SEQUENCE LISTING

<110> Glenmark Pharmaceuticals S.A.

<120> HETERO-DIMERIC IMMUNOGLOBULINS

<130> PCT

<160> 97

<170> PatentIn version 3.3

<210> 1
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> T cell receptor constant domain alpha
<222> (1)..(91)

<400> 1

Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30

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

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
85 90

<210> 2
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> T cell receptor constant domain beta [Homo sapiens]
<222> (1)..(128)

<400> 2

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

```
Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35                  40                  45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
    50                  55                  60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65                  70                  75                  80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
                85                  90                  95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
            100                 105                 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
        115                 120                 125
```

<210> 3
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT alpha chain

<400> 3

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
```

```
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Lys
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Tyr Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 4
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT beta chain

<400> 4

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val
        115                 120                 125

Ala Thr Phe Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Asp Pro Pro
                165                 170                 175

Leu Leu Glu Ser Asp Gly Ser Phe Cys Leu Ser Ser Arg Leu Arg Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 5
<211> 108
<212> PRT
<213> Artificial

<220>
<223> VL: modified VBASE2-humIGKV115-IGKJ*01

<400> 5

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Asn
                85                  90                  95
```

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

<210> 6
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-BT beta chain

<400> 6

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

```
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro
225                 230                 235                 240

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu
                245                 250                 255

Val Thr Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser
        275                 280                 285

Asp Gly Ser Phe Cys Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 7
<211> 233
<212> PRT
<213> Artificial

<220>
<223> BT alpha His chain

<400> 7

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Lys
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Tyr Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys His His His His His His
225                 230
```

<210> 8
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding CH3-BT alpha chain

<400> 8
ggccagccca gagaacccca ggtgtacacc ctgcccccca gcagagatga gctgaccaag 60

aaccaggtca agctcgtgtg cctggtcacc ggcttctacc ccagcgatat cgccgtggag 120

tgggagagca acggccagcc tgaaaacaac tactacacca ccccccctgt gctggacagc 180

gacggcagct tcagcctggt gtcctggctg aacgtggaca agagccggtg gcagcagggc 240

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 300

ctgagcctgt ctcctggcaa g 321

<210> 9
<211> 321
<212> DNA
<213> Artificial

<220>

<223> cDNA coding CH3-BT beta chain

<400> 9
ggacagccca gggaacctga ggtggccaca ttcccaccta gccgggacga gctgacaaaa 60

aatcaggtca ccctcgtctg tctcgtgacc ggcttttacc cttccgacat tgccgtggaa 120

tgggaatcca atgggcagcc cgagaacaat tacaagacag acccccccct gctggaatcc 180

gatggcagct tctgcctgag cagccggctg cgggtggaca agtccagatg gcagcagggg 240

aatgtctttt cctgctccgt catgcatgaa gccctccaca atcattatac acagaaaagc 300

ctgagcctga gccccggcaa g 321

<210> 10
<211> 699
<212> DNA
<213> Artificial

<220>
<223> cDNA coding BT alpha His chain

<400> 10
gacaaaactc acacatgccc cccctgccct gcccctgagc tgctgggcgg accctccgtg 60

ttcctgttcc cccccaagcc caaggacacc ctgatgatca gccggacccc cgaggtgacc 120

tgcgtggtgg tggacgtgag ccacgaggac cctgaggtga agttcaattg gtacgtggac 180

ggcgtggagg tgcacaacgc caagaccaag ccccgggagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa ggaatacaag 300

tgcaaggtct ccaacaaggc cctgcctgcc cccatcgaga aaaccatctc caaagccaaa 360

ggccagccca gagaacccca ggtgtacacc ctgcccccca gcagagatga gctgaccaag 420

aaccaggtca agctcgtgtg cctggtcacc ggcttctacc ccagcgatat cgccgtggag 480

tgggagagca acggccagcc tgaaaacaac tactacacca ccccccctgt gctggacagc 540

gacggcagct tcagcctggt gtcctggctg aacgtggaca agagccggtg gcagcagggc 600

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 660

ctgagcctgt ctcctggcaa gcatcaccat caccatcac 699

<210> 11
<211> 1005
<212> DNA
<213> Artificial

<220>
<223> cDNA coding VL-BT beta chain

<400> 11
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga ccgggtgacc 60

atcacctgcc gggccagcca gagcatcagc tcctacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctatgct gcctcctctc tccagagcgg cgtgcccagc 180

cggttttccg ggtctgggtc cgggacagat ttcaccctga ccatcagcag cctccagccc 240

gaggatttcg ccacctacta ctgccagcag agctacagca cccccaacac cttcggccag 300

ggaacaaagg tggagatcaa gcgggacaaa actcacactt gcccaccgtg cccagcacct 360

gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 420

atctcccgga cccctgaggt cacctgcgtg gtggtggacg tgagccacga ggaccctgag 480

gtgaagttca attggtacgt ggacggcgtg gaggtgcaca acgccaagac caagccccgg 540

gaggaacagt acaacagcac ctaccgggtg gtgtccgtgc tgaccgtgct gcaccaggac 600

tggctgaacg gcaaggaata caagtgcaag gtctccaaca aggccctgcc tgcccccatc 660

gaaaagacca tcagcaaggc caagggacag cccagggaac ctgaggtggc cacattccca 720

cctagccggg acgagctgac aaaaaatcag gtcaccctcg tctgtctcgt gaccggcttt 780

taccccttccg acattgccgt ggaatgggaa tccaatgggc agcccgagaa caattacaag 840

acagaccccc ccctgctgga atccgatggc agcttctgcc tgagcagccg gctgcgggtg 900

gacaagtcca gatggcagca ggggaatgtc ttttcctgct ccgtcatgca tgaagccctc 960

cacaatcatt atacacagaa aagcctgagc ctgagccccg gcaag 1005

<210> 12
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Human IGHG1 Fc chain

<400> 12

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 13
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CH3-BT alpha domain

<400> 13

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1               5                   10                  15

Glu Leu Thr Lys Asn Gln Val Lys Leu Val Cys Leu Val Thr Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

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

Ser Leu Val Ser Trp Leu Asn Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95
```

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 14
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CH3-BT beta domain with substitution F405A

<400> 14

Gly Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu Val Thr Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser Asp Gly Ser Phe
50 55 60

Ala Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 15
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CH3-BT beta domain

<400> 15

Gly Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu Val Thr Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser Asp Gly Ser Phe
50 55 60

Cys Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 16
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CH3-BT beta domain with substitution F405S

<400> 16

Gly Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu Val Thr Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser Asp Gly Ser Phe
50 55 60

Ser Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 17
<211> 236
<212> PRT
<213> Artificial

<220>
<223> BT beta (F405A) HA chain

<400> 17

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val
        115                 120                 125

Ala Thr Phe Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Asp Pro Pro
                165                 170                 175

Leu Leu Glu Ser Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
225                 230                 235
```

<210> 18
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc (BTA)-Y407V-K409W

<400> 18

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Trp Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 19
<211> 227
<212> PRT
<213> Artificial

<220>

<223> Fc (BTA)-K392Y-K409W

<400> 19

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Tyr Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Trp Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 20
<211> 227

<212> PRT
<213> Artificial

<220>
<223> Fc (BTA)-T366V-K409W

<400> 20

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Trp Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 21
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc (BTA)-Y407V-K409W-T411N

<400> 21

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Trp Leu Asn Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
```

Pro Gly Lys
225

<210> 22
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc (BTA)-F405S-Y407V-K409W-T411N

<400> 22

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 23
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc (BTA)-S364K-T366V-K370T-K392Y-K409W-T411N

<400> 23

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Lys
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Tyr Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Trp Leu Asn Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 24
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc (BTB)-F405A-Y407S

<400> 24

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Ala Leu Ser Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335


<210>  25
<211>  335
<212>  PRT
<213>  Artificial

<220>
<223>  VL-Fc (BTB)-F405A-K409R

<400>  25

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320
```

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 26
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc (BTB)-Y407S-K409R

<400> 26

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

```
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 27
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc (BTB)-K409R-T411R

<400> 27

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Asn
                85                  90                  95
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 28
<211> 335
<212> PRT
<213> Artificial

<220>

<223> VL-Fc (BTB)-F405A-Y407S-K409R

<400> 28

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255
```

```
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 29
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc (BTB)-F405A-Y407S-K409R-T411R

<400> 29

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140
```

```
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Ser Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 30
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc-T366W (knob)

<400> 30

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 31
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc-T366S-L368A-Y407V (hole)

<400> 31

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

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270
```

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 32
<211> 87
<212> PRT
<213> Artificial

<220>
<223> T cell receptor constant domain delta [Homo sapiens]

<400> 32

Arg Ser Gln Pro His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly
1 5 10 15

Thr Asn Val Ala Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg
20 25 30

Ile Asn Leu Val Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile
35 40 45

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

Glu Asp Ser Asn Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr
65 70 75 80

Val His Ser Thr Asp Phe Glu
85

<210> 33
<211> 101
<212> PRT
<213> Artificial

<220>
<223> T cell receptor constant domain gamma [Homo sapiens]

<400> 33

Val Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys
1 5 10 15

Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Phe Pro
20 25 30

```
Asp Val Ile Lys Ile His Trp Glu Glu Lys Lys Ser Asn Thr Ile Leu
        35                  40                  45

Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys
    50                  55                  60

Phe Ser Trp Leu Thr Val Pro Glu Lys Ser Leu Asp Lys Glu His Arg
65                  70                  75                  80

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

Ile Phe Pro Pro Ile
            100
```

<210> 34
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT delta chain

<400> 34

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Met Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Asn
    130                 135                 140
```

```
Leu Ala Cys Leu Val Lys Glu Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Phe Thr Ala Pro Pro
                165                 170                 175

Val Leu Ser Ser Asp Gly Ser Phe Asn Leu Val Ser Leu Leu Lys Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 35
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT gamma chain

<400> 35

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Lys Val
        115                 120                 125
```

```
Thr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Gly Pro Pro
                165                 170                 175

Met Leu Asp Ser Asp Gly Ser Phe Met Leu Phe Ser Trp Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 36
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-BT gamma chain

<400> 36

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Lys Val Thr Thr Leu Pro
225                 230                 235                 240

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr Leu Leu Cys Leu
                245                 250                 255

Val Glu Lys Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Gly Pro Pro Met Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Met Leu Phe Ser Trp Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 37
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the engineered CH3 domain of the BT delta chain

<400> 37
ggccagccca gagaacccca ggtgtacacc atgcccccca gcagggacga gctgaccaag 60

aaccaggtca acctggcctg cctggtcaaa gagttctacc ccagcgatat cgccgtggaa 120

tgggagagca acggccagcc tgagaacaac tacttcaccg cccctcccgt gctgagcagc 180

gacggcagct tcaacctggt gtccctgctg aaggtggaca agagccggtg gcagcagggc 240

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 300

ctgagcctga gccccggaaa g 321

<210> 38
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the engineered CH3 domain of the BT gamma chain

<400> 38
ggccagcccc gcgagcccaa agtgacaacc ctgcccccca gccgggacga gctgaccaag 60

aatcaggtca cactgctgtg cctggtggaa aagttctacc ccagcgatat cgccgtggaa 120

tgggagagca acggccagcc cgagaacaac tacaagaccg gccctcccat gctggacagc 180

gacggcagct tcatgctgtt cagctggctg accgtggaca agagccggtg gcagcagggc 240

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 300

ctgagcctga gccccggaaa g 321

<210> 39
<211> 98
<212> PRT
<213> Artificial

<220>
<223> CH1 delta domain

<400> 39

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Met Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Asn Leu Ala Cys Leu Val Lys Glu Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Val Ser Leu Val Lys Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 40
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CK gamma domain

<400> 40

Arg Thr Val Ala Ala Pro Lys Val Thr Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Gly Val Met Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Met Leu Phe Ser Trp Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 41
<211> 461
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hCD19)-CH1 delta-BT beta c-myc chain

<400> 41

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Ser Leu Pro Asp Tyr
20 25 30

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

```
Ala Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys
    50                  55                  60

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

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

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp 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 Met Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Asn
    130                 135                 140

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

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

Leu Ser Ser Ser Gly Leu Tyr Asn Leu Val Ser Leu Val Lys 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 Glu Val Ala
            340                 345                 350

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

Val Cys Leu Val Thr 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 Asp Pro Pro Leu
385                 390                 395                 400

Leu Glu Ser Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg 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 Lys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
    450                 455                 460
```

<210> 42
<211> 214
<212> PRT
<213> Artificial

<220>
<223> VL(anti-hCD19)-CK gamma chain

<400> 42

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Ile Lys Leu Leu Ile
        35                  40                  45

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

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Ala Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Thr Val Leu Cys Leu Leu Glu Lys 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 Gly Val Met Glu Gln Asp Ser Lys Asp Ser Thr Tyr Met Leu Phe
                165                 170                 175

Ser Trp 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> 43
<211> 1383
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VH(anti-hCD19)-CH1 delta-BT beta c-myc chain

<400> 43

```
caggtccagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cctctggcgt gagcctgccc gactacggcg tgagctgggt ccgccaggct    120

ccaggcaagg ggctggagtg ggtggcagtg atctggggct ccgagacaac ctactacaac    180

agcgccctga agagccgatt caccatctcc agagacaatt ccaagaacac gctgtatttg    240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgaa gcactactac    300

tacggcggca gctacgccat ggactactgg ggccagggaa ccctggtcac cgtctcctca    360

gcgtcgacca agggccccag cgtgttcccg atggccccca gcagcaagag caccagcggc    420

ggcacagcca acctggcctg cctggtgaag gagtacttcc ccgagcccgt gaccgtgtcc    480

tggaactctg gagccctgac ctccggcgtg ttcaccgccc ccgccgtgct ctccagcagc    540
```

ggcctgtaca acctggtgag cctcgtgaag gtgcccagca gcagcctggg aacccagacc 600

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc 660

aagagctgcg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag gacagcccag ggaacctgag gtggccacat tcccacctag ccgggacgag 1080

ctgacaaaaa atcaggtcac cctcgtctgt ctcgtgaccg gcttttaccc ttccgacatt 1140

gccgtggaat gggaatccaa tgggcagccc gagaacaatt acaagacaga ccccccccctg 1200

ctggaatccg atggcagctt cgccctgagc agccggctgc gggtggacaa gtccagatgg 1260

cagcagggga atgtcttttc ctgctccgtc atgcatgaag ccctccacaa tcattataca 1320

cagaaaagcc tgagcctgtc tcctggcaag gaacaaaaac tcatctcaga agaggatctg 1380

aat 1383

<210> 44
<211> 642
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VL(anti-hCD19)-CK gamma chain

<400> 44
gatattcaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagcca ggacatcagc aagtacctga actggtatca gcagaaacca 120

gggaaagcca tcaagctcct gatctatcac accagccggc tgcacagcgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcagcaa ggcgccacac tgccctacac cttcggccct 300

gggaccaaag tggatatcaa acgtacggtg gccgctccca aggtgaccat cttcccccc 360

agcgacgagc agctgaagag cggcaccgcc accgtgctgt gcctgctgga gaagttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tccagagcgg caacagccag 480

gaaggcgtca tggagcagga cagcaaggac tccacctaca tgctgttcag ctggctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gc 642

<210> 45
<211> 294

<212> DNA
<213> Artificial

<220>
<223> cDNA coding the CH1 delta domain

<400> 45
gcgtcgacca agggccccag cgtgttcccg atggccccca gcagcaagag caccagcggc 60

ggcacagcca acctggcctg cctggtgaag gagtacttcc ccgagcccgt gaccgtgtcc 120

tggaactctg gagccctgac ctccggcgtg ttcaccgccc ccgccgtgct ctccagcagc 180

ggcctgtaca acctggtgag cctcgtgaag gtgcccagca gcagcctggg aacccagacc 240

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtg 294

<210> 46
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the CK gamma domain

<400> 46
cgtacggtgg ccgctcccaa ggtgaccatc ttccccccca gcgacgagca gctgaagagc 60

ggcaccgcca ccgtgctgtg cctgctggag aagttctacc cccgggaggc caaggtgcag 120

tggaaggtgg acaacgccct ccagagcggc aacagccagg aaggcgtcat ggagcaggac 180

agcaaggact ccacctacat gctgttcagc tggctgaccc tgagcaaggc cgactacgag 240

aagcacaagg tgtacgcctg cgaggtgacc caccagggcc tgtccagccc cgtgaccaag 300

agcttcaacc ggggcgagtg c 321

<210> 47
<211> 107
<212> PRT
<213> Artificial

<220>
<223> human CH3 (isotype gamma 1) constant domain

<400> 47

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 48
<211> 98
<212> PRT
<213> Artificial

<220>
<223> CH13 domain

<400> 48

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

Glu Thr Ser Gly Gly Gln Ala Ser Leu Thr Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Tyr Ser Lys Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 49
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CK3 domain

<400> 49

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

Glu Leu Lys Ser Gly Thr Ala Ser Val Thr Cys Leu Leu Lys Asn Phe
20 25 30

```
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Lys Glu Thr Val Val Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
```

<210> 50
<211> 461
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hCD19)-CH13-BT beta c-myc chain

<400> 50

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Ser Leu Pro Asp Tyr
            20                  25                  30

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

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

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

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

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

Tyr Pro Leu Ala Pro Ser Ser Asp Glu Thr Ser Gly Gly Gln Ala Ser
    130                 135                 140
```

```
Leu Thr 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 Lys Thr Thr Pro Ala Val
                165                 170                 175

Leu Asp Ser Ser Gly Leu Tyr Phe Leu Tyr Ser Lys 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 Glu Val Ala
            340                 345                 350

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

Val Cys Leu Val Thr 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 Asp Pro Pro Leu
385                 390                 395                 400
```

Leu Glu Ser Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg 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 Lys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
450 455 460

<210> 51
<211> 214
<212> PRT
<213> Artificial

<220>
<223> VL(anti-hCD19)-CK3 chain

<400> 51

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Ile Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Ala Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Thr Cys Leu Leu Lys 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 Lys
145 150 155 160

Glu Thr Val Val Glu Gln Asp Ser Lys Asp Ser Thr Tyr Phe Leu Tyr
165 170 175

Ser Lys 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> 52
<211> 1383
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VH(anti-hCD19)-CH13-BT beta c-myc chain

<400> 52
caggtccagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggcgt gagcctgccc gactacggcg tgagctgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtg atctggggct ccgagacaac ctactacaac 180

agcgccctga agagccgatt caccatctcc agagacaatt ccaagaacac gctgtatttg 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgaa gcactactac 300

tacggcggca gctacgccat ggactactgg ggccagggaa ccctggtcac cgtctcctca 360

gccagcacca agggccccca ggtgtaccct ctggccccca gcagcgacga gacaagcgga 420

ggccaggcca gcctgacctg cctggtgaaa gactacttcc ccgagcccgt gaccgtgtcc 480

tggaactctg gcgccctgac cagcggcgtg aaaaccaccc ctgctgtgct ggacagcagc 540

ggcctgtact tcctgtacag caaagtgacc gtgcctagca gcagcctggg cacccagacc 600

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa agtggaaccg 660

aaaagctgcg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag gacagcccag ggaacctgag gtggccacat tcccacctag ccgggacgag 1080

ctgacaaaaa atcaggtcac cctcgtctgt ctcgtgaccg gcttttaccc ttccgacatt 1140

gccgtggaat gggaatccaa tgggcagccc gagaacaatt acaagacaga ccccccccctg 1200

ctggaatccg atggcagctt cgccctgagc agccggctgc gggtggacaa gtccagatgg 1260

cagcagggga atgtcttttc ctgctccgtc atgcatgaag ccctccacaa tcattataca 1320

cagaaaagcc tgagcctgtc tcctggcaag gaacaaaaac tcatctcaga agaggatctg 1380

aat 1383

<210> 53
<211> 642
<212> DNA
<213> Artificial

<220>
<223> cDNA coding VL(anti-hCD19)-CK3 chain

<400> 53
gatattcaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagcca ggacatcagc aagtacctga actggtatca gcagaaacca 120

gggaaagcca tcaagctcct gatctatcac accagccggc tgcacagcgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcagcaa ggcgccacac tgccctacac cttcggccct 300

gggaccaaag tggatatcaa aagaaccgtg gctgctcctc aggtgtacat cctgcctccc 360

agcgacgatg agctgaagtc tggcaccgcc agcgtgacat gtctgctgaa gaacttctac 420

ccccgcgagg ccaaggtgca gtggaaagtg gacaacgccc tgcagagcgg caacagcaaa 480

gaaaccgtgg tggaacagga cagcaaggac tccacctact ttctgtactc caagctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgagcagcc ccgtgaccaa gagcttcaac cggggcgagt gc 642

<210> 54
<211> 294
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the CH13 domain

<400> 54
gccagcacca agggccccca ggtgtaccct ctggccccca gcagcgacga gacaagcgga 60

ggccaggcca gcctgacctg cctggtgaaa gactacttcc ccgagcccgt gaccgtgtcc 120

tggaactctg gcgccctgac cagcggcgtg aaaaccaccc ctgctgtgct ggacagcagc 180

ggcctgtact tcctgtacag caaagtgacc gtgcctagca gcagcctggg cacccagacc 240

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa agtg 294

<210> 55
<211> 321
<212> DNA
<213> Artificial

<220>

<223> cDNA coding the CK3 domain

<400> 55
agaaccgtgg ctgctcctca ggtgtacatc ctgcctccca gcgacgatga gctgaagtct 60

ggcaccgcca gcgtgacatg tctgctgaag aacttctacc cccgcgaggc caaggtgcag 120

tggaaagtgg acaacgccct gcagagcggc aacagcaaag aaaccgtggt ggaacaggac 180

agcaaggact ccacctactt tctgtactcc aagctgaccc tgagcaaggc cgactacgag 240

aagcacaagg tgtacgcctg cgaagtgacc caccagggcc tgagcagccc cgtgaccaag 300

agcttcaacc ggggcgagtg c 321

<210> 56
<211> 1347
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VH(anti-EGFR)-CH1-BT alpha chain

<400> 56
caggtccagc tgaagcagag cggcccaggc ctcgtgcagc cctctcagtc tctcagcatc 60

acctgcaccg tgtccggctt cagcctgacc aactacggcg tgcactgggt ccgccagagc 120

cccggcaagg gcctggaatg gctgggcgtg atctggtccg gcggcaacac cgactacaac 180

acccccttca ccagcaggct gtccatcaac aaggacaaca gcaagagcca ggtgttcttc 240

aagatgaaca gcctgcagag caacgacacc gccatctact actgcgccag ggctctgacc 300

tactacgact acgagttcgc ctactgggga cagggcaccc tggtcactgt ctccgccgcc 360

agcaccaagg gccccagcgt gttccccctg gcccccagca gcaagagcac ctctggcggc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg agcccgtgac agtgtcctgg 480

aacagcggag ccctgacctc cggcgtccac accttccccg ccgtgctgca gagcagcggc 540

ctgtacagcc tgagcagcgt ggtcacagtg ccctctagca gcctcggcac ccagacctac 600

atctgcaacg tgaaccacaa gcccagcaac accaaggtgg acaagaaggt ggagcccaag 660

agctgcgaca aaactcacac atgccccccc tgccctgccc ctgagctgct gggcggaccc 720

tccgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagccg gacccccgag 780

gtgacctgcg tggtggtgga cgtgagccac gaggaccctg aggtgaagtt caattggtac 840

gtggacggcg tggaggtgca caacgccaag accaagcccc gggaggaaca gtacaacagc 900

acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 960

tacaagtgca aggtctccaa caaggccctg cctgccccca tcgagaaaac catctccaaa 1020

gccaaaggcc agcccagaga accccaggtg tacaccctgc cccccagcag agatgagctg 1080

accaagaacc aggtcaagct cgtgtgcctg gtcaccggct tctaccccag cgatatcgcc 1140

gtggagtggg agagcaacgg ccagcctgaa aacaactact acaccacccc ccctgtgctg 1200

gacagcgacg gcagcttcag cctggtgtcc tggctgaacg tggacaagag ccggtggcag 1260

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctga gcctgtctcc tggcaag 1347

<210> 57
<211> 642
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VL(anti-EGFR)-CK chain

<400> 57
gacatcctgc tgacccagag ccccgtgatc ctgagcgtgt ccccaggcga gagggtgtcc 60

ttcagctgca gagccagcca gagcatcggc accaacatcc actggtatca gcagaggacc 120

aacggcagcc ccaggctgct gatcaagtac gccagcgagt ccatcagcgg catccccagc 180

aggttcagcg gcagcggctc cggcaccgac ttcaccctga gcatcaacag cgtggagagc 240

gaggacatcg ccgactacta ctgccagcag aacaacaact ggcccaccac cttcggagcc 300

ggcaccaagc tggaactgaa gaggaccgtg gctgccccca gcgtgttcat cttcccccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtggtct gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtcac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 58
<211> 1422
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the scFv(anti-HER2)-BT beta chain

<400> 58
gaggtgcagc tggtcgagtc tggcggcgga ctggtgcagc ctggcggctc cctgcggctg 60

tcctgcgccg cctccggctt caacatcaag gacacctaca tccactgggt gcggcaggcc 120

cctggcaagg gcctggagtg ggtggcccgg atctacccta ccaacggcta caccagatac 180

gccgactccg tgaagggccg gttcaccatc tccgccgaca cctccaagaa caccgcctac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgctc cagatgggga 300

ggagatggct tctacgccat ggactactgg ggccagggca ccctggtgac cgtgtcctcc 360

ggtggcggtg gcagcggcgg tggtggttcc ggaggcggcg gttctgacat ccagatgacc 420

cagtcccccct ccagcctgtc tgcctccgtg ggcgaccggg tgaccatcac ctgccgggcc 480

tcccaggacg tgaacaccgc cgtggcctgg tatcagcaga agcctggcaa ggcccctaag 540

ctgctgatct actccgcctc cttcctgtac tccggcgtgc cttcccggtt ctccggctcc 600

cggtccggca ccgacttcac cctgaccatc tcctccctgc agcctgagga cttcgccacc 660

tactactgcc agcagcacta caccacccct cctaccttcg gccagggcac caaggtggag 720

atcaagggag gaggagggtc agacaaaact cacacttgcc caccgtgccc agcacctgaa 780

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 840

tcccggaccc ctgaggtcac ctgcgtggtg gtggacgtga gccacgagga ccctgaggtg 900

aagttcaatt ggtacgtgga cggcgtggag gtgcacaacg ccaagaccaa gccccgggag 960

gaacagtaca acagcaccta ccgggtggtg tccgtgctga ccgtgctgca ccaggactgg 1020

ctgaacggca aggaatacaa gtgcaaggtc tccaacaagg ccctgcctgc ccccatcgaa 1080

aagaccatca gcaaggccaa gggacagccc agggaacctg aggtggccac attcccacct 1140

agccgggacg agctgacaaa aaatcaggtc accctcgtct gtctcgtgac cggcttttac 1200

ccttccgaca ttgccgtgga atgggaatcc aatgggcagc ccgagaacaa ttacaagaca 1260

gacccccccc tgctggaatc cgatggcagc ttctgcctga gcagccggct gcgggtggac 1320

aagtccagat ggcagcaggg gaatgtcttt tcctgctccg tcatgcatga agccctccac 1380

aatcattata cacagaaaag cctgagcctg agccccggca ag 1422

<210> 59
<211> 449
<212> PRT
<213> Artificial

<220>
<223> VH(anti-EGFR)-CH1-BT alpha chain

<400> 59

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

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

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

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val Asp Lys
                405                 410                 415

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

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

Lys
```

<210> 60
<211> 214
<212> PRT
<213> Artificial

<220>
<223> VL(anti-EGFR)-CK chain

<400> 60

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

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

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

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu 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> 61
<211> 474
<212> PRT
<213> Artificial

<220>
<223> scFv(anti-HER2)-BT beta chain

<400> 61

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30

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

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

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125
```

```
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

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

Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro Pro Ser Arg Asp Glu
    370                 375                 380

Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu Val Thr Gly Phe Tyr
385                 390                 395                 400
```

```
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser Asp Gly Ser Phe Ala
            420                 425                 430

Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  62
<211>  851
<212>  PRT
<213>  Artificial

<220>
<223>  human EGFR-Fc

<400>  62

Leu Glu Glu Lys Lys Val Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln
1               5                   10                  15

Leu Gly Thr Phe Glu Asp His Phe Leu Ser Leu Gln Arg Met Phe Asn
            20                  25                  30

Asn Cys Glu Val Val Leu Gly Asn Leu Glu Ile Thr Tyr Val Gln Arg
        35                  40                  45

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

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

Gln Ile Ile Arg Gly Asn Met Tyr Tyr Glu Asn Ser Tyr Ala Leu Ala
                85                  90                  95

Val Leu Ser Asn Tyr Asp Ala Asn Lys Thr Gly Leu Lys Glu Leu Pro
            100                 105                 110

Met Arg Asn Leu Gln Glu Ile Leu His Gly Ala Val Arg Phe Ser Asn
        115                 120                 125

Asn Pro Ala Leu Cys Asn Val Glu Ser Ile Gln Trp Arg Asp Ile Val
    130                 135                 140
```

```
Ser Ser Asp Phe Leu Ser Asn Met Ser Met Asp Phe Gln Asn His Leu
145                 150                 155                 160

Gly Ser Cys Gln Lys Cys Asp Pro Ser Cys Pro Asn Gly Ser Cys Trp
                165                 170                 175

Gly Ala Gly Glu Glu Asn Cys Gln Lys Leu Thr Lys Ile Ile Cys Ala
            180                 185                 190

Gln Gln Cys Ser Gly Arg Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys
        195                 200                 205

His Asn Gln Cys Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys
    210                 215                 220

Leu Val Cys Arg Lys Phe Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys
225                 230                 235                 240

Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn
                245                 250                 255

Pro Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro
            260                 265                 270

Arg Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly
        275                 280                 285

Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys
    290                 295                 300

Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu
305                 310                 315                 320

Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys
                325                 330                 335

Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe
            340                 345                 350

Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu
        355                 360                 365

Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln
    370                 375                 380

Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu
385                 390                 395                 400
```

```
Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val
                405                 410                 415

Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile
            420                 425                 430

Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala
        435                 440                 445

Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr
    450                 455                 460

Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
465                 470                 475                 480

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
                485                 490                 495

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
            500                 505                 510

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
        515                 520                 525

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
    530                 535                 540

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
545                 550                 555                 560

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
                565                 570                 575

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
            580                 585                 590

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
        595                 600                 605

Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Gly Gly Gly
    610                 615                 620

Gly Gly Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
625                 630                 635                 640

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                645                 650                 655

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            660                 665                 670
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        675                 680                 685

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    690                 695                 700

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
705                 710                 715                 720

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                725                 730                 735

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            740                 745                 750

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        755                 760                 765

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    770                 775                 780

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
785                 790                 795                 800

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                805                 810                 815

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            820                 825                 830

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        835                 840                 845

Pro Gly Lys
    850
```

<210> 63
<211> 862
<212> PRT
<213> Artificial

<220>
<223> human HER2-Fc

<400> 63

```
Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser
1               5                   10                  15

Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln
            20                  25                  30
```

```
Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser
        35                  40                  45

Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile
    50                  55                  60

Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val
65                  70                  75                  80

Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp
                85                  90                  95

Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro
            100                 105                 110

Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
        115                 120                 125

Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr
    130                 135                 140

Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr
145                 150                 155                 160

Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met
                165                 170                 175

Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser
            180                 185                 190

Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro
        195                 200                 205

Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly
    210                 215                 220

Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly
225                 230                 235                 240

Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr
                245                 250                 255

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

Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser
        275                 280                 285
```

```
Cys Thr Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp
    290                 295                 300

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

Tyr Gly Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser
                325                 330                 335

Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu
            340                 345                 350

Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala
        355                 360                 365

Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile
    370                 375                 380

Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu
385                 390                 395                 400

Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn
                405                 410                 415

Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly
            420                 425                 430

Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His
        435                 440                 445

Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe
    450                 455                 460

Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp
465                 470                 475                 480

Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly
                485                 490                 495

His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe
            500                 505                 510

Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu
        515                 520                 525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
    530                 535                 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545                 550                 555                 560
```

```
Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
                565                 570                 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
            580                 585                 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
        595                 600                 605

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln
    610                 615                 620

Arg Ala Ser Pro Leu Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
625                 630                 635                 640

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
                645                 650                 655

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            660                 665                 670

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        675                 680                 685

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    690                 695                 700

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
705                 710                 715                 720

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                725                 730                 735

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            740                 745                 750

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        755                 760                 765

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    770                 775                 780

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
785                 790                 795                 800

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                805                 810                 815
```

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
820 825 830

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
835 840 845

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
850 855 860

<210> 64
<211> 2577
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the human EGFR-Fc

<400> 64
ctggaggaaa agaaagtttg ccaaggcacg agtaacaagc tcacgcagtt gggcactttt 60

gaagatcatt ttctcagcct ccagaggatg ttcaataact gtgaggtggt ccttgggaat 120

ttggaaatta cctatgtgca gaggaattat gatctttcct tcttaaagac catccaggag 180

gtggctggtt atgtcctcat tgccctcaac acagtggagc gaattccttt ggaaaacctg 240

cagatcatca gaggaaatat gtactacgaa aattcctatg ccttagcagt cttatctaac 300

tatgatgcaa ataaaaccgg actgaaggag ctgcccatga gaaatttaca ggaaatcctg 360

catggcgccg tgcggttcag caacaaccct gccctgtgca acgtggagag catccagtgg 420

cgggacatag tcagcagtga ctttctcagc aacatgtcga tggacttcca gaaccacctg 480

ggcagctgcc aaaagtgtga tccaagctgt cccaatggga gctgctgggg tgcaggagag 540

gagaactgcc agaaactgac caaaatcatc tgtgcccagc agtgctccgg gcgctgccgt 600

ggcaagtccc ccagtgactg ctgccacaac cagtgtgctg caggctgcac aggcccccgg 660

gagagcgact gcctggtctg ccgcaaattc cgagacgaag ccacgtgcaa ggacacctgc 720

cccccactca tgctctacaa ccccaccacg taccagatgg atgtgaaccc cgagggcaaa 780

tacagctttg gtgccacctg cgtgaagaag tgtccccgta attatgtggt gacagatcac 840

ggctcgtgcg tccgagcctg tggggccgac agctatgaga tggaggaaga cggcgtccgc 900

aagtgtaaga agtgcgaagg gccttgccgc aaagtgtgta acggaatagg tattggtgaa 960

tttaaagact cactctccat aaatgctacg aatattaaac acttcaaaaa ctgcacctcc 1020

atcagtggcg atctccacat cctgccggtg gcatttaggg gtgactcctt cacacatact 1080

cctcctctgg atccacagga actggatatt ctgaaaaccg taaaggaaat cacagggttt 1140

ttgctgattc aggcttggcc tgaaaacagg acggacctcc atgcctttga gaacctagaa 1200

atcatacgcg gcaggaccaa gcaacatggt cagttttctc ttgcagtcgt cagcctgaac 1260

ataacatcct tgggattacg ctcccctcaag gagataagtg atggagatgt gataatttca 1320

ggaaacaaaa atttgtgcta tgcaaataca ataaactgga aaaaactgtt tgggacctcc 1380

ggtcagaaaa ccaaaattat aagcaacaga ggtgaaaaca gctgcaaggc cacaggccag 1440

gtctgccatg ccttgtgctc ccccgagggc tgctggggcc cggagcccag ggactgcgtc 1500

tcttgccgga atgtcagccg aggcagggaa tgcgtggaca agtgcaacct tctggagggt 1560

gagccaaggg agtttgtgga gaactctgag tgcatacagt gccacccaga gtgcctgcct 1620

caggccatga acatcacctg cacaggacgg ggaccagaca actgtatcca gtgtgcccac 1680

tacattgacg gcccccactg cgtcaagacc tgcccggcag gagtcatggg agaaaacaac 1740

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cccgaggtga cctgcgtggt ggtggacgtg agccacgagg accctgaggt gaagttcaat 2040

tggtacgtgg acggcgtgga ggtgcacaac gccaagacca agccccggga ggagcagtac 2100

aactccacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 2160

aaggaataca agtgcaaggt gtccaacaag gccctgcctg cccccatcga aaagaccatc 2220

agcaaggcca agggccagcc cagggagccc caggtgtaca ccctgccccc cagccgggag 2280

gagatgacca agaaccaggt gtccctgacc tgcctggtga agggcttcta ccccagcgac 2340

atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cacccccccct 2400

gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagagcagg 2460

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 2520

acccagaaga gcctgagcct gtcccccggc aagagcgccc atcatcacca tcaccat 2577

<210> 65
<211> 2586
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the human HER2-Fc

<400> 65
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ctggacatgc tccgccacct ctaccagggc tgccaggtgg tgcagggaaa cctggaactc 120

acctacctgc ccaccaatgc cagcctgtcc ttcctgcagg atatccagga ggtgcagggc 180

tacgtgctca tcgctcacaa ccaagtgagg caggtcccac tgcagaggct gcggattgtg 240

cgaggcaccc agctctttga ggacaactat gccctggccg tgctagacaa tggagacccg 300

ctgaacaata ccacccctgt cacaggggcc tccccaggag gcctgcggga gctgcagctt 360

cgaagcctca cagagatctt gaaaggaggg gtcttgatcc agcggaaccc ccagctctgc 420

taccaggaca cgattttgtg gaaggacatc ttccacaaga acaaccagct ggctctcaca 480

ctgatagaca ccaaccgctc tcgggcctgc cacccctgtt ctccgatgtg taagggctcc 540

cgctgctggg gagagagttc tgaggattgt cagagcctga cgcgcactgt ctgtgccggt 600

ggctgtgccc gctgcaaggg gccactgccc actgactgct gccatgagca gtgtgctgcc 660

ggctgcacgg gccccaagca ctctgactgc ctggcctgcc tccacttcaa ccacagtggc 720

atctgtgagc tgcactgccc agccctggtc acctacaaca cagacacgtt tgagtccatg 780

cccaatcccg agggccggta tacattcggc gccagctgtg tgactgcctg tccctacaac 840

tacctttcta cggacgtggg atcctgcacc ctcgtctgcc ccctgcacaa ccaagaggtg 900

acagcagagg atggaacaca gcggtgtgag aagtgcagca agccctgtgc ccgagtgtgc 960

tatggtctgg gcatggagca cttgcgagag gtgagggcag ttaccagtgc caatatccag 1020

gagtttgctg gctgcaagaa gatctttggg agcctggcat ttctgccgga gagctttgat 1080

ggggacccag cctccaacac tgccccgctc cagccagagc agctccaagt gtttgagact 1140

ctggaagaga tcacaggtta cctatacatc tcagcatggc cggacagcct gcctgacctc 1200

agcgtcttcc agaacctgca agtaatccgg ggacgaattc tgcacaatgg cgcctactcg 1260

ctgaccctgc aagggctggg catcagctgg ctggggctgc gctcactgag ggaactgggc 1320

agtggactgg ccctcatcca ccataacacc cacctctgct tcgtgcacac ggtgccctgg 1380

gaccagctct ttcggaaccc gcaccaagct ctgctccaca ctgccaaccg gccagaggac 1440

gagtgtgtgg gcgagggcct ggcctgccac cagctgtgcg cccgagggca ctgctggggt 1500

ccagggccca cccagtgtgt caactgcagc cagttccttc ggggccagga gtgcgtggag 1560

gaatgccgag tactgcaggg gctccccagg gagtatgtga atgccaggca ctgtttgccg 1620

tgccaccctg agtgtcagcc ccagaatggc tcagtgacct gttttggacc ggaggctgac 1680

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ggtgtgaaac ctgacctctc ctacatgccc atctggaagt ttccagatga ggagggcgca 1800

tgccagcctt gccccatcaa ctgcacccac tcctgtgtgg acctggatga caagggctgc 1860

cccgccgagc agagagccag ccctctgacg gagcccaaga gctgcgacaa gacccacacc 1920

tgcccccccc gccctgcccc tgagctgctg ggcggaccca gcgtgttcct gttccccccc 1980

aagcccaagg acaccctgat gatcagccgg acccccgagg tgacctgcgt ggtggtggac 2040

gtgagccacg aggaccctga ggtgaagttc aattggtacg tggacggcgt ggaggtgcac 2100

aacgccaaga ccaagccccg ggaggagcag tacaactcca cctaccgggt ggtgtccgtg 2160

ctgaccgtgc tgcaccagga ctggctgaac ggcaaggaat acaagtgcaa ggtgtccaac 2220

aaggccctgc ctgccccat cgaaaagacc atcagcaagg ccaagggcca gcccagggag 2280

ccccaggtgt acaccctgcc ccccagccgg gaggagatga ccaagaacca ggtgtccctg 2340

acctgcctgg tgaagggctt ctaccccagc gacatcgccg tggagtggga gagcaacggc 2400

cagcccgaga acaactacaa gaccaccccc cctgtgctgg acagcgacgg cagcttcttc 2460

ctgtacagca agctgaccgt ggacaagagc aggtggcagc agggcaacgt gttcagctgc 2520

agcgtgatgc acgaggccct gcacaaccac tacacccaga agagcctgag cctgtccccc 2580

ggcaag 2586

<210> 66
<211> 1365
<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VH(anti-hVLA2)-CH1-BT alpha His chain

<400> 66
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acctgcaccg tgagcggctt cagcctgacc aactacggca tccactggat caggcagccc 120

ccaggcaagg gcctggagtg gctgggcgtg atctgggcca ggggcttcac caactacaac 180

agcgccctga tgagcaggct gaccatcagc aaggacaaca gcaagaacca ggtgtccctg 240

aagctgtcca gcgtgacagc cgccgacacc gccgtgtact actgcgccag ggccaacgac 300

ggcgtgtact acgccatgga ctactggggc cagggcaccc tggtcaccgt cagctcagcg 360

tcgaccaagg gccccagcgt gttcccgcta gcccccagca gcaagagcac cagcggcggc 420

acagccgccc tgggctgcct ggtgaaggac tacttccccg agcccgttac cgtgtcctgg 480

aactctggag ccctgacctc cggcgtgcac accttccccg ccgtgctcca gagcagcggc 540

ctgtacagcc tgagcagcgt ggtgacagtg cccagcagca gcctgggaac ccagacctac 600

atctgcaacg tgaaccacaa gcccagcaac accaaggtgg acaagaaggt ggagcccaag 660

agctgcgaca aaactcacac atgccccccc tgccctgccc ctgagctgct gggcggaccc 720

tccgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagccg gacccccgag 780

gtgacctgcg tggtggtgga cgtgagccac gaggaccctg aggtgaagtt caattggtac 840

gtggacggcg tggaggtgca caacgccaag accaagcccc gggaggaaca gtacaacagc 900

acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 960

tacaagtgca aggtctccaa caaggccctg cctgccccca tcgagaaaac catctccaaa 1020

gccaaaggcc agcccagaga accccaggtg tacaccctgc cccccagcag agatgagctg 1080

accaagaacc aggtcaagct cgtgtgcctg gtcaccggct tctaccccag cgatatcgcc 1140

gtggagtggg agagcaacgg ccagcctgaa aacaactact acaccacccc ccctgtgctg 1200

gacagcgacg gcagcttcag cctggtgtcc tggctgaacg tggacaagag ccggtggcag 1260

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctga gcctgtctcc tggcaagcat caccatcacc atcac 1365

<210> 67
<211> 639

<212> DNA
<213> Artificial

<220>
<223> cDNA coding the VL(anti-hVLA2)-CK chain

<400> 67
gacttcgtga tgacccagag ccccgccttc ctgagcgtga ccccaggcga gaaggtgacc 60

atcacctgca gcgcccagag cagcgtgaac tacatccact ggtaccagca gaagcccgac 120

caggccccca agaagctgat ctacgacacc agcaagctgg ccagcggcgt gcccagcagg 180

ttcagcggca gcggctccgg caccgactac accttcacca tcagcagcct ggaggccgag 240

gacgccgcca cctactactg ccagcagtgg accaccaacc ccctgacctt cggccagggc 300

accaaggtgg agatcaagag gaccgtggcc gcccccagcg tgttcatctt cccccccagc 360

gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc 420

cgggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag 480

agcgtcaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 540

agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 600

tccagccccg tgaccaagag cttcaacagg ggcgagtgc 639

<210> 68
<211> 455
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hVLA2)-CH1-BT alpha His chain

<400> 68

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

Gly Val Ile Trp Ala Arg Gly Phe Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

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

Arg Ala Asn Asp Gly Val Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val Asp Lys
                405                 410                 415

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

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

Lys His His His His His His
    450                 455
```

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

<220>
<223> VL(anti-hVLA2)-CK chain

<400> 69

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

Glu Lys Val Thr Ile Thr Cys Ser Ala Gln Ser Ser Val Asn Tyr Ile
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ala Pro Lys Lys Leu Ile Tyr
        35                  40                  45

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

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

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

Phe Gly Gln Gly Thr Lys Val 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> 70
<211> 450
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hCD19)-CH1 delta-BT beta chain

<400> 70

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Ser Leu Pro Asp Tyr
            20                  25                  30

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

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

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

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

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp 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 Met Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Asn
    130                 135                 140

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

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

Leu Ser Ser Ser Gly Leu Tyr Asn Leu Val Ser Leu Val Lys 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 Glu Val Ala
            340                 345                 350

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

Val Cys Leu Val Thr 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 Asp Pro Pro Leu
385                 390                 395                 400
```

```
Leu Glu Ser Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg 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 Lys
    450
```

<210> 71
<211> 445
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hCD19)-CH13-BT beta chain

<400> 71

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Ser Leu Pro Asp Tyr
            20                  25                  30

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

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

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

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

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

Tyr Pro Leu Ala Pro Ser Ser Asp Glu Thr Ser Gly Gly Gln Ala Ser
    130                 135                 140

Leu Thr 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 Lys Thr Thr Pro Ala Val
                165                 170                 175

Leu Asp Ser Ser Gly Leu Tyr Phe Leu Tyr Ser Lys 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 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 Glu Val Ala Thr Phe Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu Val Thr
        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 Asp Pro Pro Leu Leu Glu Ser Asp Gly
385                 390                 395                 400

Ser Phe Ala Leu Ser Ser Arg Leu Arg 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> 72
<211> 449
<212> PRT
<213> Artificial

<220>
<223> VH(anti-hVLA2)-CH1-BT alpha chain

<400> 72

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

Gly Val Ile Trp Ala Arg Gly Phe Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

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

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

Arg Ala Asn Asp Gly Val Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val Asp Lys
                405                 410                 415

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

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

Lys
```

<210> 73
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT alpha IGHG3 chain

<400> 73

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Lys
130 135 140

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

Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Tyr Thr Thr Pro Pro
165 170 175

Met Leu Asp Ser Asp Gly Ser Phe Ser Leu Val Ser Trp Leu Asn Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 74
<211> 227
<212> PRT
<213> Artificial

<220>
<223> BT beta F405A chain

<400> 74

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val
115 120 125

Ala Thr Phe Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Asp Pro Pro
165 170 175

Leu Leu Glu Ser Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 75
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-BT beta F405A chain

<400> 75

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val Ala Thr Phe Pro
225 230 235 240

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr Leu Val Cys Leu
245 250 255

Val Thr Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Asp Pro Pro Leu Leu Glu Ser
275 280 285

Asp Gly Ser Phe Ala Leu Ser Ser Arg Leu Arg Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 76
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CH3-BT alpha IGHG3 domain

<400> 76

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15

Glu Met Thr Lys Asn Gln Val Lys Leu Val Cys Leu Val Thr Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu
35 40 45

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

Ser Leu Val Ser Trp Leu Asn Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 77
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding CH3-BT alpha IGHG3 domain

<400> 77
ggccagccca gagaacccca ggtgtacacc ctgcccccca gccgggaaga gatgaccaag 60

aaccaggtga aactggtgtg cctggtgaca ggcttctacc ccagcgatat cgccgtggaa 120

tgggagagca gcggccagcc tgagaacaac tactacacca ccccccccat gctggacagc 180

gacggcagct tcagcctggt gtcctggctg aacgtggaca agagccggtg gcagcagggc 240

aacatcttca gctgcagcgt gatgcacgag gccctgcaca accggttcac ccagaagtcc 300

ctgagcctga gccccggcaa g 321

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

<220>
<223> CH3 IGHAG domain

<400> 78

Gly Gln Pro Arg Glu Pro Glu Val His Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Arg Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Arg Leu Glu Ser Asp Gly Ser Phe
50 55 60

Ala Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

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

<220>
<223> CH3 IGHGA domain

<400> 79

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Thr Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

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

Phe Leu Tyr Ser Ile Leu Arg Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 80
<211> 227
<212> PRT
<213> Artificial

<220>
<223> Fc IGHAG chain

<400> 80

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Glu Val
        115                 120                 125

His Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Arg Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Arg Leu Glu Ser Asp Gly Ser Phe Ala Leu Thr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 81
<211> 335
<212> PRT
<213> Artificial

<220>
<223> VL-Fc IGHGA chain

<400> 81

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Thr Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser
        275                 280                 285

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 82
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding CH3 IGHAG domain

<400> 82
ggccagccta gagaacctga ggtgcacacc ctgccccca gcagagatga gctgaccaag 60

aaccaggtgt ccctgacctg tctcgtgcgg ggcttctacc cctccgatat cgccgtggaa 120

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccccag actggaaagc 180

gacggcagct ttgccctgac cagcaagctg accgtggaca agagcagatg gcagcagggc 240

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 300

ctgagcctga gccccggcaa g 321

<210> 83
<211> 321
<212> DNA
<213> Artificial

<220>
<223> cDNA coding CH3 IGHGA domain

<400> 83
ggccagccta gagaacccca ggtgtacaca ctgccccca gcagagatga gctgaccaag 60

aaccaagtga ccctgacctg cctcgtgaag ggcttctacc cctccgatat cgccgtggaa 120

tgggagagca acggccagcc cgagaacaac tacctgacct ggccccctgt gctggacagc 180

gacggctcat tcttcctgta cagcatcctg cgggtggaca agagcagatg gcagcagggc 240

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 300

ctgagcctga gccccggcaa g 321

<210> 84
<211> 113
<212> PRT
<213> Artificial

<220>
<223> IGHM CH4 alpha domain

<400> 84

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
1 5 10 15

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

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
35 40 45

Pro Leu Ser Pro Glu Lys Tyr Tyr Thr Ser Ala Pro Met Pro Glu Pro
50 55 60

Gln Ala Pro Gly Arg Tyr Ser Ala Val Ser Trp Leu Asn Val Ser Glu
65 70 75 80

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
85 90 95

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
100 105 110

Lys

<210> 85
<211> 113
<212> PRT
<213> Artificial

<220>
<223> IGHM CH4 beta domain

<400> 85

Gly Val Ala Leu His Arg Pro Glu Val Ala Leu Phe Pro Pro Ala Arg
1 5 10 15

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

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
35 40 45

Pro Leu Ser Pro Glu Lys Tyr Val Thr Asp Ala Pro Leu Pro Glu Pro
50 55 60

Gln Ala Pro Gly Arg Tyr Ala Ala Ser Ser Arg Leu Arg Val Ser Glu
65 70 75 80

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
85 90 95

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
100 105 110

Lys

<210> 86
<211> 339
<212> DNA
<213> Artificial

<220>
<223> cDNA coding IGHM CH4 alpha domain

<400> 86
ggcgtggccc tgcacagacc cgacgtgtac ctgctgcctc ctgccagaga gcagctgaac 60

ctgcgggaaa gcgccaagat cgtgtgtctc gtgaccggct tctcccctgc cgacgtgttc 120

gtgcagtgga tgcagagagg ccagcccctg agccccgaga agtactacac aagcgccccc 180

atgcctgagc cacaggcccc tggaagatac agcgccgtgt cttggctgaa cgtgtccgag 240

gaagagtgga acaccggcga gacatacacc tgtgtggtgg cccatgaggc cctgcccaat 300

agagtgaccg agcggaccgt ggacaagagc accggaaag 339

<210> 87
<211> 339
<212> DNA
<213> Artificial

<220>
<223> cDNA coding IGHM CH4 beta domain

<400> 87
ggcgtggccc tgcacagacc agaggtggcc ctgtttccac ccgccagaga gcagctgaac 60

ctgcgggaaa gcgccaccat cgtgtgtctc gtgaccggct tcagccctgc cgacgtgttc 120

gtgcagtgga tgcagagagg ccagcccctg tcccccgaga aatacgtgac agacgccccc 180

ctgcctgagc cacaggcccc tggaagatat gccgccagca gcagactgcg ggtgtccgag 240

gaagagtgga acaccggcga gacatacacc tgtgtggtgg cccatgaggc cctgcccaat 300

agagtgaccg aacggaccgt ggacaagagc accggcaag 339

<210> 88
<211> 239
<212> PRT
<213> Artificial

<220>
<223> BT alpha IGHM-4 His chain

<400> 88

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Val Ala Leu His Arg Pro Asp
        115                 120                 125

Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser
    130                 135                 140

Ala Lys Ile Val Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe
145                 150                 155                 160

Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Tyr
                165                 170                 175

Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Ser Ala
            180                 185                 190

Val Ser Trp Leu Asn Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr
        195                 200                 205

Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu
    210                 215                 220

Arg Thr Val Asp Lys Ser Thr Gly Lys His His His His His His
225                 230                 235


<210>  89
<211>  341
<212>  PRT
<213>  Artificial

<220>
<223>  VL-BT beta IGHM-4 chain

<400>  89

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
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```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Val Ala Leu His Arg Pro Glu Val Ala Leu Phe
225                 230                 235                 240

Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Val
                245                 250                 255

Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met
            260                 265                 270

Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Asp Ala Pro
        275                 280                 285
```

Leu Pro Glu Pro Gln Ala Pro Gly Arg Tyr Ala Ala Ser Ser Arg Leu
290 295 300

Arg Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val
305 310 315 320

Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp
325 330 335

Lys Ser Thr Gly Lys
340

<210> 90
<211> 110
<212> PRT
<213> Artificial

<220>
<223> IGHE CH4 alpha domain

<400> 90

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
1 5 10 15

Pro Gly Ser Arg Asp Lys Arg Lys Leu Val Cys Leu Ile Thr Asn Phe
20 25 30

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
35 40 45

Pro Asp Ala Arg His Tyr Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
50 55 60

Gly Phe Ser Val Val Ser Trp Leu Asn Val Thr Arg Ala Glu Trp Glu
65 70 75 80

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
85 90 95

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
100 105 110

<210> 91
<211> 110
<212> PRT
<213> Artificial

<220>
<223> IGHE CH4 beta domain

<400> 91

Gly Pro Arg Ala Ala Pro Glu Val Ala Ala Phe Ala Thr Pro Glu Trp
1 5 10 15

Pro Gly Ser Arg Asp Lys Arg Thr Leu Val Cys Leu Ile Thr Asn Phe
20 25 30

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
35 40 45

Pro Asp Ala Arg His Ser Thr Asp Gln Pro Leu Lys Glu Lys Gly Ser
50 55 60

Gly Phe Ala Val Ser Ser Leu Leu Arg Val Thr Arg Ala Glu Trp Glu
65 70 75 80

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
85 90 95

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
100 105 110

<210> 92
<211> 330
<212> DNA
<213> Artificial

<220>
<223> cDNA coding IGHE CH4 alpha domain

<400> 92
ggacctagag ccgcccctga ggtgtacgcc tttgccacac ctgagtggcc cggcagccgg 60

gacaagagaa aactcgtgtg cctgatcacc aacttcatgc ccgaggacat cagcgtgcag 120

tggctgcaca acgaggtgca gctgcccgac gccagacact acaccaccca gcccagaaag 180

accaagggca gcggcttcag cgtggtgtcc tggctgaatg tgaccagagc cgagtgggag 240

cagaaggacg agttcatctg cagagccgtg cacgaggccg ccagcccttc tcagacagtg 300

cagagggccg tgtccgtgaa ccctggaaaa 330

<210> 93
<211> 330
<212> DNA
<213> Artificial

<220>
<223> cDNA coding IGHE CH4 beta domain

<400> 93
ggacctagag ccgctcctga agtggccgcc tttgccacac ctgagtggcc cggcagcaga 60

gacaagagaa ccctcgtgtg cctgatcacc aacttcatgc ccgaggacat cagcgtgcag 120

tggctgcaca acgaggtgca gctgcccgat gccagacaca gcaccgacca gcccctgaaa 180

gagaagggca gcggctttgc cgtgtccagc ctgctgagag tgaccagagc cgagtgggag 240

cagaaggacg agttcatctg cagagccgtg cacgaggccg ccagcccttc tcagacagtg 300

cagagggccg tgtccgtgaa ccctggaaaa 330

<210> 94
<211> 236
<212> PRT
<213> Artificial

<220>
<223> BT alpha IGHE-4 His chain

<400> 94

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Pro Arg Ala Ala Pro Glu Val
115 120 125

Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg Lys
130 135 140

Leu Val Cys Leu Ile Thr Asn Phe Met Pro Glu Asp Ile Ser Val Gln
145 150 155 160

Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His Tyr Thr Thr
165 170 175

Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Ser Val Val Ser Trp Leu
180 185 190

Asn Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg
195 200 205

Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr Val Gln Arg Ala Val
210 215 220

Ser Val Asn Pro Gly Lys His His His His His His
225 230 235

<210> 95
<211> 338
<212> PRT
<213> Artificial

<220>
<223> VL-BT beta IGHE-4 chain

<400> 95

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

```
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Pro Arg Ala Ala Pro Glu Val Ala Ala Phe Ala
225                 230                 235                 240

Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Val Cys Leu
                245                 250                 255

Ile Thr Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn
            260                 265                 270

Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr Asp Gln Pro Leu Lys
        275                 280                 285

Glu Lys Gly Ser Gly Phe Ala Val Ser Ser Leu Leu Arg Val Thr Arg
    290                 295                 300

Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu
305                 310                 315                 320

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

Gly Lys
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<210> 96
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> human CH3 (isotype alpha 1) constant domain
<222> (1)..(111)

<400> 96

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Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1               5                   10                  15

Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
            20                  25                  30

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

```
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
    50                  55                  60

Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
65                  70                  75                  80

Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
                85                  90                  95

Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
            100                 105                 110
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<210> 97
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> human CH3 (isotype alpha 2) constant domain
<222> (1)..(111)

<400> 97

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Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1               5                   10                  15

Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
            20                  25                  30

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

Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
    50                  55                  60

Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
65                  70                  75                  80

Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
                85                  90                  95

Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
            100                 105                 110
```