcaatgga tcagcgaccc tcctactttc 360

ggacagggaa caaaattgga aattaagcgt acg 393

<210> 150
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-57

<400> 150
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atgacctgca gtgccacctc aagtgtgact tacatgcact ggtaccagca gaagtcaggc 120

acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg agtgataacc cacccacgtt cggctcgggg 300

acaaagttgg aaataaagcg g 321

<210> 151

<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 151
gaattcgcca ccatggggtg gtcctgtatt atcctgttcc tggtcgcaac cgccacaggc 60

gttcactccg agatcgtgtt gactcagagc ccagccacca tgtccgcttc ccccggggag 120

agagtgacaa tgacttgttc cgccacaagt tctgtaacct acatgcattg gtaccagcaa 180

aaaccaggac agagtccccg tcgttggatt tatgatacct ctaacctggc ttcaggcgtt 240

cctgcccgct tttctggtag tggatctggg acttcctata gccttaccat aagctctatg 300

gaagccgagg acgccgctac atactactgc cagcagtgga gtgataaccc ccccaccttc 360

gggcagggaa ccaaattgga gatcaaacgt acg 393

<210> 152
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 152
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gtcctatcac aggtgcaggt gaaggagtca ggacctggcc tggtggcgcc ctcacagagc 120

ctgtccatta catgcactgt ctcagggttc tcattaacca cctctggtgt aagctgggtt 180

cgccagcctc caggaaaggg tctggagtgg ctgggagtaa tatggggtga cgggagcaca 240

aactatcatt cagctctcaa atccagactg agcatcaaga aggatcactc caagagccaa 300

gttttcttaa aactgaacag tctgcaaact gatgacacag ccacgtacta ctgtgccaaa 360

ggaggctact cgttggctca ctggggccaa gggactctgg tcacagtctc tgcagcctct 420

acgaagggcc catcagtttt ccccttggct ccaagttcta aatccacaag cggtggaaca 480

gctgcactgg gatgcctcgt taaagattat ttccctgagc ctgtgacagt gagctggaat 540

agcggagcat tgacttcagg tgtgcacact tttcccgctg tgttgcagtc ctccggtctg 600

tactcactgt ccagtgtcgt aaccgtccct tctagcagct tgggaaccca gacctacatc 660

tgtaacgtca accataaacc atccaacaca aaggtggata agaaggttga accaaagagc 720

tgtgataaga cacatacatg ccctccttgt cctgcaccag agctcctcgg aggtccatct 780

gtgttcctgt ttcccccaa acccaaggac actcttatga tctctcgtac tccagaggtc 840

acctgtgttg ttgtcgacgt gagccatgaa gatcccgagg ttaaattcaa ctggtacgtg 900

gatggagtcg aggttcacaa tgccaagacc aagcccaggg aggagcaata taattctaca 960

tatcgggtag tgagcgttct gaccgtgctc caccaagatt ggctcaatgg aaaagagtac 1020

aagtgcaagg tgtccaacaa ggctcttccc gctcccattg agaaaactat ctccaaagcc 1080

aaggggcagc cacgggaacc ccaggtgtat acattgcccc catctagaga cgagctgacc 1140

aagaaccagg tgagtctcac ttgtctggtc aaggggtttt acccttctga cattgctgta 1200

gagtgggagt ctaacggaca gccagaaaac aactacaaga caactccccc agtgctggac 1260

agcgacggga gcttcttcct ctactccaag ttgactgtag acaagtctag atggcagcaa 1320

ggaaacgttt tctcctgctc agtaatgcat gaggctctgc acaatcacta tacccagaaa 1380

tcactgtccc ttagcccagg gtgactcgag 1410

<210> 153
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3v1.0

<400> 153
aagcttgcca ccatgggttg gagctgcatt attctgtttc tggtggccac cgccaccggt 60

gtgcactcac aagtccaagt ccaagaatct ggtccaggtc tggtggcccc ttcccaaact 120

ctgagcatca cctgtaccgt ttctggtttt agccttacca cctctggtgt gagttgggta 180

cgccaaccac ccggtaaggg tctcgaatgg ctgggtgtaa tctggggtga tggttccaca 240

aattaccatc cttccctcaa gtcccgcctt agcatcaaaa aggatcacag caaaagtcaa 300

gttttcctga aactgaatag tctgacagca gccgatacag ccacctacta ttgcgccaag 360

ggtggttata gtcttgcaca ctggggtcaa ggtaccctcg ttaccgtctc ctcagctagt 420

accaagggcc catcagtttt ccccttggct ccaagttcta aatccacaag cggtggaaca 480

gctgcactgg gatgcctcgt taaagattat ttccctgagc ctgtgacagt gagctggaat 540

agcggagcat tgacttcagg tgtgcacact tttcccgctg tgttgcagtc ctccggtctg 600

tactcactgt ccagtgtcgt aaccgtccct tctagcagct tgggaaccca gacctacatc 660

tgtaacgtca accataaacc atccaacaca aaggtggata agaaggttga accaaagagc 720

tgtgataaga cacatacatg ccctccttgt cctgcaccag agctcctcgg aggtccatct 780

gtgttcctgt ttcccccaa acccaaggac actcttatga tctctcgtac tccagaggtc 840

acctgtgttg ttgtcgacgt gagccatgaa gatcccgagg ttaaattcaa ctggtacgtg 900

gatggagtcg aggttcacaa tgccaagacc aagcccaggg aggagcaata taattctaca 960

tatcgggtag tgagcgttct gaccgtgctc caccaagatt ggctcaatgg aaaagagtac 1020

aagtgcaagg tgtccaacaa ggctcttccc gctcccattg agaaaactat ctccaaagcc 1080

aaggggcagc cacgggaacc ccaggtgtat acattgcccc catctagaga cgagctgacc 1140

aagaaccagg tgagtctcac ttgtctggtc aaggggtttt acccttctga cattgctgta 1200

gagtgggagt ctaacggaca gccagaaaac aactacaaga caactccccc agtgctggac 1260

agcgacggga gcttcttcct ctactccaag ttgactgtag acaagtctag atggcagcaa 1320

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tcactgtccc ttagcccagg gtgactcgag 1410

<210> 154
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 154
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gtccactccc aagtgcaggt acaagagtcc gggcctggat tggtcgcacc aagccagacc 120

ctctctatca cttgtaccgt tagcgggttc tctctgacaa ccagtggagt gagttgggtg 180

aggcagccac caggaaaggg actggagtgg ctgggggtga tttggggcga cggcagcaca 240

aactatcatt ccagtcttaa atctcggttg tccattaaaa aagaccatag taaatctcaa 300

gttttcctga aactcaatag cctgacagcc gcagacactg ctacgtatta ctgcgccaaa 360

ggaggataca gtctggctca ctggggacag gggaccctgg tgaccgtgtc atccgcatca 420

acaaagggcc catcagtttt ccccttggct ccaagttcta aatccacaag cggtggaaca 480

gctgcactgg gatgcctcgt taaagattat ttccctgagc ctgtgacagt gagctggaat 540

agcggagcat tgacttcagg tgtgcacact tttcccgctg tgttgcagtc ctccggtctg 600

tactcactgt ccagtgtcgt aaccgtccct tctagcagct tgggaaccca gacctacatc 660

tgtaacgtca accataaacc atccaacaca aaggtggata agaaggttga accaaagagc 720

tgtgataaga cacatacatg ccctccttgt cctgcaccag agctcctcgg aggtccatct 780

gtgttcctgt ttcccccaa acccaaggac actcttatga tctctcgtac tccagaggtc 840

acctgtgttg ttgtcgacgt gagccatgaa gatcccgagg ttaaattcaa ctggtacgtg 900

gatggagtcg aggttcacaa tgccaagacc aagcccaggg aggagcaata taattctaca 960

tatcgggtag tgagcgttct gaccgtgctc caccaagatt ggctcaatgg aaaagagtac 1020

aagtgcaagg tgtccaacaa ggctcttccc gctcccattg agaaaactat ctccaaagcc 1080

aaggggcagc cacgggaacc ccaggtgtat acattgcccc catctagaga cgagctgacc 1140

aagaaccagg tgagtctcac ttgtctggtc aaggggtttt acccttctga cattgctgta 1200

gagtgggagt ctaacggaca gccagaaaac aactacaaga caactccccc agtgctggac 1260

agcgacggga gcttcttcct ctactccaag ttgactgtag acaagtctag atggcagcaa 1320

ggaaacgttt tctcctgctc agtaatgcat gaggctctgc acaatcacta tacccagaaa 1380

tcactgtccc ttagcccagg gtgactcgag 1410

<210> 155
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 155
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gtgcactcac agattcagct ggttcaaagt ggcccagagc tgaaaaagcc aggggaaaca 120

gtgaaaataa gttgcaaggc atccggttac actttcacaa agtacggcat gaactgggtc 180

aagcaggccc agggcaaggg gctcaaatgg atgggttgga tcaataccaa cactggcgag 240

tctaggaatg ctgaggagtt taagggccgg tttgccttca gcctggagac aagtgccagc 300

acagcttacc tgcaaatcaa caatctgaag tatgaggata cagcaaccta tttctgcggc 360

cgcggcactg tcgttgcaga ctggggacaa ggtaccacct tgactgtatc cagtgccagc 420

actaagggcc catcagtttt ccccttggct ccaagttcta aatccacaag cggtggaaca 480

gctgcactgg gatgcctcgt taaagattat ttccctgagc ctgtgacagt gagctggaat 540

agcggagcat tgacttcagg tgtgcacact tttcccgctg tgttgcagtc ctccggtctg 600

tactcactgt ccagtgtcgt aaccgtccct tctagcagct tgggaaccca gacctacatc 660

tgtaacgtca accataaacc atccaacaca aaggtggata agaaggttga accaaagagc 720

tgtgataaga cacatacatg ccctccttgt cctgcaccag agctcctcgg aggtccatct 780

gtgttcctgt ttcccccaa acccaaggac actcttatga tctctcgtac tccagaggtc 840

acctgtgttg ttgtcgacgt gagccatgaa gatcccgagg ttaaattcaa ctggtacgtg 900

gatggagtcg aggttcacaa tgccaagacc aagcccaggg aggagcaata taattctaca 960

tatcgggtag tgagcgttct gaccgtgctc caccaagatt ggctcaatgg aaaagagtac 1020

aagtgcaagg tgtccaacaa ggctcttccc gctcccattg agaaaactat ctccaaagcc 1080

aaggggcagc cacgggaacc ccaggtgtat acattgcccc catctagaga cgagctgacc 1140

aagaaccagg tgagtctcac ttgtctggtc aaggggtttt acccttctga cattgctgta 1200

gagtgggagt ctaacggaca gccagaaaac aactacaaga caactccccc agtgctggac 1260

agcgacggga gcttcttcct ctactccaag ttgactgtag acaagtctag atggcagcaa 1320

ggaaacgttt tctcctgctc agtaatgcat gaggctctgc acaatcacta tacccagaaa 1380

tcactgtccc ttagcccagg gtgactcgag 1410

<210> 156
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 156
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ctctccctga cctgcactgt tacaggatac tcaatcacat caggctttgg ctggcactgg 180

atcagacaat ttcccgggaa caagttggaa tggatggctt acattctgta tagcgggggt 240

accgattaca atccttccct caagagccga atctctatca ccagggatac aagcaagaac 300

caatttttc tccgcctcag ctctgtgact accgaagata ccgctactta ctattgtgcc 360

aggggctact atggatatgg tgcatggttc gtctattggg gccagggaac cctggtgact 420

gtgagcgctg cctctaccaa gggcccatca gttttccccc tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

acccagacct acatctgtaa cgtcaaccat aaaccatcca acacaaaggt ggataagaag 720

gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

ctcggaggtc catctgtgtt cctgtttccc cccaaaccca aggacactct tatgatctct 840

cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

ttcaactggt acgtggatgg agtcgaggtt cacaatgcca agaccaagcc cagggaggag 960

caatataatt ctacatatcg ggtagtgagc gttctgaccg tgctccacca agattggctc 1020

aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 157
<211> 1425

<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 157
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ctcagtctca cctgtactgt ctctggctac tctattacca gtgggttcgg ctggcattgg 180

attaggcagt ttcccggtaa ggggctggag tggatggcat atatcctgta cagcggagga 240

accgattaca acccaagtct gaagagcagg atcagcatta cccgggacac aagcaaaaac 300

cagtttttcc ttcggctgtc tagtgttaca gctgcagaca ccgctactta ctattgtgct 360

cggggttact atggctatgg ggcttggttt gtgtattggg gacaaggcac tcttgtgacc 420

gtgagcagcg cctcaacaaa gggcccatca gttttcccct tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

acccagacct acatctgtaa cgtcaaccat aaaccatcca acacaaaggt ggataagaag 720

gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

ctcggaggtc catctgtgtt cctgtttccc cccaaaccca aggacactct tatgatctct 840

cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

ttcaactggt acgtggatgg agtcgaggtt cacaatgcca agaccaagcc cagggaggag 960

caatataatt ctacatatcg ggtagtgagc gttctgaccg tgctccacca agattggctc 1020

aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 158
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 158
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ctgagtctga cttgtactgt ttctggctac agcataacca gcggtttcgc ttggcactgg 180

atcagacagc atcccggcaa caaactggag tggatgggat acatactgta ctcaggctca 240

actgtctatt ccccctccct gaaatcccgg atcagtatta cccgtgacac ttctaagaac 300

catttttttc tgcagctgaa cagcgttacc gcagctgaca ctgcaaccta ctactgtgcc 360

cggggatatt atggatacgg agcttggttc gcttactggg gccaaggcac cctcgtaact 420

gtgagtgctg cttccaccaa gggcccatca gttttcccct tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

acccagacct acatctgtaa cgtcaaccat aaaccatcca acacaaaggt ggataagaag 720

gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

ctcggaggtc catctgtgtt cctgtttccc cccaaaccca aggacactct tatgatctct 840

cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

ttcaactggt acgtggatgg agtcgaggtt cacaatgcca agaccaagcc cagggaggag 960

caatataatt ctacatatcg ggtagtgagc gttctgaccg tgctccacca agattggctc 1020

aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 159
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 159
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gtgcattcag aagttcagtt ggtggagtcc ggcccagaag tgctgaaacc cggcgaatca 120

ctgtccctga cttgtaccgt gtcaggttat agcatcagca gcggctttgc ttggcactgg 180

attcggcagt ttccaggcaa gggactggaa tggatgggct acatccatta cagtggctca 240

accaattaca gccctagcct gcagggccga atctctatta ccagggatag ttctattaac 300

cagtttttcc tgcagcttaa ttccgtgact gcctctgaca cagcaactta ctattgcgcc 360

cgtggctact acgggttcgg agcctggttt gtatactggg gtcagggcac cctggtcact 420

gtctcagccg cctctaccaa gggcccatca gttttcccct tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

acccagacct acatctgtaa cgtcaaccat aaaccatcca acacaaaggt ggataagaag 720

gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

ctcggaggtc catctgtgtt cctgtttccc cccaaaccca aggacactct tatgatctct 840

cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

ttcaactggt acgtggatgg agtcgaggtt cacaatgcca agaccaagcc cagggaggag 960

caatataatt ctacatatcg ggtagtgagc gttctgaccg tgctccacca agattggctc 1020

aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 160
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 160
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gtccactccc aggtgcagct gcaagaaagc gggccaggat tggtaaaacc ttcccagtct 120

ctgagtctta cttgtaccgt atctggatac agtatcacat ctggcttcgc ctggcattgg 180

attcgccagt ttcccggcaa ggggcttgag tggatggggt atattcatta ttctggaggt 240

accaactaca acccttccct gaagagtcga gtctcaatta ccagggacac ttccaagaac 300

caattctttt tgcagcttaa ttcagtgacc gctgccgaca ccgctactta ctactgcgcc 360

cggggctact atgggtttgg tgcctggttc gcctactggg gccaggggac cctggtgccc 420

gtgtctgctg cctccacaaa gggcccatca gttttcccct tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

acccagacct acatctgtaa cgtcaaccat aaaccatcca acacaaaggt ggataagaag 720

gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

ctcggaggtc catctgtgtt cctgtttccc cccaaaccca aggacactct tatgatctct 840

cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

ttcaactggt acgtggatgg agtcgaggtt cacaatgcca agaccaagcc cagggaggag 960

caatataatt ctacatatcg ggtagtgagc gttctgaccg tgctccacca agattggctc 1020

aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 161
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 161
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gttcacagtc aagtccaact gcaggagagc ggccccggac tcctgaaacc atctcagtca 120

ctcagtctga catgtactgt gagcggctac agcattacct caggcttcgc ttggcattgg 180

atcaggcagt tccccggaaa aggtctggag tggatggggt acattctgta cagcggcagt 240

acagtgtatt caccctcctt gaaatctagg atatcaatca cacgtgatac aagcaaaaat 300

cagttcttcc tccagctgaa ctccgtcacc gccgcagaca cagcaaccta ttattgtgct 360

cgcggatact acggatatgg cgcatggttc gcctattggg gccaggggac actcgtgacc 420

gtttccgccg cctccacaaa gggcccatca gttttcccct tggctccaag ttctaaatcc 480

acaagcggtg gaacagctgc actgggatgc ctcgttaaag attatttccc tgagcctgtg 540

acagtgagct ggaatagcgg agcattgact tcaggtgtgc acacttttcc cgctgtgttg 600

cagtcctccg gtctgtactc actgtccagt gtcgtaaccg tcccttctag cagcttggga 660

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gttgaaccaa agagctgtga taagacacat acatgccctc cttgtcctgc accagagctc 780

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cgtactccag aggtcacctg tgttgttgtc gacgtgagcc atgaagatcc cgaggttaaa 900

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aatggaaaag agtacaagtg caaggtgtcc aacaaggctc ttcccgctcc cattgagaaa 1080

actatctcca aagccaaggg gcagccacgg gaaccccagg tgtatacatt gcccccatct 1140

agagacgagc tgaccaagaa ccaggtgagt ctcacttgtc tggtcaaggg gttttaccct 1200

tctgacattg ctgtagagtg ggagtctaac ggacagccag aaaacaacta caagacaact 1260

cccccagtgc tggacagcga cgggagcttc ttcctctact ccaagttgac tgtagacaag 1320

tctagatggc agcaaggaaa cgttttctcc tgctcagtaa tgcatgaggc tctgcacaat 1380

cactataccc agaaatcact gtcccttagc ccagggtgac tcgag 1425

<210> 162
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 162
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gatgccagat gtgacatcca gatgactcag tctccagcct ccctttctgt atctgtggga 120

gaaactgtca ccatcacatg tcgagcaagt gagaatattc gcagtaattt agcatggtat 180

cagcagaaac agggaaaatc tcctcagctc ctggtcaatg ttgcaacaaa cttagcagat 240

ggtgtgccat caaggttcag tggcagtgga tcaggcacac agtattccct caagatcaac 300

agcctgcagt ctgaagattt tgggacttat tactgtcaac attattgggg tactacgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgtacgg tggctgcacc atctgtcttc 420

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 480

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 540

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 660

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttag 717

<210> 163
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3 (1.0 and 1.1)

<400> 163
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cgcgtaacaa tcacctgtag agctagtgaa aacatccgca gtaatctcgc atggtaccaa 180

caaaagccag gtaagtcacc taagctcctc gtgaatgttg ctaccaacct cgctgatggt 240

gtgccttcac gattctctgg ttcaggttcc ggtaccgatt attcacttaa gatcaactca 300

ctccaaccag aagatttcgg tacatattac tgtcaacact actggggtac gacctggaca 360

ttcggtcaag gtactaagct ggaaatcaag cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg ttag 714

<210> 164
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 164
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cgtgccacca tctcctgccg ggcctcacag tccgtgagca ctagctctta ttcctatctc 180

tactggtttc aacagaagcc aggacagccc cctaagctgc tgatcaagta cgcctccaac 240

ctcgccagcg gcgttcccgc tagattctct ggttccggta gcggaactga tttcactttg 300

aacatccacc ccgttgagga agaggatacc gccacttact attgtcaaca ctcttgggag 360

attccttaca cctttggagg aggaacaaag ctcgaaatta agcgtacggt ggctgcacca 420

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agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 720

tgttag 726

<210> 165
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 165
gaattcgcca ccatgggctg gtcctgtatc atcctgtttc tcgtggccac agctacaggt 60

gttcattctc agattgtgct gacccaatca ccagctatta tgtccgctag ccccggcgag 120

aaagtgacaa tgacatgtag cgctagctct tctgtgactt acatgcattg gtatcaacag 180

aagtcaggta ccagtcccaa gcgttggatc tacgacacat ccaaactggc ctccggagtc 240

cctgccaggt tcagcggagg tgggtccggc accagttatt cactgaccat atcctctatg 300

gaagctgaag atgctgctac ttattattgt caacaatgga tttctaaccc ccccaccttt 360

ggtggcggaa caaagctgga gatcaagcgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 166
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 166
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cgggtgacca tgacatgctc tgccagttcc tccgtgacat atatgcattg gtatcagcaa 180

aaacccggta cctctccaaa aagatggatc tacgacactt caaagcttgc atcaggcgtt 240

cctgccagat tttccgggtc tgggtctggc acttcataca gtctgaccat tagttccatg 300

gaagctgaag atgcagccac ctattactgt cagcagtgga tttcaaatcc tcctaccttc 360

ggcggcggaa ccaaactgga gataaagcgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

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<210> 167
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<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 167
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cgtgtgacca tgacttgctc tgcaacctca agtgtgacat acatgcattg gtatcagcaa 180

aagcctggcc aatcccctaa aaggtggatc tacgatactt ctaatctgcc atacggtgtg 240

cccgcaaggt tctccgggag tggcagtggc accagttata gtctgaccat cagttcaatg 300

gaagcagagg atgcagcaac ctattattgt cagcagtggt ccgataatcc ccctactttt 360

ggtcagggta caaagctgga gattaagcgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 168
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 168
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aaacctggac agtctccaaa gcgttggatt tacgacacct ccaacctggc ttcaggagtt 240

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ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 169
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 169
gaattcgcca ccatgggctg gtcctgtatc atcctgtttc tggtggcaac cgctactggg 60

gttcactctg atattgtcct gacacagagt ccagccttca tgagtgcttc tcccggagaa 120

aaggtcacaa tgacttgttc agcttcctcc tccgtcacat acatgcattg gtaccagcag 180

aagcctgacc agagtcctaa gaggtggatc tatgatacaa gcaatctggc ttccggtgtc 240

ccctcccgct tttcaggcgg cggaagcgga actgactata gccttaccat ctcctcaatg 300

gaagccgagg acgctgctac atattactgc cagcaatgga tcagcgaccc tcctactttc 360

ggacagggaa caaaattgga aattaagcgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 170
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 170
gaattcgcca ccatggggtg gtcctgtatt atcctgttcc tggtcgcaac cgccacaggc 60

gttcactccg agatcgtgtt gactcagagc ccagccacca tgtccgcttc ccccggggag 120

agagtgacaa tgacttgttc cgccacaagt tctgtaacct acatgcattg gtaccagcaa 180

aaaccaggac agagtccccg tcgttggatt tatgatacct ctaacctggc ttcaggcgtt 240

cctgcccgct tttctggtag tggatctggg acttcctata gccttaccat aagctctatg 300

gaagccgagg acgccgctac atactactgc cagcagtgga gtgataaccc ccccaccttc 360

gggcagggaa ccaaattgga gatcaaacgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VH-CDR1

<400> 171

Ser Tyr Gly Met Ser
1 5

<210> 172
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VH-CDR2

<400> 172

Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Ser Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 173
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VH-CDR3

<400> 173

His Ser Tyr Tyr Asp Thr Ser Val Asp Tyr
1 5 10

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VL-CDR1

<400> 174

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 175
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VL-CDR2

<400> 175

Tyr Thr Ser Lys Leu His Ser
1 5

<210> 176
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VL-CDR3

<400> 176

Gln Gln Gly Asn Ala Leu Pro Trp Thr
1 5

<210> 177
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VH

<400> 177

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Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Ser Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg His Ser Tyr Tyr Asp Thr Ser Val Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Ser Val Thr Val Ser Ser
        115


<210>  178
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  252-3 VL

<400>  178

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80
```

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 179
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 Full-Length Heavy Chain

<400> 179

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Ser Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Ser Tyr Tyr Asp Thr Ser Val Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser

180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
210 215 220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
325 330 335

Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
340 345 350

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
435 440 445

Lys

<210> 180
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 Full-length Light Chain

<400> 180

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

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

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr

180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 181
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 252-3 VH-CDR2

<400> 181

Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr
1 5 10

<210> 182
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> VH 252-3

<400> 182
gaggtgcagg tggtggagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt agctatggca tgtcttgggt tcgccagact 120

ccagacaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagtta cacctactct 180

ccagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa aaccctgtac 240

ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtgc aagacatagt 300

tactacgata ctagcgtcga ctactggggt caaggaacct cagtcaccgt ctcctca 357

<210> 183
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> VL 252-3

<400> 183
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atcagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaaccc 120

gatggaactg ttaaactcct gatctactac acatcaaaat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggagcaa 240

gaagatattg ccacttactt ttgccaacag ggtaatgcgc ttccgtggac gttcggtgga 300

ggcaccaagc tggaactcaa acgg 324

<210> 184
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37-M1

<400> 184

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1 5 10 15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val Leu Arg Thr Ile Gln
115 120 125

Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala Glu Glu Ser Trp Asp
130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
165 170 175

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

```
Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280


<210>  185
<211>  128
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  muCD37-R176

<400>  185

Ile Ser Thr Gln Arg Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val
1               5                   10                  15

Leu Arg Thr Ile Gln Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala
            20                  25                  30

Glu Glu Ser Trp Asp Tyr Ala Gln Phe Gln Leu Arg Cys Cys Gly Trp
        35                  40                  45

Gln Ser Pro Arg Asp Trp Asn Lys Ala Gln Met Leu Lys Ala Asn Glu
    50                  55                  60

Ser Glu Glu Pro Arg Val Pro Cys Ser Cys Tyr Asn Ser Thr Ala Thr
65                  70                  75                  80

Asn Asp Ser Thr Val Phe Asp Lys Leu Phe Phe Ser Gln Leu Ser Arg
                85                  90                  95

Leu Gly Pro Arg Ala Lys Leu Arg Gln Thr Ala Asp Ile Cys Ala Leu
            100                 105                 110
```

Pro Ala Lys Ala His Ile Tyr Arg Glu Gly Cys Ala Gln Ser Leu Gln
115 120 125

<210> 186
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37-M45

<400> 186

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1 5 10 15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
115 120 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
165 170 175

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

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly Pro Arg Ala

195 200 205

Lys Leu Arg Gln Thr Ala Asp Ile Cys Ala Leu Pro Ala Lys Ala His
210 215 220

Ile Tyr Arg Glu Gly Cys Ala Gln Ser Leu Gln Lys Trp Leu His Asn
225 230 235 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
245 250 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
260 265 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
275 280

<210> 187
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37m ECD-H45

<400> 187

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1 5 10 15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val Leu Arg Thr Ile Gln
115 120 125

```
Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

Tyr Ala Gln Phe Gln Leu Arg Cys Cys Gly Trp Gln Ser Pro Arg Asp
145                 150                 155                 160

Trp Asn Lys Ala Gln Met Leu Lys Ala Asn Glu Ser Glu Glu Pro Arg
                165                 170                 175

Val Pro Cys Ser Cys Tyr Asn Ser Thr Ala Thr Asn Asp Ser Thr Val
            180                 185                 190

Phe Asp Lys Leu Phe Phe Ser Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280


<210>  188
<211>  281
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  hCD37m ECD-H5

<400>  188

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1               5                   10                  15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
            20                  25                  30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45
```

```
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val Leu Arg Thr Ile Gln
        115                 120                 125

Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

Tyr Ala Gln Phe Gln Leu Arg Cys Cys Gly Trp Gln Ser Pro Arg Asp
145                 150                 155                 160

Trp Asn Lys Ala Gln Met Leu Lys Ala Asn Glu Ser Glu Glu Pro Arg
                165                 170                 175

Val Pro Cys Ser Cys Tyr Asn Ser Thr Ala Thr Asn Asp Ser Thr Val
            180                 185                 190

Phe Asp Lys Leu Phe Phe Ser Gln Leu Ser Arg Leu Gly Pro Arg Ala
        195                 200                 205

Lys Leu Arg Gln Thr Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280
```

<210> 189
<211> 281

<212> PRT
<213> Artificial Sequence

<220>
<223> hCD37m ECD-H4

<400> 189

```
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1               5                   10                  15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
            20                  25                  30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

Val Arg Leu Glu Arg Arg Val Gln Glu Leu Val Leu Arg Thr Ile Gln
        115                 120                 125

Ser Tyr Arg Thr Asn Pro Asp Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

Tyr Ala Gln Phe Gln Leu Arg Cys Cys Gly Trp Gln Ser Pro Arg Asp
145                 150                 155                 160

Trp Asn Lys Ala Gln Met Leu Lys Ala Asn Glu Ser Glu Glu Pro Arg
                165                 170                 175

Val Pro Cys Ser Cys Tyr Asn Ser Thr Ala Thr Asn Asp Ser Thr Val
            180                 185                 190

Phe Asp Lys Leu Phe Phe Ser Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Leu Pro Ala Lys Ala His
    210                 215                 220
```

```
Ile Tyr Arg Glu Gly Cys Ala Gln Ser Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240


Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255


Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270


Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280


<210>  190
<211>  281
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  hCD37-Mac4

<400>  190

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1               5                   10                  15


Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
            20                  25                  30


Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45


Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60


Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80


Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95


Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110


Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
        115                 120                 125


Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140
```

```
Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145                 150                 155                 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
                165                 170                 175

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

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly Gln Leu Ala
        195                 200                 205

Arg Ser Arg His Ser Thr Asp Ile Cys Ala Val Pro Ala Glu Ser His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
                245                 250                 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
            260                 265                 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
        275                 280


<210>  191
<211>  280
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  hCD37-Mac45

<400>  191

Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1               5                   10                  15

Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
            20                  25                  30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
```

65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
115 120 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
165 170 175

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

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly Gln Leu Ala
195 200 205

Arg Ser Arg His Ser Thr Asp Ile Cys Ala Val Pro Ala Asn Ser His
210 215 220

Ile Tyr Arg Glu Gly Cys Ala Arg Ser Leu Gln Lys Trp Leu His Asn
225 230 235 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
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Val Tyr Asn Arg Leu Ala Arg Tyr
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Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
        35                  40                  45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
    50                  55                  60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65                  70                  75                  80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
                85                  90                  95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
            100                 105                 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
        115                 120                 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
    130                 135                 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145                 150                 155                 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
                165                 170                 175

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

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
        195                 200                 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Asn Ser His
    210                 215                 220

Ile Tyr Arg Glu Gly Cys Ala Arg Ser Leu Gln Lys Trp Leu His Asn
225                 230                 235                 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
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actgtctatt ccccctccct gaaatcccgg atcagtatta cccgtgacac ttctaagaac 300

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