SEQUENCE LISTING

<110> Trubion Pharmaceuticals Inc.
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<120> TCR COMPLEX IMMUNOTHERAPEUTICS

<130> 910180.416PC

<140> PCT
<141> 2009-10-09

<160> 434

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3 VH nucleotide sequence

<400> 1
caggtccagc tgcagcagtc tggggctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcaagc 357

<210> 2
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VH amino acid sequence

<400> 2
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 3

<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3 VL nucleotide sequence

<400> 3
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagtcaggc 120
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcac 180
ttcaggggca gtgggtctgg gacctcttac tctctcacaa tcagcggcat ggaggctgaa 240
gatgctgcca cttattactg ccagcagtgg agtagtaacc cattcacgtt cggctcgggg 300
acaaagttgg aaataaac 318

<210> 4
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VL amino acid sequence

<400> 4
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1   5   10   15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser
    50   55   60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu
65   70   75   80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
                85   90   95
Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
            100   105

<210> 5
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3 VH nucleotide sequence

<400> 5
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta caccttttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagc 369

<210> 6
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 VH amino acid sequence

<400> 6
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15

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


<210> 7
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3 VL nucleotide sequence

<400> 7
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 120
acctccccca aaagatggat ttatgacaca tccaaactgg cctctggcgt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 240
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 300
accaagctgg agctgaaa                                              318

<210> 8
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 VL amino acid sequence

<400> 8
Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1               5                  10                  15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65                  70                  75                  80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
                85                  90                  95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105


<210> 9
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified human 2H7 Leader (for BC3, OKT3, 2C11 and
      H57)

<400> 9
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
```

 1   5   10   15
Val Ile Met Ser Arg Gly
            20

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified huIgG1-SCCP hinge ; Linker 87

<220>
<221> SITE
<222> (1)...(2)
<223> junction amino acids

<400> 10
Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 1   5   10   15
Pro

<210> 11
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> G1 N297A CH2-CH3 (N297ST - A297ST)

<400> 11
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100   105   110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115   120   125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130   135   140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145   150   155   160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165   170   175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180   185   190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195   200   205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210   215

<210> 12
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 AA N297A CH2CH3 (Ala substitutions at 234, 235, 237 and 297; 236 deleted)

<400> 12
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            100   105   110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
        115   120   125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130   135   140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145   150   155   160
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165   170   175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180   185   190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195   200   205
Ser Leu Ser Leu Ser Pro Gly Lys
    210   215

<210> 13
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> G2 AA N297A CH2CH3 (Ala substitution at 234, 236 and 297)

<400> 13
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
            100   105   110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
        115   120   125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130   135   140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145   150   155   160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165   170   175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

```
            180                 185                 190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205
Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 14
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> G4 AA N297A CH2CH3 (Ala substitutions at 234, 235, 237 and 297; 236 deleted)

<400> 14

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

<210> 15
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> HM1 (IgM-CH3::IgG1-CH3) with C-terminal tail

<400> 15

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

```
Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro Arg Glu Pro
            100                 105                 110
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        115                 120                 125
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    130                 135                 140
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
145                 150                 155                 160
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                165                 170                 175
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            180                 185                 190
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        195                 200                 205
Leu Ser Pro Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
    210                 215                 220
Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys
225                 230                 235                 240
Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys His His His
                245                 250                 255
His His His
```

<210> 16
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> DeltaCH2 (g1CH3 only)

<400> 16

```
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 Thr Gly Leu Asn Asp
            100                 105                 110
Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp
        115                 120                 125
Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp
    130                 135                 140
Asp Asp Lys His His His His His His
145                 150
```

<210> 17
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-VH-VL Nucleotide (includes g4s linker)

<400> 17

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caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
```

atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg tctctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaa 738

<210> 18
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-VH-VL amino acid sequence (includes g4s
linker)

<400> 18
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50   55   60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130   135   140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145   150   155   160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165   170   175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180   185   190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210   215   220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225   230   235   240
Thr Lys Leu Glu Leu Lys
                245

<210> 19
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-VH-VL Nucleotide (includes g4s linker)

<400> 19
caggtccagc tgcagcagtc tggggctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcaagcggt 360
ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgcacaaca aattgttctc 420
acccagtctc cagcaatcat gtctgcatct ccaggggaga aggtcaccat gacctgcagt 480
gccagctcaa gtgtaagtta catgaactgg taccagcaga agtcaggcac ctcccccaaa 540
agatggattt atgacacatc caaactggct tctggagtcc ctgctcactt caggggcagt 600
gggtctggga cctcttactc tctcacaatc agcggcatgg aggctgaaga tgctgccact 660
tattactgcc agcagtggag tagtaaccca ttcacgttcg gctcggggac aaagttggaa 720
ataaac 726

<210> 20
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-VH-VL amino acid sequence (includes g4s
linker)

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

<210> 21
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-G1 N297A Nucleotide- human 2H7 leader through
CH3

<400> 21
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300

gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaactcctg ggtggaccgt cagtcttcct cttccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag tacgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1140
aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200
ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500
ggtaaatga 1509

<210> 22
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-g1 N297A amino acid sequence- 2H7L leader
through CH3

<400> 22
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
20 25 30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65 70 75 80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
115 120 125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
165 170 175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
180 185 190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
195 200 205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
210 215 220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225 230 235 240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
245 250 255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
260 265 270
Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

```
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
            340                 345                 350
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    370                 375                 380
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495
Ser Leu Ser Pro Gly Lys
            500
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<210> 23
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-g1 AA N297A Nucleotide - human 2H7 leader through CH3

<400> 23

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atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaagccgca gctccgtcag tcttcctctt ccccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020
gccaagacaa agccgcggga ggagcagtac gccagcacgt accgtgtggt cagcgtcctc 1080
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1140
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500
aaatga                                                            1506
```

<210> 24

<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-g1 AA N297A - human 2H7 leader through CH3

<400> 24
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65   70   75   80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
        115   120   125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
    130   135   140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145   150   155   160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
                165   170   175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            180   185   190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
        195   200   205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    210   215   220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225   230   235   240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                245   250   255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
            260   265   270
Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275   280   285
Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290   295   300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305   310   315   320
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325   330   335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            340   345   350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355   360   365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370   375   380
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385   390   395   400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                405   410   415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420   425   430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435   440   445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450   455   460
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465   470   475   480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
485 490 495
Leu Ser Pro Gly Lys
500

<210> 25
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-g2 AA N297A Nucleotide - human 2H7 leader through CH3

<400> 25
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaagccgca gctccgtcag tcttcctctt cccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 960
agccacgaag accccgaggt ccagttcaac tggtacgtgg acggcatgga ggtgcataat 1020
gccaagacaa agccacggga ggagcagttc gccagcacgt tccgtgtggt cagcgtcctc 1080
accgtcgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 1140
ggcctcccag ccccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca 1200
caggtgtaca ccctgccccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1260
tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcctc 1380
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtctccgggt 1500
aaatga 1506

<210> 26
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-g2 AA N297A - human 2H7 leader through CH3

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

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Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
    130                 135                 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
                165                 170                 175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            180                 185                 190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
        195                 200                 205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    210                 215                 220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225                 230                 235                 240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                245                 250                 255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
            260                 265                 270
Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285
Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320
Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met
                325                 330                 335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser
            340                 345                 350
Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
        355                 360                 365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
    370                 375                 380
Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
                405                 410                 415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445
Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450                 455                 460
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
Leu Ser Pro Gly Lys
            500
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<210> 27
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-g4 AA N297A Nucleotide - human 2H7 leader through CH3

<400> 27
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480

gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaagccgca gctccgtcag tcttcctctt cccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 960
agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 1020
gccaagacaa agccgcggga ggagcagttc gccagcacgt accgtgtggt cagcgtcctc 1080
accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 1140
ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1200
caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1260
tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380
tacagcaggc taaccgtgga caagagccgg tggcaggagg ggaatgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtctccgggt 1500
aaatga 1506

<210> 28
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-g4 AA N297A - human 2H7 leader through CH3

<400> 28
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65   70   75   80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
        115   120   125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
    130   135   140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145   150   155   160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
                165   170   175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            180   185   190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
        195   200   205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    210   215   220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225   230   235   240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                245   250   255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
            260   265   270
Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275   280   285
Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290   295   300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305   310   315   320

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Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser
            340                 345                 350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
    370                 375                 380
Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
                405                 410                 415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
    450                 455                 460
Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
Leu Ser Pro Gly Lys
            500
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<210> 29
<211> 1635
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-HM1 Nucleotide - human 2H7 leader through g1
CH3

<400> 29

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atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttgtgacaa aactcacaca 840
tgcccaccgt gcccagatca agacacagcc atccgggtct tcgccatccc cccatccttt 900
gccagcatct tcctcaccaa gtccaccaag ttgacctgcc tggtcacaga cctgaccacc 960
tatgacagcg tgaccatctc ctggacccgc cagaatggcg aagctgtgaa aacccacacc 1020
aacatctccg agagccaccc caatgccact ttcagcgccg tgggtgaggc cagcatctgc 1080
gaggatgact ggaattccgg ggagaggttc acgtgcaccg tgacccacac agacctgccc 1140
tcgccactga agcagaccat ctcccggccc aaggggcagc cccgagaacc acaggtgtac 1200
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1260
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1320
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1380
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1440
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtccccggg taaaaccggt 1500
ctgaacgaca tcttcgaggc tcagaaaatc gaatggcacg aagattacaa ggatgacgac 1560
gataaggatt acaaggatga cgacgataag gattacaagg atgacgacga taagcatcat 1620
catcatcatc actga                                                   1635
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<210> 30
<211> 544
<212> PRT

<213> Artificial Sequence

<220>
<223> BC3-HM1 - human 2H7 leader through g1 CH3

<400> 30
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65   70   75   80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
        115   120   125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
    130   135   140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145   150   155   160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
                165   170   175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            180   185   190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
        195   200   205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    210   215   220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225   230   235   240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                245   250   255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
            260   265   270
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asp Gln Asp
        275   280   285
Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe
    290   295   300
Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr
305   310   315   320
Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val
                325   330   335
Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser
            340   345   350
Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu
        355   360   365
Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys
    370   375   380
Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385   390   395   400
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
                405   410   415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
            420   425   430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        435   440   445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
    450   455   460
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
465   470   475   480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                485   490   495

Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
500 505 510
His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
515 520 525
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
530 535 540

<210> 31
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> BC3-delta CH2 Nucleotide - human 2H7 leader
through g1 CH3

<400> 31
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctgca gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca gtgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagtag tggatatatt 240
gggtacagtc agaagttcaa ggacaagacc acattgactg cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag tctgacatct gaggactctg cggtctatta ctgtgcaaga 360
tcgaaggtct actatgatta cgacgtttat tctatggact actggggtca aggaacctcg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttattctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgcactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggtctc tggcgtccct 660
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaatccact cacgttcggt 780
gctgggacca agctggagct gaaacgaact gagcccaaat cttgtgacaa aactcacaca 840
tgcccaccgt gcccagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 900
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 960
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1020
cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1080
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1140
tacacgcaga agagcctctc cctgtccccg ggtaaaaccg gtctgaacga catcttcgag 1200
gctcagaaaa tcgaatggca cgaagattac aaggatgacg acgataagga ttacaaggat 1260
gacgacgata aggattacaa ggatgacgac gataagcatc atcatcatca tcactga 1317

<210> 32
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-delta CH2 - human 2H7 leader through g1 CH3

<400> 32
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
20 25 30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65 70 75 80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
115 120 125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
130 135 140

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

<210> 33
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-G1 N297A Nucleotide - human 2H7 leader
through CH3

<400> 33

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atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 840
ccagcacctg aactcctggg tggaccgtca gtcttcctct tccccccaaa acccaaggac 900
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 960
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1020
aagccgcggg aggagcagta cgccagcacg taccgtgtgg tcagcgtcct caccgtcctg 1080
```

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1140
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1200
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1260
aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1320
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1380
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1440
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga 1497

<210> 34
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-G1 N297A - human 2H7 leader through CH3

<400> 34
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260   265   270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
        275   280   285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
    290   295   300
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
305   310   315   320
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
                325   330   335
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg
            340   345   350
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
        355   360   365
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
    370   375   380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385   390   395   400
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu

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                405                 410                 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
            420                 425                 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        435                 440                 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
    450                 455                 460
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
465                 470                 475                 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                485                 490                 495
Gly Lys
```

<210> 35
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-G1 AA N297A Nucleotide - human 2H7 leader through CH3

<400> 35
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 840
ccagcacctg aagccgcagc tccgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020
ccgcgggagg agcagtacgc cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga   1494

<210> 36
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-G1 AA N297A - human 2H7 leader through CH3

<400> 36
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50                  55                  60
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Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65                  70                  75                  80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85                  90                  95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115                 120                 125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145                 150                 155                 160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165                 170                 175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180                 185                 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195                 200                 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210                 215                 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225                 230                 235                 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245                 250                 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260                 265                 270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro
        275                 280                 285
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    290                 295                 300
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305                 310                 315                 320
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                325                 330                 335
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val
            340                 345                 350
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        355                 360                 365
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    370                 375                 380
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385                 390                 395                 400
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                405                 410                 415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420                 425                 430
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        435                 440                 445
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    450                 455                 460
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465                 470                 475                 480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490                 495
Lys
```

<210> 37
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-G2 AA N297A Nucleotide - human 2H7 leader through CH3

<400> 37

atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 840
ccagcacctg aagccgcagc tccgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900
ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccacgaagac 960
cccgaggtcc agttcaactg gtacgtggac ggcatggagg tgcataatgc caagacaaag 1020
ccacgggagg agcagttcgc cagcacgttc cgtgtggtca gcgtcctcac cgtcgtgcac 1080
caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccagcc 1140
cccatcgaga aaaccatctc caaaaccaaa gggcagcccc gagaaccaca ggtgtacacc 1200
ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260
ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320
tacaagacca cacctcccat gctggactcc gacggctcct tcttcctcta cagcaagctc 1380
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440
gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 38
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-G2 AA N297A - human 2H7 leader through CH3

<400> 38
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp

```
            260                 265                 270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro
        275                 280                 285
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    290                 295                 300
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305                 310                 315                 320
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn
                325                 330                 335
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val
            340                 345                 350
Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
        355                 360                 365
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
    370                 375                 380
Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385                 390                 395                 400
Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                405                 410                 415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420                 425                 430
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
        435                 440                 445
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    450                 455                 460
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465                 470                 475                 480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490                 495
Lys
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<210> 39
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-G4 AA N297A Nucleotide - human 2H7 leader
through CH3

<400> 39

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atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 840
ccagcacctg aagccgcagc tccgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900
ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 960
cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 1020
ccgcgggagg agcagttcgc cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080
caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 1140
tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 1200
ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260
ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1380
accgtggaca agagccggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1440
gctctgcaca accactacac acagaagagc ctctccctgt ctccgggtaa atga       1494
```

<210> 40
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-G4 AA N297A - human 2H7 leader through CH3

<400> 40
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260   265   270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro
        275   280   285
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    290   295   300
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
305   310   315   320
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                325   330   335
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val
            340   345   350
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        355   360   365
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
    370   375   380
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385   390   395   400
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                405   410   415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420   425   430
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        435   440   445
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
    450   455   460

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495
Lys

<210> 41
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-HM1 Nucleotide - human 2H7 leader through G1
CH3

<400> 41
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 840
ccagatcaag acacagccat ccgggtcttc gccatccccc catcctttgc cagcatcttc 900
ctcaccaagt ccaccaagtt gacctgcctg gtcacagacc tgaccaccta tgacagcgtg 960
accatctcct ggacccgcca gaatggcgaa gctgtgaaaa cccacaccaa catctccgag 1020
agccacccca atgccacttt cagcgccgtg ggtgaggcca gcatctgcga ggatgactgg 1080
aattccgggg agaggttcac gtgcaccgtg acccacacag acctgccctc gccactgaag 1140
cagaccatct cccggcccaa ggggcagccc cgagaaccac aggtgtacac cctgccccca 1200
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1260
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 1380
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tccccgggta aaaccggtct gaacgacatc 1500
ttcgaggctc agaaaatcga atggcacgaa gattacaagg atgacgacga taaggattac 1560
aaggatgacg acgataagga ttacaaggat gacgacgata agcatcatca tcatcatcac 1620
tga 1623

<210> 42
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-HM1 - human 2H7 leader through g1 CH3

<400> 42
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
20 25 30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65 70 75 80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
85 90 95

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Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115                 120                 125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145                 150                 155                 160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165                 170                 175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180                 185                 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195                 200                 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210                 215                 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225                 230                 235                 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245                 250                 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp
            260                 265                 270
Lys Thr His Thr Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg
        275                 280                 285
Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
    290                 295                 300
Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
305                 310                 315                 320
Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
                325                 330                 335
Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
            340                 345                 350
Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
        355                 360                 365
Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
    370                 375                 380
Arg Pro Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385                 390                 395                 400
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Gly
                485                 490                 495
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr
            500                 505                 510
Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr
        515                 520                 525
Lys Asp Asp Asp Asp Lys His His His His His His
    530                 535                 540
```

<210> 43
<211> 1305
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3 delta CH2 Nucleotide - human 2H7 leader
through g1 CH3

<400> 43

atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggacagg tccagctgca gcagtctggg gctgaactgg caagacctgg ggcctcagtg 120
aagatgtcct gcaaggcttc tggctacacc tttactaggt acacgatgca ctgggtaaaa 180
cagaggcctg gacagggtct ggaatggatt ggatacatta atcctagccg tggttatact 240
aattacaatc agaagttcaa ggacaaggcc acattgacta cagacaaatc ctccagcaca 300
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtgcaaga 360
tattatgatg atcattactg ccttgactac tggggccaag gcaccacggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaacaaatt 480
gttctcaccc agtctccagc aatcatgtct gcatctccag gggagaaggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagtc aggcacctcc 600
cccaaaagat ggatttatga cacatccaaa ctggcttctg gagtccctgc tcacttcagg 660
ggcagtgggt ctgggacctc ttactctctc acaatcagcg gcatggaggc tgaagatgct 720
gccacttatt actgccagca gtggagtagt aacccattca cgttcggctc ggggacaaag 780
ttggaaataa accgaactga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 840
ccagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 900
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 960
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1020
tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1080
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1140
agcctctccc tgtccccggg taaaaccggt ctgaacgaca tcttcgaggc tcagaaaatc 1200
gaatggcacg aagattacaa ggatgacgac gataaggatt acaaggatga cgacgataag 1260
gattacaagg atgacgacga taagcatcat catcatcatc actga 1305

<210> 44
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 delta CH2 - human 2H7 leader through g1 CH3

<400> 44
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp
            260   265   270
Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln
        275   280   285

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



<210> 45
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Leader-VH-Linker-VL

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


<210> 46
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<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> H57 Null2 Nucleotide - human 2H7 leader through
muG2a CH3

<400> 46
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggagaag tttacctggt ggagtcaggg ggagatttag tgcagcctgg aagttccctg 120
aaagtctcct gtgcagcctc tggattcacc ttcagtgact tctggatgta ctgggtccgc 180
caggctccag ggaaggggct ggagtgggtt ggtagaatta aaaacaaacc taataattat 240
gcaacagaat atgcggattc cgtgagaggc agattcacca tctcaagaga cgactcaaga 300
aacagcatct atctgcaaat gaataggtta agagtcgatg acacagccat ttattactgt 360
actagagccg ggaggttcga ccacttcgat tactggggcc aaggaaccat ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaatat 480
gagctgatcc aaccatcttc agcatcagtc actgtaggag agacggtcaa aatcacttgc 540
tctggggacc agttgccaaa aaattttgct tattggtttc agcaaaagtc agacaagaac 600
attttactac tcatatacat ggataataag cgaccatcag ggatcccaga acgattctct 660
gggtccactt caggtacaac agccaccttg accatcagtg gagcccagcc tgaggatgag 720
gctgcctatt actgtttgtc ttcatatggt gataataacg atttagtttt tggcagcgga 780
acccagctca ccgtcctacg aactgagccc agagtgccca taacacagaa cccctgtcct 840
ccactcaaag agtgtccccc atgcgcagct ccagacgcag cgggtgcgcc atccgtcttc 900
atcttccctc caaagatcaa ggatgtactc atgatctccc tgagccccat ggtcacatgt 960
gtggtggtgg atgtgagcga ggatgaccca gacgtccaga tcagctggtt tgtgaacaac 1020
gtggaagtac acacagctca gacacaaacc catagagagg attacaacag tactctccgg 1080
gtggtcagtg ccctccccat ccagcaccag gactggatga gtggcaaggc gttcgcatgc 1140
gcggtcaaca acagagccct cccatccccc atcgagaaaa ccatctcaaa acccagaggg 1200
ccagtaagag ctccacaggt atatgtcttg cctccaccag cagaagagat gactaagaaa 1260
gagttcagtc tgacctgcat gatcacaggc ttcttacctg ccgaaattgc tgtggactgg 1320
accagcaatg ggcgtacaga gcaaaactac aagaacaccg caacagtcct ggactctgat 1380
ggttcttact tcatgtacag caagctcaga gtacaaaaga gcacttggga aagaggaagt 1440
cttttcgcct gctcagtggt ccacgagggt ctgcacaatc accttacgac taagaccatc 1500
tcccggtctc tgggtaaatg a 1521

<210> 47
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - human 2H7 leader through mouse
g2a CH3

<400> 47
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Glu Val Tyr Leu Val Glu Ser Gly Gly Asp
            20   25   30
Leu Val Gln Pro Gly Ser Ser Leu Lys Val Ser Cys Ala Ala Ser Gly
        35   40   45
Phe Thr Phe Ser Asp Phe Trp Met Tyr Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Val Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr
65   70   75   80
Ala Thr Glu Tyr Ala Asp Ser Val Arg Gly Arg Phe Thr Ile Ser Arg
                85   90   95
Asp Asp Ser Arg Asn Ser Ile Tyr Leu Gln Met Asn Arg Leu Arg Val
            100   105   110
Asp Asp Thr Ala Ile Tyr Tyr Cys Thr Arg Ala Gly Arg Phe Asp His
        115   120   125
Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
    130   135   140
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr
145   150   155   160
Glu Leu Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr Val
                165   170   175

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

<210> 48
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 VH-Linker-VL (without leader)

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

115 120 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr Glu Leu Ile Gln Pro Ser
130 135 140
Ser Ala Ser Val Thr Val Gly Glu Thr Val Lys Ile Thr Cys Ser Gly
145 150 155 160
Asp Gln Leu Pro Lys Asn Phe Ala Tyr Trp Phe Gln Gln Lys Ser Asp
165 170 175
Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp Asn Lys Arg Pro Ser Gly
180 185 190
Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser Gly Thr Thr Ala Thr Leu
195 200 205
Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Ala Tyr Tyr Cys Leu
210 215 220
Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val Phe Gly Ser Gly Thr Gln
225 230 235 240
Leu Thr Val Leu

<210> 49
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - VH amino acid

<400> 49
Glu Val Tyr Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Ser
1 5 10 15
Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr Ala Thr Glu Tyr Ala Asp
50 55 60
Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Arg Asn Ser
65 70 75 80
Ile Tyr Leu Gln Met Asn Arg Leu Arg Val Asp Asp Thr Ala Ile Tyr
85 90 95
Tyr Cys Thr Arg Ala Gly Arg Phe Asp His Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 50
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse IGHG2c mutated CH2 (alanine substitutions at
positions L234, L235, G237, E318, K320 and K322)

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

Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg
100 105 110

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - VL amino acid sequence

<400> 51
Tyr Glu Leu Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr
1 5 10 15
Val Lys Ile Thr Cys Ser Gly Asp Gln Leu Pro Lys Asn Phe Ala Tyr
20 25 30
Trp Phe Gln Gln Lys Ser Asp Lys Asn Ile Leu Leu Leu Ile Tyr Met
35 40 45
Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr
50 55 60
Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
65 70 75 80
Glu Ala Ala Tyr Tyr Cys Leu Ser Ser Tyr Gly Asp Asn Asn Asp Leu
85 90 95
Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu
100 105

<210> 52
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - Spacer and Hinge (RT is part of design); Linker 112

<400> 52
Arg Thr Glu Pro Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu
1 5 10 15
Lys Glu Cys Pro Pro Cys Ala
20

<210> 53
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - CH2 amino acid (same as 2C11 CH2 domain; is a mutated mouse IGHG2c (an allele of IgG2a isotype) CH2 domain

<400> 53
Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15
Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45
Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80
Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val Asn Asn Arg
85 90 95

Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg
100 105 110

<210> 54
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 CH3 region

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

<210> 55
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP nucleotide sequence

<400> 55
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcg 60
cgaggagagg tgcagctggt ggagtctggg ggaggcttgg tgcagcctgg aaagtccctg 120
aaactctcct gtgaggcctc tggattcacc ttcagcggct atggcatgca ctgggtccgc 180
caggctccag ggaggggggct ggagtcggtc gcatacatta ctagtagtag tattaatatc 240
aaatatgctg acgctgtgaa aggccggttc accgtctcca gagacaatgc caagaactta 300
ctgtttctac aaatgaacat tctcaagtct gaggacacag ccatgtacta ctgtgcaaga 360
ttcgactggg acaaaaatta ctggggccaa ggaaccatgg tcaccgtctc aagcggtggc 420
ggagggtctg ggggtggcgg atccggaggt ggtggctctg cacaagacat ccagatgacc 480
cagtctccat catcactgcc tgcctccctg ggagacagag tcactatcaa ttgtcaggcc 540
agtcaggaca ttagcaatta tttaaactgg taccagcaga aaccagggaa agctcctaag 600
ctcctgatct attatacaaa taaattggca gatggagtcc catcaaggtt cagtggcagt 660
ggttctggga gagattcttc tttcactatc agcagcctgg aatccgaaga tattggatct 720
tattactgtc aacagtatta taactatccg tggacgttcg gacctggcac caagctggaa 780
atcaaacgaa ctgagcccag agtgcccata acacagaacc cctgtcctcc actcaaagag 840
tgtcccccat gcgcagctcc agacgcagcg ggtgcgccat ccgtcttcat cttccctcca 900
aagatcaagg atgtactcat gatctccctg agccccatgg tcacatgtgt ggtggtggat 960
gtgagcgagg atgacccaga cgtccagatc agctggtttg tgaacaacgt ggaagtacac 1020
acagctcaga cacaaaccca tagagaggat tacaacagta ctctccgggt ggtcagtgcc 1080
ctccccatcc agcaccagga ctggatgagt ggcaaggcgt tcgcatgcgc ggtcaacaac 1140
agagccctcc catcccccat cgagaaaacc atctcaaaac ccagagggcc agtaagagct 1200
ccacaggtat atgtcttgcc tccaccagca gaagagatga ctaagaaaga gttcagtctg 1260
acctgcatga tcacaggctt cttacctgcc gaaattgctg tggactggac cagcaatggg 1320
cgtacagagc aaaactacaa gaacaccgca acagtcctgg actctgatgg ttcttacttc 1380
atgtacagca agctcagagt acaaaagagc acttgggaaa gaggaagtct tttcgcctgc 1440
tcagtggtcc acgagggtct gcacaatcac cttacgacta agaccatctc ccggtctctg 1500
ggtaaatga 1509

<210> 56
<211> 502
<212> PRT

<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP -human 2H7 leader through mouse g2a CH3

<400> 56
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20   25   30
Leu Val Gln Pro Gly Lys Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly
        35   40   45
Phe Thr Phe Ser Gly Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Arg Gly Leu Glu Ser Val Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile
65   70   75   80
Lys Tyr Ala Asp Ala Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn
                85   90   95
Ala Lys Asn Leu Leu Phe Leu Gln Met Asn Ile Leu Lys Ser Glu Asp
            100   105   110
Thr Ala Met Tyr Tyr Cys Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp
        115   120   125
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
145   150   155   160
Gln Ser Pro Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165   170   175
Asn Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180   185   190
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asn Lys
        195   200   205
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg
    210   215   220
Asp Ser Ser Phe Thr Ile Ser Ser Leu Glu Ser Glu Asp Ile Gly Ser
225   230   235   240
Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp Thr Phe Gly Pro Gly
                245   250   255
Thr Lys Leu Glu Ile Lys Arg Thr Glu Pro Arg Val Pro Ile Thr Gln
            260   265   270
Asn Pro Cys Pro Pro Leu Lys Glu Cys Pro Pro Cys Ala Ala Pro Asp
        275   280   285
Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
    290   295   300
Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp
305   310   315   320
Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
                325   330   335
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
            340   345   350
Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
        355   360   365
Met Ser Gly Lys Ala Phe Ala Cys Ala Val Asn Asn Arg Ala Leu Pro
    370   375   380
Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg Gly Pro Val Arg Ala
385   390   395   400
Pro Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys Lys
                405   410   415
Glu Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu Ile
            420   425   430
Ala Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn
        435   440   445
Thr Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
    450   455   460
Leu Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys
465   470   475   480
Ser Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr Ile

485 490 495
Ser Arg Ser Leu Gly Lys
500

<210> 57

<400> 57
000

<210> 58
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP - VH amino acid

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

<210> 59
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP without leader

<400> 59
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val
35 40 45
Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe
65 70 75 80
Leu Gln Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val
100 105 110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140
Pro Ala Ser Leu Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln
145 150 155 160
Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

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


<210> 60
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP - VL amino acid

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


<210> 61
<211> 262
<212> PRT
```

<213> Artificial Sequence

<220>
<223> 2C11 Leader-VH-Linker-VL

<400> 61
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20   25   30
Leu Val Gln Pro Gly Lys Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly
        35   40   45
Phe Thr Phe Ser Gly Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Arg Gly Leu Glu Ser Val Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile
65   70   75   80
Lys Tyr Ala Asp Ala Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn
                85   90   95
Ala Lys Asn Leu Leu Phe Leu Gln Met Asn Ile Leu Lys Ser Glu Asp
            100   105   110
Thr Ala Met Tyr Tyr Cys Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp
        115   120   125
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
145   150   155   160
Gln Ser Pro Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165   170   175
Asn Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180   185   190
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asn Lys
        195   200   205
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg
    210   215   220
Asp Ser Ser Phe Thr Ile Ser Ser Leu Glu Ser Glu Asp Ile Gly Ser
225   230   235   240
Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp Thr Phe Gly Pro Gly
                245   250   255
Thr Lys Leu Glu Ile Lys
            260

<210> 62
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 VH-Linker-VL (without leader)

<400> 62
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
 1   5   10   15
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val
        35   40   45
Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
    50   55   60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe
65   70   75   80
Leu Gln Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val
            100   105   110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu

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


<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 hinge; Linker 50

<400> 63
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1               5                  10                  15


<210> 64
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG1 CH2

<400> 64
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110


<210> 65
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG1 CH3

<400> 65
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 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> 66
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG2 CH2

<400> 66
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
            100   105

<210> 67
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG2 CH3

<400> 67
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 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 Met 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> 68
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG4 CH2

<400> 68
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 69
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG4 CH3

<400> 69
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 1   5   10   15
Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu 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> 70
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail sequence

<400> 70
Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 1   5   10   15
Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys
            20   25   30
Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
        35   40   45

<210> 71
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgM CH3

<400> 71

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

<210> 72
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse IGHG2c hinge; Linker 107

<400> 72
Glu Pro Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys Glu
 1   5   10   15
Cys Pro Pro Cys Ala
            20

<210> 73
<211> 110
<212> PRT
<213> Mus musculus

<220>
<223> Human IGHG2c CH2 domain

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

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

<220>
<223> HM1 (IgM CH3:IgG1 CH3) without C-terminal tail

<400> 74
Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala
 1   5   10   15
Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp

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


<210> 75
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 AA CH2

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


<210> 76
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 HM1 SMIP without C-terminal tail

<400> 76
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
```

50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65 70 75 80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
115 120 125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
165 170 175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
180 185 190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
195 200 205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
210 215 220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225 230 235 240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
245 250 255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
260 265 270
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asp Gln Asp
275 280 285
Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe
290 295 300
Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr
305 310 315 320
Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val
325 330 335
Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser
340 345 350
Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu
355 360 365
Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys
370 375 380
Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385 390 395 400
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
405 410 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
420 425 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
435 440 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
450 455 460
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
465 470 475 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
485 490 495
Gly Lys

<210> 77
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 delta CH2 SMIP without C-terminal tail

<400> 77

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Ala Ala Glu
            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met Gln Trp Val Lys Gln Arg Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile
65                  70                  75                  80
Gly Tyr Ser Gln Lys Phe Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys
                85                  90                  95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp
        115                 120                 125
Val Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
    130                 135                 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160
Ala Gln Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
                165                 170                 175
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            180                 185                 190
Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
        195                 200                 205
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    210                 215                 220
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
225                 230                 235                 240
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                245                 250                 255
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro
            260                 265                 270
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro
        275                 280                 285
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    290                 295                 300
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
305                 310                 315                 320
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                325                 330                 335
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            340                 345                 350
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        355                 360                 365
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    370                 375                 380
Ser Leu Ser Leu Ser Pro Gly Lys
385                 390


<210> 78
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 HM1 SMIP without C-terminal tail

<400> 78
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
```

50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65 70 75 80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
130 135 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145 150 155 160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
165 170 175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
180 185 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
195 200 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
210 215 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225 230 235 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
245 250 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp
260 265 270
Lys Thr His Thr Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg
275 280 285
Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
290 295 300
Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
305 310 315 320
Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
325 330 335
Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
340 345 350
Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
355 360 365
Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
370 375 380
Arg Pro Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385 390 395 400
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
405 410 415
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
420 425 430
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
435 440 445
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
450 455 460
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465 470 475 480
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 79
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 delta CH2 SMIP without C-terminal tail

<400> 79
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

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


<210> 80
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A SMIP without leader

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

65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr
245 250 255
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
260 265 270
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
275 280 285
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
290 295 300
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
305 310 315 320
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
325 330 335
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
340 345 350
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
355 360 365
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
370 375 380
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
385 390 395 400
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
405 410 415
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
420 425 430
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
435 440 445
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
450 455 460
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475 480

<210> 81
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 AA SMIP without leader

<400> 81
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

```
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 82
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G2 AA SMIP without leader

<400> 82
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
```

```
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
```

<210> 83
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G4 AA SMIP without leader

<400> 83

```
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
    290                 295                 300
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
```

<210> 84
<211> 522
<212> PRT
<213> Artificial Sequence

<220>

<223> BC3 HM1 SMIP without leader

<400> 84
```
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe
            260                 265                 270
Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys
        275                 280                 285
Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile
    290                 295                 300
Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile
305                 310                 315                 320
Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser
                325                 330                 335
Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val
            340                 345                 350
Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro
        355                 360                 365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370                 375                 380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385                 390                 395                 400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405                 410                 415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420                 425                 430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435                 440                 445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450                 455                 460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Gly Leu Asn
465                 470                 475                 480
Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp
                485                 490                 495
Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp
            500                 505                 510
Asp Asp Asp Lys His His His His His His
```

515 520

<210> 85
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 delta CH2 SMIP without leader

<400> 85
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr
245 250 255
His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr
260 265 270
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
275 280 285
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
290 295 300
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
305 310 315 320
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
325 330 335
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
340 345 350
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
355 360 365
Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
370 375 380
His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
385 390 395 400
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
405 410 415

<210> 86
<211> 476

<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 HM1 SMIP without N-terminal leader or
C-terminal tail

<400> 86
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50   55   60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130   135   140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145   150   155   160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165   170   175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180   185   190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210   215   220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225   230   235   240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr
                245   250   255
His Thr Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe
            260   265   270
Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys
        275   280   285
Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile
    290   295   300
Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile
305   310   315   320
Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser
                325   330   335
Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val
            340   345   350
Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro
        355   360   365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370   375   380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385   390   395   400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405   410   415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420   425   430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435   440   445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450   455   460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 87
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 delta CH2 SMIP without N-terminal leader or
C-terminal tail

<400> 87
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr
245 250 255
His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr
260 265 270
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
275 280 285
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
290 295 300
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
305 310 315 320
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
325 330 335
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
340 345 350
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
355 360 365
Gly Lys
370

<210> 88
<211> 476
<212> PRT
<213> Artificial Sequence

<220>

<223> OKT3 G1 N297A SMIP without leader

<400> 88
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130   135   140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145   150   155   160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165   170   175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180   185   190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195   200   205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210   215   220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225   230   235   240
Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245   250   255
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
            260   265   270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275   280   285
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290   295   300
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305   310   315   320
Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                325   330   335
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            340   345   350
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        355   360   365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370   375   380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385   390   395   400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405   410   415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420   425   430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435   440   445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450   455   460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 89
<211> 475
<212> PRT

<213> Artificial Sequence

<220>
<223> OKT3 G1 AA SMIP without leader

<400> 89
```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130                 135                 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195                 200                 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225                 230                 235                 240
Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320
Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            340                 345                 350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
```

<210> 90
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 G2 AA SMIP without leader

<400> 90
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130   135   140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145   150   155   160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165   170   175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180   185   190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195   200   205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210   215   220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225   230   235   240
Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245   250   255
Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro
            260   265   270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275   280   285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
    290   295   300
Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg
305   310   315   320
Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
                325   330   335
Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            340   345   350
Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
        355   360   365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
    370   375   380
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385   390   395   400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405   410   415
Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
            420   425   430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435   440   445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450   455   460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

465 470 475

<210> 91
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 G4 AA SMIP without leader

<400> 91
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
130 135 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145 150 155 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
165 170 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
180 185 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
195 200 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
210 215 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240
Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
245 250 255
Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro
260 265 270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
275 280 285
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
290 295 300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320
Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
370 375 380
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450   455   460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 92
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 HM1 SMIP without leader

<400> 92
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130   135   140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145   150   155   160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165   170   175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180   185   190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195   200   205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210   215   220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225   230   235   240
Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
                245   250   255
Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
            260   265   270
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
        275   280   285
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
    290   295   300
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
305   310   315   320
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
                325   330   335
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
            340   345   350
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro
        355   360   365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    370   375   380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385   390   395   400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405   410   415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

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            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu
465                 470                 475                 480
Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp Asp Lys
                485                 490                 495
Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys
            500                 505                 510
His His His His His His
        515


<210> 93
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 delta CH2 SMIP without leader

<400> 93
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130                 135                 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195                 200                 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225                 230                 235                 240
Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            260                 265                 270
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        275                 280                 285
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    290                 295                 300
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
305                 310                 315                 320
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                325                 330                 335
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            340                 345                 350
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Gly
        355                 360                 365
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr
    370                 375                 380
Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr
385                 390                 395                 400
Lys Asp Asp Asp Asp Lys His His His His His His
                405                 410


<210> 94
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 HM1 SMIP without N-terminal leader or
      C-terminal tail

<400> 94
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130                 135                 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195                 200                 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225                 230                 235                 240
Ile Asn Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
            260                 265                 270
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
        275                 280                 285
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
    290                 295                 300
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
305                 310                 315                 320
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
                325                 330                 335
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
            340                 345                 350
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    370                 375                 380
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Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405 410 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
420 425 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460
Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 95
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 delta CH2 without N-terminal leader or
C-terminal tail

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        355   360   365

<210> 96
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 null2 SMIP without leader

<400> 96
Glu Val Tyr Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Ser
 1   5   10   15
Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
            20   25   30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr Ala Thr Glu Tyr Ala Asp
    50   55   60
Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Arg Asn Ser
65   70   75   80
Ile Tyr Leu Gln Met Asn Arg Leu Arg Val Asp Asp Thr Ala Ile Tyr
                85   90   95
Tyr Cys Thr Arg Ala Gly Arg Phe Asp His Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115   120   125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr Glu Leu Ile Gln Pro Ser
    130   135   140
Ser Ala Ser Val Thr Val Gly Glu Thr Val Lys Ile Thr Cys Ser Gly
145   150   155   160
Asp Gln Leu Pro Lys Asn Phe Ala Tyr Trp Phe Gln Gln Lys Ser Asp
                165   170   175
Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp Asn Lys Arg Pro Ser Gly
            180   185   190
Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser Gly Thr Thr Ala Thr Leu
        195   200   205
Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Ala Tyr Tyr Cys Leu
    210   215   220
Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val Phe Gly Ser Gly Thr Gln
225   230   235   240
Leu Thr Val Leu Arg Thr Glu Pro Arg Val Pro Ile Thr Gln Asn Pro
                245   250   255
Cys Pro Pro Leu Lys Glu Cys Pro Pro Cys Ala Ala Pro Asp Ala Ala
            260   265   270
Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
        275   280   285
Met Ile Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp Val Ser
    290   295   300
Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
305   310   315   320
Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
                325   330   335
Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
            340   345   350
Gly Lys Ala Phe Ala Cys Ala Val Asn Asn Arg Ala Leu Pro Ser Pro
        355   360   365
Ile Glu Lys Thr Ile Ser Lys Pro Arg Gly Pro Val Arg Ala Pro Gln
    370   375   380
Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys Lys Glu Phe
385   390   395   400
Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu Ile Ala Val
                405   410   415
Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr Ala
            420   425   430
Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg

435 440 445
Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser Val
450 455 460
Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr Ile Ser Arg
465 470 475 480
Ser Leu Gly Lys

<210> 97
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 null2 SMIP without leader

<400> 97
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val
35 40 45
Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe
65 70 75 80
Leu Gln Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val
100 105 110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140
Pro Ala Ser Leu Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln
145 150 155 160
Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175
Pro Lys Leu Leu Ile Tyr Tyr Thr Asn Lys Leu Ala Asp Gly Val Pro
180 185 190
Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Ser Ser Phe Thr Ile
195 200 205
Ser Ser Leu Glu Ser Glu Asp Ile Gly Ser Tyr Tyr Cys Gln Gln Tyr
210 215 220
Tyr Asn Tyr Pro Trp Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
225 230 235 240
Arg Thr Glu Pro Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu
245 250 255
Lys Glu Cys Pro Pro Cys Ala Ala Pro Asp Ala Ala Gly Ala Pro Ser
260 265 270
Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu
275 280 285
Ser Pro Met Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro
290 295 300
Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
305 310 315 320
Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val
325 330 335
Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe
340 345 350
Ala Cys Ala Val Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr
355 360 365
Ile Ser Lys Pro Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu
370 375 380
Pro Pro Pro Ala Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys
385 390 395 400

Met Ile Thr Gly Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser
405 410 415
Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp
420 425 430
Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser
435 440 445
Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly
450 455 460
Leu His Asn His Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys
465 470 475 480

<210> 98
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified (G4S)3 linker (AQ as junction amino acids); Linker 85

<400> 98
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
1 5 10 15
Gln

<210> 99
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human mutated IgG1 Hinge (SCC-P); Linker 47

<400> 99
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 100
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 WT hinge (RT as junction amino acids); Linker 86

<400> 100
Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15
Pro

<210> 101
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Null2 CH2-CH3

<400> 101
Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15

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


<210> 102
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 N297A CH2

<400> 102
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110


<210> 103
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 AA CH2

<400> 103
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1               5                  10                  15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        35                  40                  45
```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105

<210> 104
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG2 AA CH2

<400> 104
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
            100   105

<210> 105
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 6

<400> 105
Gly Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 7

<400> 106
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 107
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 8

<400> 107
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 108
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 9

<400> 108
Gly Cys Pro Pro Cys Pro Gly Asn Ser
 1   5

<210> 109
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 10

<400> 109
Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1   5

<210> 110
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 11

<400> 110
Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1   5

<210> 111
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 12

<400> 111
Glu Glu Glu Glu Asp Glu Gly Asn Ser
 1   5

<210> 112
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 13

<400> 112
Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser

 1   5   10

<210> 113
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 14

<400> 113
Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10

<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 15

<400> 114
Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Pro
 1   5   10

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 16

<400> 115
Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
 1   5   10

<210> 116
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 17

<400> 116
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Asn Ser
 1   5   10

<210> 117
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 18

<400> 117
Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10

<210> 118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 19

<400> 118
Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10

<210> 119
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 20

<400> 119
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Cys Pro
 1   5   10

<210> 120
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 21

<400> 120
Glu Pro Lys Ser Cys Asp Lys Thr Cys Pro Pro Cys Pro
 1   5   10

<210> 121
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 22

<400> 121
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10

<210> 122
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 23

<400> 122
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1   5   10

<210> 123
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> Linker 24

<400> 123
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1   5   10

<210> 124
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 25

<400> 124
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1   5   10

<210> 125
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 26

<400> 125
Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1   5   10

<210> 126
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 27

<400> 126
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 127
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 28

<400> 127
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 128
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker 29

<400> 128
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10   15

<210> 129
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 30

<400> 129
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 130
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 31

<400> 130
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 131
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 32

<400> 131
Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
 1   5   10   15

<210> 132
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 33

<400> 132
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
 1   5   10   15

<210> 133
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 34

<400> 133

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
 1   5   10   15

<210> 134
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 35

<400> 134
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10   15

<210> 135
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 36

<400> 135
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
 1   5   10   15

<210> 136
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 37

<400> 136
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
 1   5   10   15

<210> 137
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 38

<400> 137
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10   15

<210> 138
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 39

<400> 138
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 139
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 40

<400> 139
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 140
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 41

<400> 140
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 141
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 42

<400> 141
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10   15

<210> 142
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 43

<400> 142
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 143
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 44

<400> 143
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 144
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 45

<400> 144
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
 1   5   10   15

<210> 145
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 46

<400> 145
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 146
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 48

<400> 146
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 147
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 49
<400> 147
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 148
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 51

<400> 148
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1   5   10   15

<210> 149
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker 52

<400> 149
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
 1   5   10   15

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 53

<400> 150
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1   5   10   15

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 54

<400> 151
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 152
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 55

<400> 152
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 153
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 56

<400> 153
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 154
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 57

<400> 154

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 155
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 58

<400> 155
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 156
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 59

<400> 156
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 157
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 60

<400> 157
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 158
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 61

<400> 158
Gly Gly Gly Gly Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 159
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 62

<400> 159
Glu Pro Lys Ser Cys Gly Gly Gly Gly Gly Cys Pro Pro Cys Pro
 1   5   10   15

<210> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 63

<400> 160
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Gly Gly Cys Pro
 1   5   10   15

<210> 161
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 64

<400> 161
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Gly
 1   5   10   15

<210> 162
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 65

<400> 162
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 163
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 66

<400> 163
Glu Pro Lys Ser Cys Asp Lys Cys His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 164
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 67

<400> 164
Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Cys Pro Pro Cys Pro
 1   5   10   15

<210> 165
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 68

<400> 165
Glu Pro Lys Ser Cys Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
 1   5   10   15

<210> 166
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 69

<400> 166
Pro Pro Pro Pro Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 167
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 70

<400> 167
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Trp Trp Cys Pro
 1   5   10   15

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 71

<400> 168
Glu Pro Lys Ser Cys Asp Trp Trp His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 169
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 72

<400> 169
Glu Pro Lys Cys Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 170
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 73

<400> 170
Glu Pro Lys Ser Asp Cys Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 171
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 74

<400> 171
Glu Pro Lys Ser Asp Cys Trp Trp His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 172
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 75

<400> 172
Glu Pro Lys Ser Cys Asp Phe Phe His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 173
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 76

<400> 173
Glu Pro Lys Ser Cys Asp Trp Trp Trp Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 174
<211> 15
<212> PRT
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<220>
<223> Linker 77

<400> 174
Glu Pro Lys Ser Cys Trp Trp Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 175
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 78

<400> 175
Glu Pro Trp Trp Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 176
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 79

<400> 176
Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
 1   5   10   15

<210> 177
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 80

<400> 177
Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 1   5   10   15
Pro

<210> 178
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 81

<400> 178
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 82

<400> 179
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
 1   5   10   15
Ser

<210> 180
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 83

<400> 180
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 181
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 84

<400> 181
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 182
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 88

<400> 182
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Gly Gly Gly Pro
 1   5   10   15
Cys Pro

<210> 183
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 89

<400> 183
Glu Pro Lys Ser Cys Asp Gly Gly Gly Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 184
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 90

<400> 184
Glu Pro Lys Ser Cys Asp Pro Pro Pro Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 185
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 91

<400> 185
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Pro Pro Pro
 1   5   10   15
Cys Pro

<210> 186
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 92

<400> 186
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Asn Ser

<210> 187
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 93

<400> 187
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Ala

<210> 188
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 94

<400> 188
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Ser

<210> 189
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker 95

<400> 189
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 190
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 96

<400> 190
Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 191
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 97

<400> 191
Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala
 1   5   10   15
Arg His Ser Pro
            20

<210> 192
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 98

<400> 192
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 193
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 99

<400> 193
Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 194
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 100

<400> 194
Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 195
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 101

<400> 195
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 196
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 102

<400> 196
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 197
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 103

<400> 197
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 198
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 104

<400> 198
Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu
 1   5   10   15
Asp Gly Asn Ser
            20

<210> 199
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 105

<400> 199
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 200
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 106

<400> 200
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 201
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 108

<400> 201
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Ser Cys Pro
 1   5   10   15
Pro Cys Pro Asn Ser
            20

<210> 202
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 109

<400> 202
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
 1   5   10   15
Asp Cys Pro Asn Ser
            20

<210> 203
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 110

<400> 203
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Cys Pro Asn Ser
            20

<210> 204
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 111

<400> 204
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 205
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 113

<400> 205
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            20   25   30
Gly Ser Asn Ser
        35

<210> 206
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 114

<400> 206
Arg Thr Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr Asn Arg
 1   5   10   15
Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg Leu Lys
            20   25   30
Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg Arg
        35   40   45
Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg Ala His
    50   55   60
Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg Gln Lys
65   70   75   80
Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu
                85   90   95

Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys
100 105 110
Gly Ser Ala Asp Thr Cys Cys Pro Asn Ser
115 120

<210> 207
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 1

<400> 207
Asn Ser
1

<210> 208
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 2

<400> 208
Ser Cys Pro Pro Cys Pro
1 5

<210> 209
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3

<400> 209
Gly Gly Gly Gly Ser Gly Asn Ser
1 5

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

<220>
<223> Linker 4

<400> 210
Gly Cys Pro Pro Cys Pro Asn Ser
1 5

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

<220>
<223> Linker 5

<400> 211
Gly Ser Pro Pro Ser Pro Asn Ser

1 5

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

<220>
<223> Linker 115

<400> 212
Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser
1 5 10 15
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
20 25 30
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
35 40 45
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
50 55 60
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
65 70 75 80
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
85 90 95
Phe Glu Asp Ser Thr Lys Lys Ser Ala Cys Pro Pro Cys Ser Gly
100 105 110

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

<220>
<223> Linker 116

<400> 213
Gln Glu Lys Glu Ala Ile Glu Arg Leu Lys Ala Ala Gly Ala Pro Glu
1 5 10 15
Ser Leu Val Ile Gln Ala Tyr Phe Ala Ser Glu Lys Asn Glu Asn Leu
20 25 30
Ala Ala Asn Phe Leu Leu Ser Gln Asn Phe Asp Asp Glu Cys Pro Pro
35 40 45
Cys Pro Ser Gly
50

<210> 214
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 117

<400> 214
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1 5 10 15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
20 25 30
Asn Thr Cys Pro Pro Cys Pro
35

<210> 215
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 118

<400> 215
Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
 1   5   10   15
Pro Ser Cys Pro Pro Cys Pro
            20

<210> 216
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 119

<400> 216
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Cys
 1   5   10   15
Pro Pro Cys Pro
            20

<210> 217
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 120

<400> 217
Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Cys
 1   5   10   15
Pro Pro Cys Pro
            20

<210> 218
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 122

<400> 218
Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
 1   5   10

<210> 219
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Cris7-VH murine hybridoma Nucleotide

<400> 219
caggtccagc tgcagcagtc tggggctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180
aatcagaaat tcaaggacaa ggccacattg actgcagaca aatcctccag tacagcctac 240
atgcaactga gtagcctgac atctgaggac tctgcagtct attactgtgc aagtccgcaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactctggt cactgtctct 360
gca 363

<210> 220
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-VH murine hybridoma Amino Acid

<220>
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<222> (31)...(35)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (50)...(66)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (100)...(110)
<223> complementarity-determining region

<400> 220
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 221
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Cris7-VL murine hybridoma Nucleotide

<400> 221
caagttgttc tcacccagtc tccagcaatc atgtctgcat ttccagggga gaaggtcacc 60
atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagtcaggc 120
acctccccca aaagatggat ttatgactca tccaaactgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctcttat tctctcacaa tcagcagcat ggagactgaa 240
gatgctgcca cttattactg ccagcagtgg agtcgtaacc cacccacgtt cggaggggg 300
accaagctac aaattacacg g 321

<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-VL murine hybridoma Amino Acid

<220>
<221> ACT_SITE
<222> (24)...(33)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (49)...(55)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (88)...(96)
<223> complementarity-determining region

<400> 222
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
 1   5   10   15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
65   70   75   80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg
            100   105

<210> 223
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) N297A Nucleotide

<400> 223
aagcttccgc catggatttt caagtgcaga ttttcagctt cctgctaatc agtgcttcag 60
tcataatgtc gcgaggacag gtccagctgc agcagtctgg ggctgaactg gcaagacctg 120
gggcctcagt gaagatgtcc tgcaaggctt ctggctacac ctttactaga tctacgatgc 180
actgggtaaa acagaggcct ggacagggtc tggaatggat tggatacatt aatcctagca 240
gtgcttatac taattacaat cagaaattca aggacaaggc cacattgact gcagacaaat 300
cctccagtac agcctacatg caactgagta gcctgacatc tgaggactct gcagtctatt 360
actgtgcaag tccgcaagtc cactatgatt acaacgggtt tccttactgg ggccaaggga 420
ctctggtcac tgtctctgca ggtggcggag ggtctggggg tggcggatcc ggaggtggtg 480
gctctgcaca acaagttgtt ctcacccagt ctccagcaat catgtctgca tttccagggg 540
agaaggtcac catgacctgc agtgccagct caagtgtaag ttacatgaac tggtaccagc 600
agaagtcagg cacctccccc aaaagatgga tttatgactc atccaaactg gcttctggag 660
tccctgctcg cttcagtggc agtgggtctg ggacctctta ttctctcaca atcagcagca 720
tggagactga agatgctgcc acttattact gccagcagtg gagtcgtaac ccacccacgt 780
tcggaggggg gaccaagcta caaattacac ggcgaactga gcccaaatct tctgacaaaa 840
ctcacacatg cccaccgtgc ccagcacctg aactcctggg tggaccgtca gtcttcctct 900
tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc acatgcgtgg 960
tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg 1020
aggtgcataa tgccaagaca aagccgcggg aggagcagta cgccagcacg taccgtgtgg 1080
tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac aagtgcaagg 1140
tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc aaagggcagc 1200
cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc aagaaccagg 1260
tcagcctgac ctgcctggtc aaaggcttct atccaagcga catcgccgtg gagtgggaga 1320
gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac tccgacggct 1380
ccttcttcct ctacagcaag ctcaccgtgg acaagagccg gtggcagcag gggaacgtct 1440
tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag agcctctccc 1500
tgtctccggg taaatgaaat gtacagcggc cgcctcgagt ctaga   1545

<210> 224
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) N297A (22 aa leader)

<400> 224
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Ser Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
                165   170   175
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
225   230   235   240
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260   265   270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
        275   280   285
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290   295   300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305   310   315   320
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325   330   335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            340   345   350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355   360   365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370   375   380
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385   390   395   400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                405   410   415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420   425   430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435   440   445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450   455   460

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465 470 475 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
485 490 495
Leu Ser Pro Gly Lys
500

<210> 225
<211> 1534
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG2-AA-N297A Nucleotide

<400> 225
aagcttccgc catggatttt caagtgcaga ttttcagctt cctgctaatc agtgcttcag 60
tcataatgtc gcgaggacag gtccagctgc agcagtctgg ggctgaactg gcaagacctg 120
gggcctcagt gaagatgtcc tgcaaggctt ctggctacac ctttactaga tctacgatgc 180
actgggtaaa acagaggcct ggacagggtc tggaatggat tggatacatt aatcctagca 240
gtgcttatac taattacaat cagaaattca aggacaaggc cacattgact gcagacaaat 300
cctccagtac agcctacatg caactgagta gcctgacatc tgaggactct gcagtctatt 360
actgtgcaag tccgcaagtc cactatgatt acaacgggtt tccttactgg ggccaaggga 420
ctctggtcac tgtctctgca ggtggcggag ggtctggggg tggcggatcc ggaggtggtg 480
gctctgcaca acaagttgtt ctcacccagt ctccagcaat catgtctgca tttccagggg 540
agaaggtcac catgacctgc agtgccagct caagtgtaag ttacatgaac tggtaccagc 600
agaagtcagg cacctccccc aaaagatgga tttatgactc atccaaactg gcttctggag 660
tccctgctcg cttcagtggc agtgggtctg ggacctctta ttctctcaca atcagcagca 720
tggagactga agatgctgcc acttattact gccagcagtg gagtcgtaac ccacccacgt 780
tcggaggggg gaccaagcta caaattacac ggcgaactga gcccaaatct tctgacaaaa 840
ctcacacatg cccaccgtgc ccagcacctg aagccgcagc tccgtcagtc ttcctcttcc 900
ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg 960
tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac ggcatggagg 1020
tgcataatgc caagacaaag ccacgggagg agcagttcgc cagcacgttc cgtgtggtca 1080
gcgtcctcac cgtcgtgcac caggactggc tgaacggcaa ggagtacaag tgcaaggtct 1140
ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaaccaaa gggcagcccc 1200
gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag aaccaggtca 1260
gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag tgggagagca 1320
atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc gacggctcct 1380
tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg aacgtcttct 1440
catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc ctctccctgt 1500
ctccgggtaa atgagtgcca cggctagctc taga 1534

<210> 226
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG2-AA-N297A (22 aa
leader)

<400> 226
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
20 25 30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65 70 75 80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110

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Ser Ala Val Tyr Tyr Cys Ala Ser Pro Gln Val His Tyr Asp Tyr Asn
        115                 120                 125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145                 150                 155                 160
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
                165                 170                 175
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180                 185                 190
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        195                 200                 205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210                 215                 220
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
225                 230                 235                 240
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245                 250                 255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260                 265                 270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
        275                 280                 285
Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305                 310                 315                 320
His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
                325                 330                 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr
            340                 345                 350
Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
        355                 360                 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
    370                 375                 380
Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
385                 390                 395                 400
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
                405                 410                 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        435                 440                 445
Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    450                 455                 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465                 470                 475                 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                485                 490                 495
Ser Pro Gly Lys
            500
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<210> 227
<211> 1528
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG4-AA-N297A Nucleotide

<400> 227
aagcttccgc catggatttt caagtgcaga ttttcagctt cctgctaatc agtgcttcag 60
tcataatgtc gcgaggacag gtccagctgc agcagtctgg ggctgaactg gcaagacctg 120
gggcctcagt gaagatgtcc tgcaaggctt ctggctacac ctttactaga tctacgatgc 180
actgggtaaa acagaggcct ggacagggtc tggaatggat tggatacatt aatcctagca 240
gtgcttatac taattacaat cagaaattca aggacaaggc cacattgact gcagacaaat 300
cctccagtac agcctacatg caactgagta gcctgacatc tgaggactct gcagtctatt 360
actgtgcaag tccgcaagtc cactatgatt acaacgggtt tccttactgg ggccaaggga 420

ctctggtcac tgtctctgca ggtggcggag ggtctggggg tggcggatcc ggaggtggtg 480
gctctgcaca acaagttgtt ctcacccagt ctccagcaat catgtctgca tttccagggg 540
agaaggtcac catgacctgc agtgccagct caagtgtaag ttacatgaac tggtaccagc 600
agaagtcagg cacctccccc aaaagatgga tttatgactc atccaaactg gcttctggag 660
tccctgctcg cttcagtggc agtgggtctg ggacctctta ttctctcaca atcagcagca 720
tggagactga agatgctgcc acttattact gccagcagtg gagtcgtaac ccacccacgt 780
tcggaggggg gaccaagcta caaattacac ggcgaactga gcccaaatct tctgacaaaa 840
ctcacacatg cccaccgtgc ccagcacctg aagccgcagc tccgtcagtc ttcctcttcc 900
ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg 960
tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat ggcgtggagg 1020
tgcataatgc caagacaaag ccgcgggagg agcagttcgc cagcacgtac cgtgtggtca 1080
gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag tgcaaggtct 1140
ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa gggcagcccc 1200
gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag aaccaggtca 1260
gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag tgggagagca 1320
atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc gacggctcct 1380
tcttcctcta cagcaggcta accgtggaca agagccggtg gcaggagggg aatgtcttct 1440
catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc ctctccctgt 1500
ctccgggtaa atgagtgcta gctctaga 1528

<210> 228
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG4-AA-N297A (22 aa
leader)

<400> 228
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Ser Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
                165   170   175
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
225   230   235   240
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260   265   270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
        275   280   285
Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290   295   300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr
340 345 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

<210> 229
<211> 1649
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) HM1 Nucleotide

<400> 229
aagcttccgc catggatttt caagtgcaga ttttcagctt cctgctaatc agtgcttcag 60
tcataatgtc gcgaggacag gtccagctgc agcagtctgg ggctgaactg gcaagacctg 120
gggcctcagt gaagatgtcc tgcaaggctt ctggctacac ctttactaga tctacgatgc 180
actgggtaaa acagaggcct ggacagggtc tggaatggat tggatacatt aatcctagca 240
gtgcttatac taattacaat cagaaattca aggacaaggc cacattgact gcagacaaat 300
cctccagtac agcctacatg caactgagta gcctgacatc tgaggactct gcagtctatt 360
actgtgcaag tccgcaagtc cactatgatt acaacgggtt tccttactgg ggccaaggga 420
ctctggtcac tgtctctgca ggtggcggag ggtctggggg tggcggatcc ggaggtggtg 480
gctctgcaca acaagttgtt ctcacccagt ctccagcaat catgtctgca tttccagggg 540
agaaggtcac catgacctgc agtgccagct caagtgtaag ttacatgaac tggtaccagc 600
agaagtcagg cacctccccc aaaagatgga tttatgactc atccaaactg gcttctggag 660
tccctgctcg cttcagtggc agtgggtctg ggacctctta ttctctcaca atcagcagca 720
tggagactga agatgctgcc acttattact gccagcagtg gagtcgtaac ccacccacgt 780
tcggaggggg gaccaagcta caaattacac ggcgaactga gcccaaatct tgtgacaaaa 840
ctcacacatg cccaccgtgc ccagatcaag acacagccat ccgggtcttc gccatccccc 900
catcctttgc cagcatcttc ctcaccaagt ccaccaagtt gacctgcctg gtcacagacc 960
tgaccaccta tgacagcgtg accatctcct ggacccgcca gaatggcgaa gctgtgaaaa 1020
cccacaccaa catctccgag agccacccca atgccacttt cagcgccgtg ggtgaggcca 1080
gcatctgcga ggatgactgg aattccgggg agaggttcac gtgcaccgtg acccacacag 1140
acctgccctc gccactgaag cagaccatct cccggcccaa ggggcagccc cgagaaccac 1200
aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc agcctgacct 1260
gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc aatgggcagc 1320
cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttcctct 1380
acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg 1440
tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tccccgggta 1500
aaaccggtct gaacgacatc ttcgaggctc agaaaatcga atggcacgaa gattacaagg 1560
atgacgacga taaggattac aaggatgacg acgataagga ttacaaggat gacgacgata 1620
agcatcatca tcatcatcac tgatctaga 1649

<210> 230
<211> 543

<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) HM1 (22 aa leader)

<400> 230
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Ser Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
                165   170   175
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
225   230   235   240
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260   265   270
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asp Gln Asp Thr
        275   280   285
Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu
    290   295   300
Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr
305   310   315   320
Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys
                325   330   335
Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala
            340   345   350
Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg
        355   360   365
Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln
    370   375   380
Thr Ile Ser Arg Pro Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385   390   395   400
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                405   410   415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            420   425   430
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        435   440   445
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    450   455   460
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465   470   475   480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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                485                 490                 495
Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
            500                 505                 510
Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp
        515                 520                 525
Lys Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His
    530                 535                 540
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<210> 231
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-IgG4-WT-N297A Nucleotide

<400> 231
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ggggcctcag tgaagatgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 180
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 240
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 300
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 360
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggcttc tggagtccct 660
gctcacttca ggggcagtgg gtctgggacc tcttactctc tcacaatcag cggcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 780
tcggggacaa agttggaaat aaaccgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaattcctg gggggaccgt cagtcttcct cttccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 960
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag ttcgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1140
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1200
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca ggctaaccgt ggacaagagc cggtggcagg aggggaatgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 1500
ggtaaatgag tgctagctct agag   1524

<210> 232
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-WT-N297A (22 aa leader)

<400> 232
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65                  70                  75                  80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85                  90                  95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100                 105                 110
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Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115                 120                 125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145                 150                 155                 160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165                 170                 175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180                 185                 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195                 200                 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210                 215                 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225                 230                 235                 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245                 250                 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260                 265                 270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
        275                 280                 285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
    290                 295                 300
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
305                 310                 315                 320
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
                325                 330                 335
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg
            340                 345                 350
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
        355                 360                 365
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
    370                 375                 380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385                 390                 395                 400
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
                405                 410                 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
            420                 425                 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        435                 440                 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
    450                 455                 460
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
465                 470                 475                 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                485                 490                 495
Gly Lys
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<210> 233
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-ALGG-N297A Nucleotide

<400> 233
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gtcataatgt cgcgaggaca ggtccagctg cagcagtctg gggctgaact ggcaagacct 120
ggggcctcag tgaagatgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 180
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 240
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 300
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 360
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 420
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gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggcttc tggagtccct 660
gctcacttca ggggcagtgg gtctgggacc tcttactctc tcacaatcag cggcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 780
tcggggacaa agttggaaat aaaccgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaagccctg gggggaccgt cagtcttcct cttccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 960
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag ttcgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1140
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1200
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca ggctaaccgt ggacaagagc cggtggcagg aggggaatgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 1500
ggtaaatgag tgctagctct agag 1524

<210> 234
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-ALGG-N297A (22 aa leader)

<400> 234
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260   265   270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Leu Gly Gly
        275   280   285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
    290   295   300
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu

305 310 315 320
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
325 330 335
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg
340 345 350
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
355 360 365
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
370 375 380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385 390 395 400
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
405 410 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
420 425 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
435 440 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
450 455 460
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
465 470 475 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
485 490 495
Gly Lys

<210> 235
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FAGG-N297A Nucleotide

<400> 235
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ggggcctcag tgaagatgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 180
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 240
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 300
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 360
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggcttc tggagtccct 660
gctcacttca ggggcagtgg gtctgggacc tcttactctc tcacaatcag cggcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 780
tcggggacaa agttggaaat aaaccgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaattcgca gggggaccgt cagtcttcct cttccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 960
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag ttcgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1140
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1200
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca ggctaaccgt ggacaagagc cggtggcagg aggggaatgt cttctcatgc 1440
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ggtaaatgag tgctagctct agag 1524

<210> 236
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FAGG-N297A (22 aa leader)

<400> 236
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260   265   270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Ala Gly Gly
        275   280   285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
    290   295   300
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
305   310   315   320
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
                325   330   335
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg
            340   345   350
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
        355   360   365
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
    370   375   380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385   390   395   400
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
                405   410   415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
            420   425   430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        435   440   445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
    450   455   460
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
465   470   475   480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                485   490   495
Gly Lys

<210> 237
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FLAG-N297A Nucleotide

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ggggcctcag tgaagatgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 180
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 240
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 300
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 360
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
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gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggcttc tggagtccct 660
gctcacttca ggggcagtgg gtctgggacc tcttactctc tcacaatcag cggcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 780
tcggggacaa agttggaaat aaaccgaact gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gcccagcacc tgaattcctg gctggaccgt cagtcttcct cttcccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 960
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag ttcgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1140
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ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca ggctaaccgt ggacaagagc cggtggcagg aggggaatgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 1500
ggtaaatgag tgctagctct agag 1524

<210> 238
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FLAG-N297A (22 aa leader)

<400> 238
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
    130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys

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                165                 170                 175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180                 185                 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195                 200                 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210                 215                 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225                 230                 235                 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245                 250                 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Thr Glu Pro Lys Ser Ser Asp
            260                 265                 270
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Ala Gly
        275                 280                 285
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
    290                 295                 300
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
305                 310                 315                 320
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
                325                 330                 335
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg
            340                 345                 350
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
        355                 360                 365
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
    370                 375                 380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385                 390                 395                 400
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
                405                 410                 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
            420                 425                 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        435                 440                 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
    450                 455                 460
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
465                 470                 475                 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                485                 490                 495
Gly Lys
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<210> 239
<211> 1524
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FLGA-N297A Nucleotide

<400> 239
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ggggcctcag tgaagatgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 180
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 240
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 300
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 360
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 420
gtcaccgtct caagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 480
gcacaacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctcc aggggagaag 540
gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 600
tcaggcacct cccccaaaag atggatttat gacacatcca aactggcttc tggagtccct 660
gctcacttca ggggcagtgg gtctgggacc tcttactctc tcacaatcag cggcatggag 720
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 780
tcggggacaa agttggaaat aaaccgaact gagcccaaat cttctgacaa aactcacaca 840
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tgcccaccgt gcccagcacc tgaattcctg ggggctccgt cagtcttcct cttcccccca 900
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 960
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag ttcgccagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1140
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1200
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
ctctacagca ggctaaccgt ggacaagagc cggtggcagg aggggaatgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctccg 1500
ggtaaatgag tgctagctct agag 1524

<210> 240
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-(VH-VL) IgG4-FLGA-N297A (22 aa leader)

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
370 375 380
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
385 390 395 400
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
405 410 415
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
420 425 430
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
435 440 445
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
450 455 460
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
465 470 475 480
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
485 490 495
Gly Lys

<210> 241
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VL.1

<220>
<221> ACT_SITE
<222> (24)...(33)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (49)...(55)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (88)...(96)
<223> complementarity-determining region

<400> 241
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg
100 105

<210> 242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VL.2

<400> 242
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 Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65   70   75   80
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
            100   105

<210> 243
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VH.1

<220>
<221> ACT_SITE
<222> (31)...(35)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (50)...(66)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (100)...(110)
<223> complementarity-determining region

<400> 243
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 244
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VH.2

<400> 244

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

<210> 245
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 VH.3

<400> 245

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

<210> 246
<211> 1540
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H1-L1 N297A Nucleotide

<400> 246

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aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaca ggtccagctg gtgcagtctg gggctgaagt gaagaagcct 120
ggggcctcag tgaaggtgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180
cactgggtaa aacaggcccc tggacagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaagg ccacattgac tgcagacaaa 300
tcctccagta cagcctacat gcaactgagt agcctgaggt ctgaggacac cgcagtctat 360
tactgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actctggtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatgacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagaagcccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc 720
ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggagggg ggaccaagct acaaattaca cgacgaactg agcccaaatc ttctgacaaa 840
```

actcacacat gcccaccgtg cccagcacct gaactcctgg gtggaccgtc agtcttcctc 900
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 960
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1020
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acgccagcac gtaccgtgtg 1080
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1140
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1200
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1260
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag 1320
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
tccttcttcc tctacagcaa gctcaccgtg gacaagagcc ggtggcagca ggggaacgtc 1440
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
ctgtctccgg gtaaatgaaa tgtacagcgg ccgcctcgag 1540

<210> 247
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H1-L1 N297A (22 aa leader) Amino Acid

<400> 247
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu
            20   25   30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Ala Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Arg Ser Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165   170   175
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225   230   235   240
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260   265   270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
        275   280   285
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290   295   300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305   310   315   320
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325   330   335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            340   345   350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355   360   365

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370                 375                 380
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                405                 410                 415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450                 455                 460
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
Leu Ser Pro Gly Lys
            500
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<210> 248
<211> 1543
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H1-L2 N297A Nucleotide

<400> 248
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aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaca ggtccagctg gtgcagtctg gggctgaagt gaagaagcct 120
ggggcctcag tgaaggtgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180
cactgggtaa aacaggcccc tggacagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaagg ccacattgac tgcagacaaa 300
tcctccagta cagcctacat gcaactgagt agcctgaggt ctgaggacac cgcagtctat 360
tactgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actctggtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatcacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagacccccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctagcc gcttcagtgg cagtgggtct gggaccgact tcaccctcac aatcagcagc 720
ctgcagcccg aagatatcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggacagg ggaccaagct acaaattaca cgaactgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa ctcctgggtg gaccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtacg ccagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagccggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgaaatgt acagcggccg cctcgagtct aga                    1543
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<210> 249
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H1-L2 N297A (22 aa leader) Amino Acid

<400> 249
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu
```

```
            20                  25                  30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Lys Gln Ala Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65                  70                  75                  80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85                  90                  95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Arg Ser Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115                 120                 125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145                 150                 155                 160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165                 170                 175
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180                 185                 190
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195                 200                 205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    210                 215                 220
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225                 230                 235                 240
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245                 250                 255
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser
            260                 265                 270
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        275                 280                 285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305                 310                 315                 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325                 330                 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
            340                 345                 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355                 360                 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370                 375                 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385                 390                 395                 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
                405                 410                 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        435                 440                 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    450                 455                 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465                 470                 475                 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                485                 490                 495
Ser Pro Gly Lys
            500
```

<210> 250
<211> 1543
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H2-L1 N297A Nucleotide

<400> 250
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gggcggtcac tgaggctgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180
cactgggtaa ggcaggcccc tggaaagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaagg ccacattgac tgcagacaaa 300
tccaagaaca cagcctacat ggagctgagt agcctgaggt ctgaggacac cgcagtctat 360
tactgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actctggtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatgacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagaagcccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc 720
ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggagggg ggaccaagct acaaattaca cgaactgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa ctcctgggtg gaccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtacg ccagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagccggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgaaatgt acagcggccg cctcgagtct aga 1543

<210> 251
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H2-L1 N297A (22 aa leader) Amino Acid

<400> 251
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly
            20   25   30
Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Lys Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165   170   175
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210   215   220

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225 230 235 240
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
245 250 255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser
260 265 270
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
340 345 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

<210> 252
<211> 1543
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H2-L2 N297A Nucleotide

<400> 252
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gggcggtcac tgaggctgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180
cactgggtaa ggcaggcccc tggaaagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaagg ccacattgac tgcagacaaa 300
tccaagaaca cagcctacat ggagctgagt agcctgaggt ctgaggacac cgcagtctat 360
tactgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actctggtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatcacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagacccccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctagcc gcttcagtgg cagtgggtct gggaccgact tcaccctcac aatcagcagc 720
ctgcagcccg aagatatcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggacagg ggaccaagct acaaattaca cgaactgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa ctcctgggtg gaccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtacg ccagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260

agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagccggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgaaatgt acagcggccg cctcgagtct aga 1543

<210> 253
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H2-L2 N297A (22 aa leader) Amino Acid

<400> 253
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly
            20   25   30
Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys
                85   90   95
Ser Lys Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165   170   175
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225   230   235   240
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser
            260   265   270
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        275   280   285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290   295   300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305   310   315   320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325   330   335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
            340   345   350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355   360   365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370   375   380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385   390   395   400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
                405   410   415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

<210> 254
<211> 1540
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H3-L1 N297A Nucleotide

<400> 254
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gtcataatgt cgcgaggaca ggtccagctg gtgcagtctg ggggcggagt ggtgcagcct 120
gggcggtcac tgaggctgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180
cactgggtaa ggcaggcccc tggaaagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaggt tcacaatcag cgcagacaaa 300
tccaagagca cagccttcct gcagatggac agcctgaggc ccgaggacac cggcgtctat 360
ttctgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actcccgtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatgacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagaagcccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc 720
ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggagggg ggaccaagct acaaattaca cgacgaactg agcccaaatc ttctgacaaa 840
actcacacat gcccaccgtg cccagcacct gaactcctgg gtggaccgtc agtcttcctc 900
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 960
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1020
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acgccagcac gtaccgtgtg 1080
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1140
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1200
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1260
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag 1320
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
tccttcttcc tctacagcaa gctcaccgtg gacaagagcc ggtggcagca ggggaacgtc 1440
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
ctgtctccgg gtaaatgaaa tgtacagcgg ccgcctcgag 1540

<210> 255
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H3-L1 N297A (22 aa leader) Amino Acid

<400> 255
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly
20 25 30
Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
50 55 60
Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65 70 75 80

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Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys
                85                  90                  95
Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp
            100                 105                 110
Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115                 120                 125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145                 150                 155                 160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165                 170                 175
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180                 185                 190
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195                 200                 205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    210                 215                 220
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225                 230                 235                 240
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245                 250                 255
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260                 265                 270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
        275                 280                 285
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            340                 345                 350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370                 375                 380
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                405                 410                 415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450                 455                 460
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
Leu Ser Pro Gly Lys
            500
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<210> 256
<211> 1540
<212> DNA
<213> Artificial Sequence

<220>
<223> HuCRIS7 H3-L2 N297A Nucleotide

<400> 256
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gtcataatgt cgcgaggaca ggtccagctg gtgcagtctg ggggcggagt ggtgcagcct 120
gggcggtcac tgaggctgtc ctgcaaggct tctggctaca cctttactag atctacgatg 180

cactgggtaa ggcaggcccc tggaaagggt ctggaatgga ttggatacat taatcctagc 240
agtgcttata ctaattacaa tcagaaattc aaggacaggt tcacaatcag cgcagacaaa 300
tccaagagca cagccttcct gcagatggac agcctgaggc ccgaggacac cggcgtctat 360
ttctgtgcac ggccccaagt ccactatgat tacaacgggt ttccttactg gggccaaggg 420
actcccgtca ctgtctctag cggtggcgga gggtctgggg gtggcggatc cggaggtggt 480
ggctctgcac aagacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 540
gacagggtca ccatcacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 600
cagacccccg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 660
gtccctagcc gcttcagtgg cagtgggtct gggaccgact tcaccctcac aatcagcagc 720
ctgcagcccg aagatatcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 780
ttcggacagg ggaccaagct acaaattaca cgacgaactg agcccaaatc ttctgacaaa 840
actcacacat gcccaccgtg cccagcacct gaactcctgg gtggaccgtc agtcttcctc 900
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 960
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1020
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acgccagcac gtaccgtgtg 1080
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1140
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1200
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1260
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag 1320
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
tccttcttcc tctacagcaa gctcaccgtg gacaagagcc ggtggcagca ggggaacgtc 1440
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
ctgtctccgg gtaaatgaaa tgtacagcgg ccgcctcgag 1540

<210> 257
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 H3-L2 N297A (22 aa leader) Amino Acid

<400> 257
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly
            20   25   30
Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys
                85   90   95
Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp
            100   105   110
Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        115   120   125
Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln
145   150   155   160
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165   170   175
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            180   185   190
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        195   200   205
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    210   215   220
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
225   230   235   240
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                245   250   255
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Arg Thr Glu Pro Lys
            260   265   270
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu

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        275                 280                 285
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            340                 345                 350
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    370                 375                 380
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                405                 410                 415
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    450                 455                 460
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
Leu Ser Pro Gly Lys
            500


<210> 258
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-(VH-VL)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 258
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
    130                 135                 140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
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            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
        195                 200                 205
Ser Leu Thr Ile Ser Ser Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg
                245


<210> 259
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 259
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg
                245


<210> 260
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2)

<220>
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<221> SITE
<222> (122)...(138)
<223> Linker

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

<210> 261
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 261
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg
                245

<210> 262
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 262
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg
                245

<210> 263

<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1)

<220>
<221> SITE
<222> (122)...(138)
<223> Liniker

<400> 263
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg
                245

<210> 264
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 264
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe

50 55 60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg
245

<210> 265
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7 IgG1-N297A (No leader)

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

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 266
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG1-AA-N297A (No leader)

<400> 266
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
    130                 135                 140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
        195                 200                 205
Ser Leu Thr Ile Ser Ser Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
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225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 267
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG2-AA-N297A (No leader)

<400> 267
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
130 135 140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
195 200 205

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

<210> 268
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) IgG4-AA-N297A (No leader)

<400> 268
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
130 135 140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala

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

<210> 269
<211> 521
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Cris7-(VH-VL) HM1 (No leader)

<400> 269
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
130 135 140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145 150 155 160

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

<210> 270
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1) IgG1-N297A (No leader)

<400> 270
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

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                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260                 265                 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275                 280                 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    290                 295                 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305                 310                 315                 320
Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340                 345                 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355                 360                 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370                 375                 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385                 390                 395                 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405                 410                 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420                 425                 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435                 440                 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450                 455                 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 271
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1) IgG1-AA-N297A (No leader)

<400> 271
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
```

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 272
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1) IgG2-AA-N297A (No leader)

<400> 272
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

```
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu
                325                 330                 335
Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350
Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365
Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
            420                 425                 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 273
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1) IgG4-AA-N297A (No leader)

<400> 273
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 274
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1) HM1 (No leader)
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<400> 274

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
            260                 265                 270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
        275                 280                 285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
    290                 295                 300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305                 310                 315                 320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
                325                 330                 335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
            340                 345                 350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
        355                 360                 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465                 470                 475                 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
                485                 490                 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
            500                 505                 510
Asp Lys His His His His His His
        515                 520
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<210> 275
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2) IgG1-N297A (No leader)

<400> 275
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260   265   270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275   280   285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    290   295   300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305   310   315   320
Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val
                325   330   335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340   345   350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355   360   365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370   375   380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385   390   395   400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405   410   415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420   425   430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435   440   445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450   455   460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 276
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2) IgG1-AA-N297A (No leader)

<400> 276
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 277
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2) IgG2-AA-N297A (No leader)

<400> 277
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
290 295 300
Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu
325 330 335
Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 278
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2) IgG4-AA-N297A (No leader)

<400> 278
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

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

<210> 279
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2) HM1 (No leader)

<400> 279
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
260 265 270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
275 280 285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
290 295 300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305 310 315 320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
325 330 335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
340 345 350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
355 360 365

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Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465                 470                 475                 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
                485                 490                 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
            500                 505                 510
Asp Lys His His His His His His
        515                 520


<210> 280
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1) IgG1-N297A (No leader)

<400> 280
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260                 265                 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275                 280                 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
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290 295 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320
Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val
325 330 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 281
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1) IgG1-AA-N297A (No leader)

<400> 281
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270

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


<210> 282
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1) IgG2-AA-N297A (No leader)

<400> 282
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
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245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
290 295 300
Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu
325 330 335
Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365
Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 283
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1) IgG4-AA-N297A (No leader)

<400> 283
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

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

<210> 284
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1) HM1 (No leader)

<400> 284
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr

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        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
            260                 265                 270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
        275                 280                 285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
    290                 295                 300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305                 310                 315                 320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
                325                 330                 335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
            340                 345                 350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
        355                 360                 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465                 470                 475                 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
                485                 490                 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
            500                 505                 510
Asp Lys His His His His His His
        515                 520


<210> 285
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2) IgG1-N297A (No leader)

<400> 285
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
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Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320
Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val
325 330 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 286
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2) IgG1-AA-N297A (No leader)

<400> 286
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly

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


<210> 287
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2) IgG2-AA-N297A (No leader)

<400> 287
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu
                325                 330                 335
Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350
Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365
Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
            420                 425                 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 288
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2) IgG4-AA-N297A (No leader)

<400> 288
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
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    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210> 289
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2) HM1 (No leader)

<400> 289
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
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Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
            260                 265                 270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
        275                 280                 285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
    290                 295                 300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305                 310                 315                 320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
                325                 330                 335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
            340                 345                 350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
        355                 360                 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465                 470                 475                 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
                485                 490                 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
            500                 505                 510
Asp Lys His His His His His His
        515                 520
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<210> 290
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1) IgG1-N297A (No leader)

<400> 290
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260   265   270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275   280   285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    290   295   300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305   310   315   320
Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val
                325   330   335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340   345   350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355   360   365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370   375   380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385   390   395   400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405   410   415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420   425   430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435   440   445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450   455   460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 291

<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1) IgG1-AA-N297A (No leader)

<400> 291
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260   265   270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275   280   285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290   295   300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305   310   315   320
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
                325   330   335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340   345   350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355   360   365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370   375   380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385   390   395   400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405   410   415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420   425   430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435   440   445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450   455   460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 292
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1) IgG2-AA-N297A (No leader)

<400> 292
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260   265   270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275   280   285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
    290   295   300
Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys
305   310   315   320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu
                325   330   335
Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340   345   350
Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355   360   365
Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370   375   380
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385   390   395   400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405   410   415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
            420   425   430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435   440   445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

    450   455   460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 293
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1) IgG4-AA-N297A (No leader)

<400> 293
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260   265   270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275   280   285
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
    290   295   300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305   310   315   320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu
                325   330   335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340   345   350
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
        355   360   365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370   375   380
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385   390   395   400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405   410   415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420   425   430

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
        435   440   445
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450   455   460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 294
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1) HM1 (No leader)

<400> 294
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
            260   265   270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
        275   280   285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
    290   295   300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305   310   315   320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
                325   330   335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
            340   345   350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
        355   360   365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370   375   380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
420 425 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465 470 475 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
485 490 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
500 505 510
Asp Lys His His His His His His
515 520

<210> 295
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2) IgG1-N297A (No leader)

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340   345   350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355   360   365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370   375   380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385   390   395   400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405   410   415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420   425   430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435   440   445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450   455   460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 296
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2) IgG1-AA-N297A (No leader)

<400> 296
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
            260   265   270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275   280   285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290   295   300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

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

<210> 297
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2) IgG2-AA-N297A (No leader)

<400> 297
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu
260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

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

<210> 298
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2) IgG4-AA-N297A (No leader)

<400> 298
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                245   250   255
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu

260 265 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
290 295 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320
Pro Arg Glu Glu Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
355 360 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 299
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2) HM1 (No leader)

<400> 299
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 Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

```
Leu Gln Ile Thr Arg Thr Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245                 250                 255
Cys Pro Pro Cys Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile
            260                 265                 270
Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr
        275                 280                 285
Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp
    290                 295                 300
Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu
305                 310                 315                 320
Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys
                325                 330                 335
Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His
            340                 345                 350
Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
        355                 360                 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 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 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr 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 Thr Gly Leu Asn Asp Ile
465                 470                 475                 480
Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp
                485                 490                 495
Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp
            500                 505                 510
Asp Lys His His His His His His
        515                 520
```

<210> 300
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 121

<400> 300
```
Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1               5                  10                  15
```

<210> 301
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 123

<400> 301
```
Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser
 1               5                  10                  15
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
            20                  25                  30
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
        35                  40                  45
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
    50                  55                  60
```

Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
65 70 75 80
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
85 90 95
Phe Glu Asp Ser Thr Lys Lys Ser Ala Cys Pro Pro Cys Pro
100 105 110

<210> 302
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 124

<400> 302
Gln Glu Lys Glu Ala Ile Glu Arg Leu Lys Ala Ala Gly Ala Pro Glu
1 5 10 15
Ser Leu Val Ile Gln Ala Tyr Phe Ala Ser Glu Lys Asn Glu Asn Leu
20 25 30
Ala Ala Asn Phe Leu Leu Ser Gln Asn Phe Asp Asp Glu Cys Pro Pro
35 40 45
Cys Pro
50

<210> 303
<211> 1615
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding H57 Half null SMIP
with human 2H7 leader sequence

<400> 303
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaga agtttacctg gtggagtcag ggggagattt agtgcagcct 120
ggaagttccc tgaaagtctc ctgtgcagcc tctggattca ccttcagtga cttctggatg 180
tactgggtcc gccaggctcc agggaagggg ctggagtggg ttggtagaat taaaaacaaa 240
cctaataatt atgcaacaga atatgcggat tccgtgagag gcagattcac catctcaaga 300
gacgactcaa gaaacagcat ctatctgcaa atgaataggt taagagtcga tgacacagcc 360
atttattact gtactagagc cgggaggttc gaccacttcg attactgggg ccaaggaacc 420
atggtcaccg tctcaagcgg tggcggaggg tctgggggtg gcggatccgg aggtggtggc 480
tctgcacaat atgagctgat ccaaccatct tcagcatcag tcactgtagg agagacggtc 540
aaaatcactt gctctgggga ccagttgcca aaaaattttg cttattggtt tcagcaaaag 600
tcagacaaga acattttact actcatatac atggataata agcgaccatc agggatccca 660
gaacgattct ctgggtccac ttcaggtaca acagccacct tgaccatcag tggagcccag 720
cctgaggatg aggctgccta ttactgtttg tcttcatatg gtgataataa cgatttagtt 780
tttggcagcg gaacccagct caccgtccta cgaactgagc ccagagtgcc cataacacag 840
aacccctgtc ctccactcaa agagtgtccc ccatgcgcag ctccagacgc agcgggtgcg 900
ccatccgtct tcatcttccc tccaaagatc aaggatgtac tcatgatctc cctgagcccc 960
atggtcacat gtgtggtggt ggatgtgagc gaggatgacc cagacgtcca gatcagctgg 1020
tttgtgaaca acgtggaagt acacacagct cagacacaaa cccatagaga ggattacgcc 1080
agtactctcc gggtggtcag tgccctcccc atccagcacc aggactggat gagtggcaag 1140
gagttcaaat gcaaggtcaa caacagagcc ctcccatccc ccatcgagaa aaccatctca 1200
aaacccagag ggccagtaag agctccacag gtatatgtct tgcctccacc agcagaagag 1260
atgactaaga aagagttcag tctgacctgc atgatcacag gcttcttacc tgccgaaatt 1320
gctgtggact ggaccagcaa tgggcgtaca gagcaaaact acaagaacac cgcaacagtc 1380
ctggactctg atggttctta cttcatgtac agcaagctca gagtacaaaa gagcacttgg 1440
gaaagaggaa gtcttttcgc ctgctcagtg gtccacgagg gtctgcacaa tcaccttacg 1500
actaagacca tctcccggtc tctgggtaaa tgagctcagc acacacaatg ctcctgggtc 1560
gaccgccggc gaagggcaag ggcgaattcg cccttagctc ggcctcgagt ctaga 1615

<210> 304
<211> 506
<212> PRT

<213> Artificial Sequence

<220>
<223> H57 Half null SMIP amino acid sequence with human
2H7 leader sequence

<400> 304
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Glu Val Tyr Leu Val Glu Ser Gly Gly Asp
20 25 30
Leu Val Gln Pro Gly Ser Ser Leu Lys Val Ser Cys Ala Ala Ser Gly
35 40 45
Phe Thr Phe Ser Asp Phe Trp Met Tyr Trp Val Arg Gln Ala Pro Gly
50 55 60
Lys Gly Leu Glu Trp Val Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr
65 70 75 80
Ala Thr Glu Tyr Ala Asp Ser Val Arg Gly Arg Phe Thr Ile Ser Arg
85 90 95
Asp Asp Ser Arg Asn Ser Ile Tyr Leu Gln Met Asn Arg Leu Arg Val
100 105 110
Asp Asp Thr Ala Ile Tyr Tyr Cys Thr Arg Ala Gly Arg Phe Asp His
115 120 125
Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
130 135 140
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr
145 150 155 160
Glu Leu Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr Val
165 170 175
Lys Ile Thr Cys Ser Gly Asp Gln Leu Pro Lys Asn Phe Ala Tyr Trp
180 185 190
Phe Gln Gln Lys Ser Asp Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp
195 200 205
Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser
210 215 220
Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu
225 230 235 240
Ala Ala Tyr Tyr Cys Leu Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val
245 250 255
Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Arg Thr Glu Pro Arg Val
260 265 270
Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys Glu Cys Pro Pro Cys
275 280 285
Ala Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro
290 295 300
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys
305 310 315 320
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
325 330 335
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
340 345 350
Glu Asp Tyr Ala Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
355 360 365
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
370 375 380
Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg Gly
385 390 395 400
Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu
405 410 415
Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu
420 425 430
Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln
435 440 445
Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe
450 455 460
Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser
465 470 475 480
Leu Phe Ala Cys Ser Val Val His Glu Gly Leu His Asn His Leu Thr

485 490 495
Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys
500 505

<210> 305
<211> 1669
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding H57-HM2 SMIP with human 2H7 leader sequence

<400> 305
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
gtcataatgt cgcgaggaga agtttacctg gtggagtcag ggggagattt agtgcagcct 120
ggaagttccc tgaaagtctc ctgtgcagcc tctggattca ccttcagtga cttctggatg 180
tactgggtcc gccaggctcc agggaagggg ctggagtggg ttggtagaat taaaaacaaa 240
cctaataatt atgcaacaga atatgcggat tccgtgagag gcagattcac catctcaaga 300
gacgactcaa gaaacagcat ctatctgcaa atgaataggt taagagtcga tgacacagcc 360
atttattact gtactagagc cgggaggttc gaccacttcg attactgggg ccaaggaacc 420
atggtcaccg tctcaagcgg tggcggaggg tctgggggtg gcggatccgg aggtggtggc 480
tctgcacaat atgagctgat ccaaccatct tcagcatcag tcactgtagg agagacggtc 540
aaaatcactt gctctgggga ccagttgcca aaaaattttg cttattggtt tcagcaaaag 600
tcagacaaga acattttact actcatatac atggataata agcgaccatc agggatccca 660
gaacgattct ctgggtccac ttcaggtaca acagccacct tgaccatcag tggagcccag 720
cctgaggatg aggctgccta ttactgtttg tcttcatatg gtgataataa cgatttagtt 780
tttggcagcg gaacccagct aaccgtccta cgaactgagc ccagagtgcc cataacacag 840
aacccctgtc ctccactcaa agagtgtccc ccatgcgcag ctagtccctc cacagacatc 900
ctaaccttca ccatcccccc ctcctttgcc gacatcttcc tcagcaagtc cgctaacctg 960
acctgtctgg tctcaaacct ggcaacctat gaaaccctga atatctcctg ggcttctcaa 1020
agtggtgaac cactggaaac caaaattaaa atcatggaaa gccatcccaa tggcaccttc 1080
agtgctaagg gtgtggctag tgtttgtgtg gaagactgga ataacaggaa ggaatttgtg 1140
tgtactgtga ctcacaggga tctgccttca ccacagaaga aattcatctc aaaacccaat 1200
gggccagtaa gagctccaca ggtatatgtc ttgcctccac cagcagaaga gatgactaag 1260
aaagagttca gtctgacctg catgatcaca ggcttcttac ctgccgaaat tgctgtggac 1320
tggaccagca atgggcgtac agagcaaaac tacaagaaca ccgcaacagt cctggactct 1380
gatggttctt acttcatgta cagcaagctc agagtacaaa agagcacttg ggaaagagga 1440
agtcttttcg cctgctcagt ggtccacgag ggtctgcaca atcaccttac gactaagacc 1500
atctcccggt ctctgggtaa aaccggtctg aacgacatct tcgaggctca gaaaatcgaa 1560
tggcacgaag attacaagga tgacgacgat aaggattaca aggatgacga cgataaggat 1620
tacaaggatg acgacgataa gcatcatcat catcatcact gactctaga 1669

<210> 306
<211> 549
<212> PRT
<213> Artificial Sequence

<220>
<223> H57-HM2 SMIP amino acid sequence with human 2H7 leader sequence

<400> 306
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Glu Val Tyr Leu Val Glu Ser Gly Gly Asp
20 25 30
Leu Val Gln Pro Gly Ser Ser Leu Lys Val Ser Cys Ala Ala Ser Gly
35 40 45
Phe Thr Phe Ser Asp Phe Trp Met Tyr Trp Val Arg Gln Ala Pro Gly
50 55 60
Lys Gly Leu Glu Trp Val Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr
65 70 75 80
Ala Thr Glu Tyr Ala Asp Ser Val Arg Gly Arg Phe Thr Ile Ser Arg
85 90 95
Asp Asp Ser Arg Asn Ser Ile Tyr Leu Gln Met Asn Arg Leu Arg Val
100 105 110

```
Asp Asp Thr Ala Ile Tyr Tyr Cys Thr Arg Ala Gly Arg Phe Asp His
        115                 120                 125
Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
    130                 135                 140
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr
145                 150                 155                 160
Glu Leu Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr Val
                165                 170                 175
Lys Ile Thr Cys Ser Gly Asp Gln Leu Pro Lys Asn Phe Ala Tyr Trp
            180                 185                 190
Phe Gln Gln Lys Ser Asp Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp
        195                 200                 205
Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser
    210                 215                 220
Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu
225                 230                 235                 240
Ala Ala Tyr Tyr Cys Leu Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val
                245                 250                 255
Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Arg Thr Glu Pro Arg Val
            260                 265                 270
Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys Glu Cys Pro Pro Cys
        275                 280                 285
Ala Ala Ser Pro Ser Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser
    290                 295                 300
Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val
305                 310                 315                 320
Ser Asn Leu Ala Thr Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln
                325                 330                 335
Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro
            340                 345                 350
Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp
        355                 360                 365
Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val Thr His Arg Asp Leu
    370                 375                 380
Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro Asn Gly Pro Val Arg
385                 390                 395                 400
Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys
                405                 410                 415
Lys Glu Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu
            420                 425                 430
Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys
        435                 440                 445
Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
    450                 455                 460
Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala
465                 470                 475                 480
Cys Ser Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr
                485                 490                 495
Ile Ser Arg Ser Leu Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala
            500                 505                 510
Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp
        515                 520                 525
Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys His
    530                 535                 540
His His His His His
545
```

<210> 307
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Half null CH2-CH3 regions

<400> 307

```
Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
```

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


<210> 308
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> HM2 (mouse CH3mu-CH3gamma) with C-termial tail

<400> 308
Ser Pro Ser Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser Phe Ala
 1               5                  10                  15
Asp Ile Phe Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val Ser Asn
            20                  25                  30
Leu Ala Thr Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln Ser Gly
        35                  40                  45
Glu Pro Leu Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro Asn Gly
    50                  55                  60
Thr Phe Ser Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp Trp Asn
65                  70                  75                  80
Asn Arg Lys Glu Phe Val Cys Thr Val Thr His Arg Asp Leu Pro Ser
                85                  90                  95
Pro Gln Lys Lys Phe Ile Ser Lys Pro Asn Gly Pro Val Arg Ala Pro
            100                 105                 110
Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys Lys Glu
        115                 120                 125
Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu Ile Ala
    130                 135                 140
Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr
145                 150                 155                 160
Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
                165                 170                 175
Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser
            180                 185                 190
Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr Ile Ser
        195                 200                 205
Arg Ser Leu Gly Lys Thr Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
    210                 215                 220
Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys
225                 230                 235                 240
```

Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Lys His His His
245 250 255
His His His

<210> 309
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> HM2 (mouse CH3mu-CH3gamma) without C-termial tail

<400> 309
Ser Pro Ser Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser Phe Ala
1 5 10 15
Asp Ile Phe Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val Ser Asn
20 25 30
Leu Ala Thr Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln Ser Gly
35 40 45
Glu Pro Leu Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro Asn Gly
50 55 60
Thr Phe Ser Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp Trp Asn
65 70 75 80
Asn Arg Lys Glu Phe Val Cys Thr Val Thr His Arg Asp Leu Pro Ser
85 90 95
Pro Gln Lys Lys Phe Ile Ser Lys Pro Asn Gly Pro Val Arg Ala Pro
100 105 110
Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys Lys Glu
115 120 125
Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu Ile Ala
130 135 140
Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr
145 150 155 160
Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
165 170 175
Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser
180 185 190
Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr Ile Ser
195 200 205
Arg Ser Leu Gly Lys
210

<210> 310
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encloding BC3 G1 N297A with
IgG1 SCC-P hinge and RSS junction amino acids

<400> 310
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcgag cccaaatctt ctgacaaaac tcacacatgc 780

ccaccgtgcc cagcacctga actcctgggt ggaccgtcag tcttcctctt ccccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960
gccaagacaa agccgcggga ggagcagtac gccagcacgt accgtgtggt cagcgtcctc 1020
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1080
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagccgg tggcagcagg ggaacgtctt ctcatgctcc 1380
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440
aaatga 1446

<210> 311
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with IgG1 SCC-P hinge and RSS
junction amino acids

<400> 311
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
245 250 255
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val
325 330 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys

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        355                 360                 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    370                 375                 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385                 390                 395                 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                405                 410                 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            420                 425                 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435                 440                 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Lys
```

<210> 312
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with hinge derived from IgA1 and RSS junction amino acids

<400> 312
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcccc tcaactccac ctaccccatc tccctcaact 780
ccacctaccc catctccctc atgcccaccg tgcccagcac ctgaactcct gggtggaccg 840
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 900
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 960
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 1020
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1080
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1140
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1200
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1260
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1320
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag ccggtggcag 1380
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1440
aagagcctct ccctgtctcc gggtaaatga   1470

<210> 313
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with hinge derived from IgA1 and RSS junction amino acids

<400> 313
```
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
```

```
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Pro Ser Thr Pro Pro Thr Pro
                245                 250                 255
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Pro Pro Cys Pro
            260                 265                 270
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        275                 280                 285
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    290                 295                 300
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305                 310                 315                 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                325                 330                 335
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            340                 345                 350
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        355                 360                 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                405                 410                 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            420                 425                 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        435                 440                 445
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485
```

<210> 314
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding BC3 G1 N297A with hinge derived from IgA2 and RSS junction amino acids

<400> 314
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcccc ccacctcccc catgcccacc gtgcccagca 780
cctgaactcc tgggtggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 840
atgatctccc ggaccccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 960
cgggaggagc agtacgccag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1020
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140
cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200
ttctatccaa gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1320
gtggacaaga gccggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatg a 1431

<210> 315
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with hinge derived from IgA2 and RSS junction amino acids

<400> 315
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50   55   60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130   135   140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145   150   155   160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165   170   175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180   185   190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210   215   220

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


<210> 316
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with
      IgG3 mini hinge and RSS junction amino acids

<400> 316
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcgag cccaaatcta gcgacacacc tcccccaagc 780
ccacggtccc catgcccacc gtgcccagca cctgaactcc tgggtggacc gtcagtcttc 840
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccccctga ggtcacatgc 900
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 960
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacgccag cacgtaccgt 1020
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1080
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1140
cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1200
caggtcagcc tgacctgcct ggtcaaaggc ttctatccaa gcgacatcgc cgtggagtgg 1260
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1320
ggctccttct tcctctacag caagctcacc gtggacaaga gccggtggca gcaggggaac 1380
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1440
```

tccctgtctc cgggtaaatg a 1461

<210> 317
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with IgG3 mini hinge and RSS
junction amino acids

<400> 317
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Thr
245 250 255
Pro Pro Pro Ser Pro Arg Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
275 280 285
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
290 295 300
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305 310 315 320
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
325 330 335
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
340 345 350
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
355 360 365
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
370 375 380
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
385 390 395 400
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
405 410 415
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
420 425 430
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
435 440 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    450   455   460
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465   470   475   480
Ser Leu Ser Pro Gly Lys
                485

<210> 318
<211> 1518
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with a
      hinge derived from IgD and RSS junction amino
      acids

<400> 318
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcgag tctccaaagg cacaggcctc ctccgtgccc 780
actgcacaac cccaagcaga gggcagcctc gccaaggcaa ccacagcccc agccaccacc 840
cgtaacacat gcccaccgtg cccagcacct gaactcctgg gtggaccgtc agtcttcctc 900
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 960
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1020
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acgccagcac gtaccgtgtg 1080
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1140
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1200
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1260
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag 1320
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
tccttcttcc tctacagcaa gctcaccgtg gacaagagcc ggtggcagca ggggaacgtc 1440
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
ctgtctccgg gtaaatga   1518

<210> 319
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with a hinge derived from IgD and
      RSS junction amino acids

<400> 319
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50   55   60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

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Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Glu Ser Pro Lys Ala Gln Ala
                245                 250                 255
Ser Ser Val Pro Thr Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys
            260                 265                 270
Ala Thr Thr Ala Pro Ala Thr Thr Arg Asn Thr Cys Pro Pro Cys Pro
        275                 280                 285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
    290                 295                 300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305                 310                 315                 320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
                325                 330                 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            340                 345                 350
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        355                 360                 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    370                 375                 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385                 390                 395                 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
                405                 410                 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            420                 425                 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        435                 440                 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    450                 455                 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465                 470                 475                 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                485                 490                 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys
            500                 505


<210> 320
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with a
      hinge derived from IgG and RSS junction amino
      acids

<400> 320
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
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agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcgag cccaaatctt ctgacaaaac tcacacaagc 780
ccaccgagcc catgcccacc gtgcccagca cctgaactcc tgggtggacc gtcagtcttc 840
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 900
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 960
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacgccag cacgtaccgt 1020
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1080
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1140
cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1200
caggtcagcc tgacctgcct ggtcaaaggc ttctatccaa gcgacatcgc cgtggagtgg 1260
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1320
ggctccttct tcctctacag caagctcacc gtggacaaga gccggtggca gcaggggaac 1380
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1440
tccctgtctc cgggtaaatg a 1461

<210> 321
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with a hinge derived from IgG and
RSS junction amino acids

<400> 321
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
245 250 255
Thr His Thr Ser Pro Pro Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu
260 265 270
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

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

<210> 322
<211> 1734
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with a hinge derived from IgE CH2 and RSS junction amino acids

<400> 322

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caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagctcc agggacttca ccccgcccac cgtgaagatc 780
ttacagtcgt ccagcgacgg cggcgggcac ttccccccga ccatccagct cctgtgcctc 840
gtctctgggt acaccccagg gactatcaac atcacctggc tggaggacgg gcaggtcatg 900
gacgtggact tgtccaccgc ctctaccacg caggagggtg agctggcctc cacacaaagc 960
gagctcaccc tcagccagaa gcactggctg tcagaccgca cctacacctg ccaggtcacc 1020
tatcaaggtc acacctttga ggacagcacc aagaagtctg catgcccacc gtgctccgga 1080
gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 1140
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1200
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1260
ccgcgggagg agcagtacgc cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1320
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1380
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1440
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1500
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1560
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1620
accgtggaca agagccggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1680
```

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1734

<210> 323
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with a hinge derived from IgE CH2 and
RSS junction amino acids

<400> 323
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Ser Arg Asp Phe Thr Pro Pro
245 250 255
Thr Val Lys Ile Leu Gln Ser Ser Ser Asp Gly Gly Gly His Phe Pro
260 265 270
Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr
275 280 285
Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu
290 295 300
Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser
305 310 315 320
Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr
325 330 335
Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys
340 345 350
Ser Ala Cys Pro Pro Cys Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro
355 360 365
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
370 375 380
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
385 390 395 400
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
405 410 415
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val
420 425 430
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
435 440 445

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

<210> 324
<211> 1557
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with a
UBA hinge and RSS junction amino acids

<400> 324
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagccag gagaaagaag ctatagagag gttgaaggcc 780
gcaggcgccc cagagagcct ggtcatccag gcctatttcg cgagtgagaa gaatgagaac 840
ttggctgcca acttcctcct gagtcagaac tttgatgacg agtgcccacc gtgcccatcc 900
ggagcacctg aactcctggg tggaccgtca gtcttcctct tccccccaaa acccaaggac 960
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1020
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1080
aagccgcggg aggagcagta cgccagcacg taccgtgtgg tcagcgtcct caccgtcctg 1140
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1200
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1260
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1320
aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1380
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1440
ctcaccgtgg acaagagccg gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1500
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga 1557

<210> 325
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with a UBA hinge and RSS junction
amino acids

<400> 325
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala

```
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130                 135                 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145                 150                 155                 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165                 170                 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
            180                 185                 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
    210                 215                 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225                 230                 235                 240
Thr Lys Leu Glu Leu Lys Arg Ser Ser Gln Glu Lys Glu Ala Ile Glu
                245                 250                 255
Arg Leu Lys Ala Ala Gly Ala Pro Glu Ser Leu Val Ile Gln Ala Tyr
            260                 265                 270
Phe Ala Ser Glu Lys Asn Glu Asn Leu Ala Ala Asn Phe Leu Leu Ser
        275                 280                 285
Gln Asn Phe Asp Asp Glu Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu
    290                 295                 300
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
305                 310                 315                 320
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                325                 330                 335
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            340                 345                 350
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
        355                 360                 365
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    370                 375                 380
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
385                 390                 395                 400
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                405                 410                 415
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            420                 425                 430
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        435                 440                 445
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    450                 455                 460
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
465                 470                 475                 480
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                485                 490                 495
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            500                 505                 510
Ser Leu Ser Pro Gly Lys
        515
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<210> 326

<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding BC3 G1 N297A with a
FOS hinge and RSS junction amino acids

<400> 326
caggtccagc tgcagcagtc tgcagctgaa ctggcaagac ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcagtgggt aaaacagagg 120
cctggacagg gtctggaatg gattggatac attaatccta gtagtggata tattgggtac 180
agtcagaagt tcaaggacaa gaccacattg actgcagaca aatcctccag cacagcctac 240
atgcaactga gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgaag 300
gtctactatg attacgacgt ttattctatg gactactggg gtcaaggaac ctcggtcacc 360
gtctcaagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 420
caaattattc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 480
atgacctgca gtgccagctc aagtgtaagt tacatgcact ggtaccagca gaagtcaggc 540
acctcccca aaagatggat ttatgacaca tccaaactgg cttctggcgt ccctgctcgc 600
ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggaggctgaa 660
gatgctgcca cttattactg ccagcagtgg agtagtaatc cactcacgtt cggtgctggg 720
accaagctgg agctgaaacg ctcgagcgag ctgactgata cactccaagc ggagacagac 780
caactagaag atgagaagtc tgctttgcag accgagattg ccaacctgct gaaggagaag 840
gaaaaactag agttcatctg cccaccgtgc ccatccggag cacctgaact cctgggtgga 900
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 960
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 1080
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1200
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 1260
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc aagcgacatc 1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagccggtgg 1440
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
cagaagagcc tctccctgtc tccgggtaaa tga 1533

<210> 327
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 G1 N297A with a FOS hinge and RSS junction
amino acids

<400> 327
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50   55   60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
    130   135   140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145   150   155   160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
                165   170   175

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


<210> 328
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 133

<400> 328
Arg Ser Ser Glu Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu
 1               5                  10                  15
Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys
            20                  25                  30
Glu Lys Glu Lys Leu Glu Phe Ile Cys Pro Pro Cys Pro Ser Gly
        35                  40                  45


<210> 329
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse CH3mu region
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<400> 329
Ser Pro Ser Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser Phe Ala
 1   5   10   15
Asp Ile Phe Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val Ser Asn
            20   25   30
Leu Ala Thr Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln Ser Gly
        35   40   45
Glu Pro Leu Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro Asn Gly
    50   55   60
Thr Phe Ser Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp Trp Asn
65   70   75   80
Asn Arg Lys Glu Phe Val Cys Thr Val Thr His Arg Asp Leu Pro Ser
                85   90   95
Pro Gln Lys Lys Phe Ile Ser Lys Pro Asn
            100   105

<210> 330
<211> 4
<212> PRT
<213> Homo sapiens

<400> 330
Cys Pro Pro Cys
 1

<210> 331
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 125

<400> 331
Arg Ser Ser Gln Glu Lys Glu Ala Ile Glu Arg Leu Lys Ala Ala Gly
 1   5   10   15
Ala Pro Glu Ser Leu Val Ile Gln Ala Tyr Phe Ala Ser Glu Lys Asn
            20   25   30
Glu Asn Leu Ala Ala Asn Phe Leu Leu Ser Gln Asn Phe Asp Asp Glu
        35   40   45
Cys Pro Pro Cys Pro Ser Gly
    50   55

<210> 332
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 126

<400> 332
Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser
 1   5   10   15
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
            20   25   30
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
        35   40   45
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
    50   55   60
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
65   70   75   80
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
                85   90   95

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

<210> 333
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 127

<400> 333
Arg Ser Ser Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala
1 5 10 15
Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala
20 25 30
Thr Thr Arg Asn Thr Cys Pro Pro Cys Pro
35 40

<210> 334
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 128

<400> 334
Arg Ser Ser Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 335
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 129

<400> 335
Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
1 5 10 15
Cys Pro

<210> 336
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 130

<400> 336
Arg Ser Ser Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg
1 5 10 15
Ser Pro Cys Pro Pro Cys Pro
20

<210> 337
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 131

<400> 337
Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 1   5   10   15
Ser Pro Cys Pro Pro Cys Pro
            20

<210> 338
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 132

<400> 338
Arg Ser Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro
 1   5   10   15
Thr Pro Ser Pro Ser Cys Pro Pro Cys Pro
            20   25

<210> 339
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 339
Gly Gly Ser
 1

<210> 340
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 340
Gly Gly Gly Ser
 1

<210> 341
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 341
Gly Gly Gly Gly Ser
 1   5

<210> 342
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Linker

<400> 342
Gly Gly Gly Gly Gly Ser
 1   5

<210> 343
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 343
Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5

<210> 344
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 344
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 345
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 345
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser

<210> 346
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 346
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Gly Ser
            20

<210> 347
<211> 25

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 347
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 348
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 348
Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5

<210> 349
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 349
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 350
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 350
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 1   5   10   15
Gly Gly Ser

<210> 351
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 351
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 1   5   10   15
Gly Gly Ser Gly Gly Gly Gly Ser
            20

<210> 352
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 352
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 1   5   10   15
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 353
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 353
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 354
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 354
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            20   25   30
Gly Gly Gly Ser
        35

<210> 355
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 355
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            20   25   30
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        35   40   45

<210> 356
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> Linker

<400> 356
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 357
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 357
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser
            20

<210> 358
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 358
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 359
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 upper hinge region

<400> 359
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 1   5   10

<210> 360
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG2 upper hinge region

<400> 360
Glu Arg Lys Cys Cys Val Glu
 1   5

<210> 361
<211> 12

<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3 upper hinge region

<400> 361
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
 1   5   10

<210> 362
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3 upper hinge region

<400> 362
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 1   5   10

<210> 363
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG4 upper hinge region

<400> 363
Glu Ser Lys Tyr Gly Pro Pro
 1   5

<210> 364
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 core hinge

<400> 364
Cys Pro Pro Cys Pro
 1   5

<210> 365
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3 core hinge

<400> 365
Cys Pro Arg Cys Pro
 1   5

<210> 366
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG4 core hinge

<400> 366
Cys Pro Ser Cys Pro
 1   5

<210> 367
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> IgG4 upper and core hinge

<400> 367
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1   5   10   15
Pro

<210> 368
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> IgG4 upper and core hinge

<400> 368
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 1   5   10   15

<210> 369
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<223> human IgD upper hinge region

<400> 369
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
 1   5   10   15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30
Asn Thr

<210> 370
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<223> human IgD upper hinge region

<400> 370
Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu Glu Gln
 1   5   10   15
Glu Glu Arg Glu Thr Lys Thr Pro
            20

<210> 371
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> human IgA1 upper hinge

<400> 371
Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
 1   5   10   15
Ser Pro Ser

<210> 372
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> human IgA2 upper hinge

<400> 372
Val Pro Pro Pro Pro Pro
 1   5

<210> 373
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> human IgECH2 upper hinge-like sequence

<400> 373
Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
 1   5   10   15
Ser Ser Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
            20   25   30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
        35   40   45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
    50   55   60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65   70   75   80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
                85   90   95
His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
            100   105

<210> 374
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> human IgM CH2 upper hinge-like sequence

<400> 374
Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
 1   5   10   15
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
            20   25   30
Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly
        35   40   45

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

<210> 375
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> huamn IgG4 AA CH2 with alanine substitutions at
      F234 and N297

<400> 375
Ala Pro Glu Ala Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 376
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG4 AA CH2 with alanine substitutions at
      L235 and N297

<400> 376
Ala Pro Glu Phe Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 377
<211> 110
<212> PRT
<213> Artificial Sequence

<220>

<223> human IgG4 AA CH2 with alanine substitutions at
G236 and N297

<400> 377
Ala Pro Glu Phe Leu Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 378
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG4 AA CH2 with alanine substitutions at
G237 and N297

<400> 378
Ala Pro Glu Phe Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 379
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 134

<400> 379
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 380
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 135

<400> 380

Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 381
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 136

<400> 381
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 382
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 137

<400> 382
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 383
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 138

<400> 383
Glu Pro Met Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 384
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 139

<400> 384
Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 385
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 140

<400> 385
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 386
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 141

<400> 386
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