SEQUENCE LISTING

<110> MEDIMMUNE, LLC

<120> BINDING MOLECULES SPECIFIC FOR IL-21 AND USES THEREOF

<130> IL21-100P1

<160> 65

<170> PatentIn version 3.5

<210> 1
<211> 564
<212> DNA
<213> Homo sapiens

<400> 1
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aaatcaagct cccaaggtca agatcgccac atgattagaa tgcgtcaact tatagatatt 180

gttgatcagc tgaaaaatta tgtgaatgac ttggtccctg aatttctgcc agctccagaa 240

gatgtagaga caaactgtga gtggtcagct ttttcctgtt ttcagaaggc ccaactaaag 300

tcagcaaata caggaaacaa tgaaaggata atcaatgtat caattaaaaa gctgaagagg 360

aaaccacctt ccacaaatgc agggagaaga cagaaacaca gactaacatg cccttcatgt 420

gattcttatg agaaaaaacc acccaaagaa ttcctagaaa gattcaaatc acttctccaa 480

aagatgattc atcagcatct gtcctctaga acacacggaa gtgaagattc ctgaggatct 540

aacttgcagt tggacattgt taca 564

<210> 2
<211> 161
<212> PRT
<213> Homo sapiens

<400> 2
Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met
1 5 10 15

Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln
20 25 30

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Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
        35                  40                  45

Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
    50                  55                  60

Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
65                  70                  75                  80

Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
                85                  90                  95

Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
            100                 105                 110

Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Glu
        115                 120                 125

Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln
    130                 135                 140

Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp
145                 150                 155                 160

Ser
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<210> 3
<211> 489
<212> DNA
<213> Macaca fascicularis

<400> 3
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caacttatag atattgttga tcagctgaaa aattatgtga atgacttgga ccctgaattt 180

ctgccagctc cagaagatgt agagacaaac tgtgagtggt cagctatttc ctgttttcag 240

aaggcccaac taaagtcagc aaatacagga aacaatgaaa ggataatcaa tttatcaatt 300

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acatgccctt catgtgattc ttatgagaaa aaaccaccca aagaattcct agaaagattc 420

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<210> 4
<211> 162
<212> PRT
<213> Macaca fascicularis

<400> 4
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Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln
20 25 30

Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
35 40 45

Leu Lys Asn Tyr Val Asn Asp Leu Asp Pro Glu Phe Leu Pro Ala Pro
50 55 60

Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Ile Ser Cys Phe Gln
65 70 75 80

Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
85 90 95

Asn Leu Ser Ile Lys Lys Leu Lys Arg Lys Ser Pro Ser Thr Gly Ala
100 105 110

Glu Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
115 120 125

Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu
130 135 140

Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
145 150 155 160

Asp Ser

<210> 5
<211> 357
<212> DNA
<213> Mus sp.

<400> 5
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ccagagaagg ggcttgagtg ggttgctgaa attagaagcg aagctgataa tcatccaaca 180

tactatgctg agtctgtgaa agggaggttc accatctcaa gagatgattc caaaagtagt 240

gtctacctgc aaatgaacag cttaagagct gaagacagtg gcatttatta ctgtactgaa 300

tatgattacg aggggtttgt acactggggc caggggacgc tggtcactgt ctctgca 357

<210> 6
<211> 116
<212> PRT
<213> Mus sp.

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

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

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

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

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

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

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

Thr Val Ser Ser
115

<210> 7
<211> 5
<212> PRT
<213> Mus sp.

<400> 7
Asp Tyr Trp Met His
1 5

<210> 8
<211> 17
<212> PRT
<213> Mus sp.

<400> 8
Thr Ile Asp Pro Ser Asp Asn Tyr Thr Ile Tyr Ser Gln Asn Phe Lys
1 5 10 15

Gly

<210> 9
<211> 7
<212> PRT
<213> Mus sp.

<400> 9
Tyr Gly Phe Ala Met Asp Tyr
1 5

<210> 10
<211> 321
<212> DNA
<213> Mus sp.

<400> 10
gatatccagc tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

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gatggaactg ttaaactcct gatctactac acatcaagat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggagcaa 240

gaagatattg ccacttactt ttgccaacag ggtcatacgc ttcctcggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 11
<211> 107
<212> PRT
<213> Mus sp.

<400> 11
Asp Ile Gln Leu Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

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

Leu Asn Trp Tyr Gln Gln Thr Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 12
<211> 11
<212> PRT
<213> Mus sp.

<400> 12
Arg Ala Ser Gln Asp Ile Ser Asn Phe Leu Asn
1 5 10

<210> 13
<211> 7
<212> PRT
<213> Mus sp.

<400> 13
Tyr Thr Ser Arg Leu His Ser
1 5

<210> 14
<211> 9
<212> PRT
<213> Mus sp.

<400> 14
Gln Gln Gly His Thr Leu Pro Arg Thr
1 5

<210> 15
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K2Ha-N56Q synthetic humanized VH region sequence

<400> 15
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 16
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K2Ha-N56Q synthetic
      humanized VH + human CH region sequence

<400> 16
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 Asp Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 17
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K2Ha-N56Q synthetic
      humanized VH region sequence

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

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

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

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

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

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

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

<210> 18
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K2Ha-N56Q synthetic humanized VL + human CL region sequence

<400> 18
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 19
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-N56Q synthetic humanized VH region sequence

<400> 19
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 20
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-N56Q synthetic humanized VH + human CH region sequence

<400> 20
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-N56Q synthetic humanized VL region sequence

<400> 21
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 22
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-N56Q synthetic humanized VL + human CL region sequence

<400> 22
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 23
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-6N56Q synthetic humanized VH region sequence

<400> 23

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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 Asp Tyr
            20                  25                  30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

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

Lys Gly Arg Val Thr Met Thr Val Asp Glu Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 24
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-6N56Q synthetic humanized VH + human CH region sequence

<400> 24
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Val Asp Glu Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
```

```
                325                 330                 335

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

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

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

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

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

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

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


<210> 25
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-6N56Q synthetic
      humanized VL region sequence

<400> 25
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 26
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: K44VHa-6N56Q synthetic humanized VL + human CL region sequence

<400> 26

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
```

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 27
<211> 357
<212> DNA
<213> Mus sp.

<400> 27
gaagtggagc ttgtggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 60

tcttgtgctg cctctggatt cacttttagt gacgcctgga tggactgggt ccgccagtct 120

ccagagaagg ggcttgagtg ggttgctgaa attagaagcg aagctgataa tcatccaaca 180

tactatgctg agtctgtgaa agggaggttc accatctcaa gagatgattc caaaagtagt 240

gtctacctgc aaatgaacag cttaagagct gaagacagtg gcatttatta ctgtactgaa 300

tatgattacg aggggtttgt acactggggc caggggacgc tggtcactgt ctctgca 357

<210> 28
<211> 119
<212> PRT
<213> Mus sp.

<400> 28
Glu Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ala
            20   25   30

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

Ala Glu Ile Arg Ser Glu Ala Asp Asn His Pro Thr Tyr Tyr Ala Glu
    50   55   60

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

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

Tyr Cys Thr Glu Tyr Asp Tyr Glu Gly Phe Val His Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ala
        115

<210> 29
<211> 5
<212> PRT
<213> Mus sp.

<400> 29
Asp Ala Trp Met Asp
1   5

<210> 30
<211> 19
<212> PRT
<213> Mus sp.

<400> 30
Glu Ile Arg Ser Glu Ala Asp Asn His Pro Thr Tyr Tyr Ala Glu Ser
1   5   10   15

Val Lys Gly

<210> 31
<211> 8
<212> PRT
<213> Mus sp.

<400> 31
Tyr Asp Tyr Glu Gly Phe Val His
1 5

<210> 32
<211> 333
<212> DNA
<213> Mus sp.

<400> 32
gacattgtgc tgacacagtc tcctgcttca ctagctgtat ctctggggca gagggccacc 60

atctcatgca gggccagcaa aagtgtcagt acatatggct atagttatat gcactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatc ttgcatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcaac acagtaggga gcttccgctc 300

acgttcggtg ctgggaccaa gctggagctg aag 333

<210> 33
<211> 111
<212> PRT
<213> Mus sp.

<400> 33
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 34
<211> 15
<212> PRT
<213> Mus sp.

<400> 34
Arg Ala Ser Lys Ser Val Ser Thr Tyr Gly Tyr Ser Tyr Met His
1 5 10 15

<210> 35
<211> 7
<212> PRT
<213> Mus sp.

<400> 35
Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 36
<211> 9
<212> PRT
<213> Mus sp.

<400> 36
Gln His Ser Arg Glu Leu Pro Leu Thr
1 5

<210> 37
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-9F11 VH-4, VH-11 synthetic humanized VH region sequence

<400> 37
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

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

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

Ala Glu Ile Arg Ser Glu Ala Asp Asn His Pro Thr Tyr Tyr Ala Glu
    50   55   60

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

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

Tyr Cys Thr Glu Tyr Asp Tyr Glu Gly Phe Val His Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 38
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-9F11 VH-6 synthetic
      humanized VH region sequence

<400> 38
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

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

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

Ala Glu Ile Arg Ser Glu Ala Asp Asn His Pro Thr Tyr Tyr Ala Glu
50 55 60

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

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

Tyr Cys Thr Glu Tyr Asp Tyr Glu Gly Phe Val His Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 39
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-9F11 VL, VL-4, VL-6 synthetic humanized VL region sequence

<400> 39
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

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

Gly Tyr Ser Tyr Met His Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro
35 40 45

Gln Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln His Ser Arg

85 90 95

Glu Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 40
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-9F11 VL-11 synthetic humanized VL region sequence

<400> 40
Asp Ile Val Leu Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

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

Gly Tyr Ser Tyr Met His Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro
35 40 45

Gln Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 41
<211> 363
<212> DNA
<213> Mus sp.

<400> 41
gaagtgcagc tggtggagtc tgggggaggc tcagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggact cactttcagt cactattaca tgtattgggt tcgccagacg 120

ccggaaaaga ggctggagtg ggtcgcaatc attagtgatg gtggtgatta cacccactac 180

tcagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caacctgtac 240

ctacaaatga gcagtctgca gtctgaggac acagccatgt attactgtgc aggagattac 300

ggatatggtt acgaggggtg gtttgcttac tggggccaag gactctggt cactgtctct 360

aca 363

<210> 42
<211> 121
<212> PRT
<213> Mus sp.

<400> 42
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser His Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Asp Gly Gly Asp Tyr Thr His Tyr Ser Asp Ser Val
50 55 60

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

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

Ala Gly Asp Tyr Gly Tyr Gly Tyr Glu Gly Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Thr
115 120

<210> 43
<211> 5

<212> PRT
<213> Mus sp.

<400> 43
His Tyr Tyr Met Tyr
1   5

<210> 44
<211> 17
<212> PRT
<213> Mus sp.

<400> 44
Ile Ile Ser Asp Gly Gly Asp Tyr Thr His Tyr Ser Asp Ser Val Lys
1   5   10   15

Gly

<210> 45
<211> 12
<212> PRT
<213> Mus sp.

<400> 45
Asp Tyr Gly Tyr Gly Tyr Glu Gly Trp Phe Ala Tyr
1   5   10

<210> 46
<211> 321
<212> DNA
<213> Mus sp.

<400> 46
gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 60

gtcacctgca aggccagtca gaatgtggat acttatgtag cctggtatca acagaaacca 120

gggcaatctc ctaaagcact gatttattcg acatcctatc ggtacagtgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagtaa tgtgcagtct 240

gaagacttgg cagagtattt ctgtcagcaa tataacagct atccgtggac gttcggtgga 300

ggcactaagc tggaaatcaa a   321

<210> 47
<211> 107

<212> PRT
<213> Mus sp.

<400> 47
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1   5   10   15

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

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

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

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

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

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

<210> 48
<211> 11
<212> PRT
<213> Mus sp.

<400> 48
Lys Ala Ser Gln Asn Val Asp Thr Tyr Val Ala
1   5   10

<210> 49
<211> 7
<212> PRT
<213> Mus sp.

<400> 49
Ser Thr Ser Tyr Arg Tyr Ser
1   5

<210> 50

<211> 9
<212> PRT
<213> Mus sp.

<400> 50
Gln Gln Tyr Asn Ser Tyr Pro Trp Thr
1   5

<210> 51
<211> 360
<212> DNA
<213> Mus sp.

<400> 51
gaggtccagc tgcaacagtt tggagctgag gtggtgaagc ctggggcttc agtgaagatg   60

tcctgcaagg cttctggcta cacattcact gactacaaca tgaactgggt gaagcagagc   120

catgaaaaga gccttgagtg gattggagat attcatccta agtttcatag tactaactac   180

aaccagaaat tcaagggaaa ggccacattg actatagaca cgtcctccag cacagcctac   240

atggagctcc gcaacctgac atctgaggac actgcagtct attactgtgc acgagttggt   300

aactacgttt actttgttat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca   360

<210> 52
<211> 120
<212> PRT
<213> Mus sp.

<400> 52
Glu Val Gln Leu Gln Gln Phe Gly Ala Glu Val Val Lys Pro Gly Ala
1   5   10   15

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

Asn Met Asn Trp Val Lys Gln Ser His Glu Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Asp Ile His Pro Lys Phe His Ser Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

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

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 53
<211> 5
<212> PRT
<213> Mus sp.

<400> 53
Asp Tyr Asn Met Asn
1 5

<210> 54
<211> 10
<212> PRT
<213> Mus sp.

<400> 54
Asp Tyr Asn Met Asn Asp Tyr Asn Met Asn
1 5 10

<210> 55
<211> 11
<212> PRT
<213> Mus sp.

<400> 55
Val Gly Asn Tyr Val Tyr Phe Val Met Asp Tyr
1 5 10

<210> 56
<211> 321
<212> DNA
<213> Mus sp.

<400> 56
agtattgtga tgacccagac tcccaaattc ctgcttgtat cagcaggaga cagggttact 60

ataacctgca aggccagtca gagtgtgagt aatgatgtag cttggtacca acagaagcca 120

gggcagtctc ctaaactcct gatatactat gcatccaatc gctacactgg agtccctgat 180

cgcttcagtg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240

gaagacctgg cagtttattt ctgtcagcag gattatacct ctccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 57
<211> 107
<212> PRT
<213> Mus sp.

<400> 57
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

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

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

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

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

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

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

<210> 58
<211> 11
<212> PRT
<213> Mus sp.

<400> 58
Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala
1 5 10

<210> 59
<211> 7
<212> PRT
<213> Mus sp.

<400> 59
Tyr Ala Ser Asn Arg Tyr Thr
1 5

<210> 60
<211> 9
<212> PRT
<213> Mus sp.

<400> 60
Gln Gln Asp Tyr Thr Ser Pro Trp Thr
1 5

<210> 61
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
synthetic humanized version of 19E3 VH sequence

<400> 61
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 62
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
synthetic humanized version of 19E3 VH sequence

<400> 62
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Met Pro Gly Ala
1 5 10 15

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

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val 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 Tyr Gly Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 63
<211> 116

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
synthetic humanized version of 19E3 VH sequence

<400> 63
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 Asp Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

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

Thr Val Ser Ser
115

<210> 64
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
synthetic humanized version of 19E3 VL sequence

<400> 64
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Phe
            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 Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

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

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

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

<210> 65
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      synthetic humanized version of 19E3 VL sequence

<400> 65
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```