

SEQUENCE LISTING

<110> UCB Biopharma Sprl

<120> Antibodies

<130> PF0130-W0

<150> GB1720975.0

<151> 2017-12-15

<160> 49

<170> PatentIn version 3.5

<210> 1

<211> 13

<212> PRT

<213> Oryctolagus cuniculus

<400> 1

Gln Ala Ser Gln Ser Val Tyr Lys Asn Asn Tyr Leu Ala
1 5 10

<210> 2

<211> 7

<212> PRT

<213> Oryctolagus cuniculus

<400> 2

Gly Ala Ser Thr Leu Ala Ser
1 5

<210> 3

<211> 12

<212> PRT

<213> Oryctolagus cuniculus

<400> 3

Ala Gly Tyr Lys Gly Gly Arg Asn Asp Gly Phe Ala
1 5 10

<210> 4

<211> 10

<212> PRT
<213> Oryctolagus cuniculus

<400> 4

Gly Ile Asp Leu Ser Ser His Asp Met Tyr
1 5 10

<210> 5
<211> 16
<212> PRT
<213> Oryctolagus cuniculus

<400> 5

Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 6
<211> 9
<212> PRT
<213> Oryctolagus cuniculus

<400> 6

Ile His Tyr Gly Asn Ser Gly Gly Leu
1 5

<210> 7
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1 N33R

<400> 7

Gln Ala Ser Gln Ser Val Tyr Lys Asn Arg Tyr Leu Ala
1 5 10

<210> 8
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-H2 S56N

<400> 8

Ala Ile Tyr Ala Ser Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H3 N102H

<400> 9

Ile His Tyr Gly His Ser Gly Gly Leu
1 5

<210> 10

<211> 140

<212> PRT

<213> Homo sapiens

<400> 10

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
35 40 45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65 70 75 80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
85 90 95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
100 105 110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
115 120 125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
130 135 140

<210> 11
<211> 112
<212> PRT
<213> Oryctolagus cuniculus

<400> 11

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

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

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

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

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

Val Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Ala Gly Tyr Lys Gly Gly
85 90 95

Arg Asn Asp Gly Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys
100 105 110

<210> 12
 <211> 336
 <212> DNA
 <213> *Oryctolagus cuniculus*

<400> 12
 gccatcgtga tgaccagac tccatcttcc aagtctgtcg ctgtgggaga cacagtcacc 60
 atcaattgcc aggccagtca gagtgtttat aagaacaact acttagcctg gtttcaacag 120
 aaaccagggc agcctcccaa acaactgatc tatgggtgcgt ccactctggc atctggggtc 180
 ccatcgcggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagcgatgtg 240
 gtgtgtgacg atgctgccac ttactactgt gcaggatata aagggtggtc taatgatggt 300
 tttgctttcg gcggagggac cgaggtggtg gtcaaaa 336

<210> 13
 <211> 114
 <212> PRT
 <213> *Oryctolagus cuniculus*

<400> 13

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

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Ser His Asp
 20 25 30

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

Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
 50 55 60

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

Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Ile His
 85 90 95

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

Ser Ser

<210> 14
<211> 342
<212> DNA
<213> Oryctolagus cuniculus

<400> 14
cagtcggtgg aggagtccgg gggtcgcctg gtcacgcctg ggacacccct gacactcacc 60
tgcacagtct ctggaatcga cctcagtagc cacgacatgt attgggtccg ccaggctcca 120
gggaaggggc tggaatacat tggagccatt tatgctagt gtagcacata ctacgcgagc 180
tgggcgaaag gccgattcac catctccaag acctcgacca cggatgatct gaaaatgacc 240
agtctgacaa ccgaggacac ggccacctat ttctgtgcca gaattcatta tggtaatagt 300
ggtgggttgt ggggccaaagg caccctgggtc accgtctcga gt 342

<210> 15
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gL3 VL

<400> 15

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 Gln Ala Ser Gln Ser Val Tyr Lys Asn
20 25 30

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

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

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

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

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

<210> 16
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gL3 VL nucl.

<400> 16
gacattcaga tgacccagtc cccttcatca ctgtccgcga gcgtgggcga cagagtgacc 60
attacgtgcc aagccagcca gtccgtgtac aagaacaact acctggcctg gttccagcaa 120
aagcccggga aggcgcaaaa acagcttatc tacggtgcat ccactctcgc ctcgggagtg 180
ccgagccgct tctcgggatc tgggtccgga actcagttca ccctgactat ctcgtccctg 240
caacccgagg atttcgccac ctactactgc gccggctata agggaggacg gaacgacggc 300
ttcgcttttg gtggaggcac caaggtcgaa atcaag 336

<210> 17
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gL3 Light chain

<400> 17

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 Gln Ala Ser Gln Ser Val Tyr Lys Asn
20 25 30

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

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

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

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

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

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 18
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gL3 Light chain nucl.

<400> 18
gacattcaga tgaccagtc cccctcatca ctgtccgcga gcgtgggcga cagagtgacc 60
attacgtgcc aagccagcca gtccgtgtac aagaacaact acctggcctg gttccagcaa 120
aagcccggga aggcgcaaaa acagcttata tacgggtgcat ccaactctgc ctcgggagtg 180
ccgagccgct tctcgggatc tgggtccgga actcagttca ccctgactat ctcgtccctg 240
caaccgagg atttcgccac ctactactgc gccggctata agggaggacg gaacgacggc 300
ttcgcttttg gtggaggcac caaggtcgaa atcaagcgta cgggtggccgc tccctccgtg 360
ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420
ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480
tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540
tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaagggtga cgcctgcgaa 600
gtgaccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 19
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gL3 VL N33R

<400> 19

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 Gln Ala Ser Gln Ser Val Tyr Lys Asn
20 25 30

Arg Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Gln
35 40 45

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

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

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

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

<210> 20
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gL3 VL N33R nucl.

<400> 20
gacattcaga tgacccagtc cccttcatca ctgtccgcga gcgtgggcga cagagtgacc 60
attacgtgcc aagccagcca gtccgtgtac aagaaccgtt acctggcctg gttccagcaa 120
aagcccggga aggcgcaaaa acagcttatc tacggtgcat ccaactctgc ctcgggagtg 180
ccgagccgct tctcgggatc tgggtccgga actcagttca ccctgactat ctcgtccctg 240
caaccgagg atttcgccac ctactactgc gccggctata agggaggacg gaacgacggc 300
ttcgcttttg gtggaggcac caaggtcgaa atcaag 336

<210> 21
<211> 219
<212> PRT
<213> Artificial Sequence

<220>

<223> 6470 gL3 Light chain N33R

<400> 21

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	Gln	Ala	Ser	Gln	Ser	Val	Tyr	Lys	Asn
			20				25						30		

Arg	Tyr	Leu	Ala	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Gln
		35				40						45			

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

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

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

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

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
		115					120					125			

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	130					135					140				

Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150					155					160

Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 22
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gL3 Light chain N33R nucl.

<400> 22
gacattcaga tgaccagtc cccttcatca ctgtccgcga gcgtgggcga cagagtgacc 60
attacgtgcc aagccagcca gtccgtgtac aagaaccgtt acctggcctg gttccagcaa 120
aagcccggga aggcgcaaaa acagcttattc tacgggtgcat ccaactctcgc ctcgggagtg 180
ccgagccgct tctcgggatc tgggtccgga actcagttca ccctgactat ctcgtccctg 240
caacccgagg atttcgccac ctactactgc gccggctata agggaggacg gaacgacggc 300
ttcgcttttg gtggaggcac caaggtcgaa atcaagcgta cggtggccgc tccctccgtg 360
ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420
ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480
tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540
tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600
gtgaccaccc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 23
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> 6470 gH23 VH

<400> 23

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

Gly Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys
50 55 60

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

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

Arg Ile His Tyr Gly Asn Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 24

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 6479gH23 VH nucl.

<400> 24

gagggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120

ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtagcac atactacgcg 180

```

agctgggcga aaggccgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg      240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat      300
ggtaatagtg gtgggttggt gggtcagggt actctgggta ccgtctcgag c                351

```

```

<210> 25
<211> 444
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 6470 gH23 Heavy chain

```

```

<400> 25

```

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
          20          25          30

```

```

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

```

```

Gly Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys
          50          55          60

```

```

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

```

```

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

```

```

Arg Ile His Tyr Gly Asn Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
          100          105          110

```

```

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

```

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 26
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470gH23 Heavy chain nucl.

<400> 26
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtagcac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtaatagtg gtgggttgtg gggtcagggt actctgggta ccgtctcgag cgcttctaca 360

```

aagggccctt ccgtgttccc tctggccctt tgctcccggt ccacctccga gtctaccgcc      420
gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgacagtgtc ctggaactct      480
ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac      540
tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt      600
aacgtggacc acaagccctc caacaccaag gtggacaagc ggggtggaatc taagtacggc      660
cctccctgcc cccctgtccc tgcccctgaa tttctgggcg gaccttccgt gttcctgttc      720
cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtgggtg      780
gtggacgtgt cccaggaaga tcccgaggtc cagttcaatt ggtacgtgga cggcgtggaa      840
gtgcacaatg ccaagaccaa gcccagagag gaacagttca actccaccta ccgggtgggtg      900
tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg      960
tccaacaagg gcctgccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc     1020
cgcgagcccc aggtgtacac cctgccccct agccaggaag agatgaccaa gaaccagggtg     1080
tccctgacct gtctgggtcaa gggcttctac ccctccgaca ttgccgtgga atgggagtcc     1140
aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggacag cgacggctcc     1200
ttcttcctgt actctcggct gaccgtggac aagtcccggt ggcaggaagg caacgtcttc     1260
tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg     1320
agcctgggca ag                                         1332

```

```

<210> 27
<211> 117
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 6470 gH23 VH S56N N102H

```

```

<400> 27

```

```

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

```

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

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

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

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

Arg Ile His Tyr Gly His Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 28
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH23 VH S56N N102H nucl.

<400> 28
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggaatac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtcacagtg gtgggttgtg gggtcagggt actctgggta ccgtctcgag c 351

<210> 29
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gH23 Heavy chain S56N N102H

<400> 29

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

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

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

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

Arg Ile His Tyr Gly His Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 30
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH23 heavy chain S56N N102H nucl.

<400> 30
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtaatac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgacaact ctaaaaacac cgtgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtcacagtg gtgggttgtg gggtcagggt actctgggta ccgtctcgag cgcttctaca 360
aaggggcccct ccgtgttccc tctggcccct tgctcccggg ccacctccga gtctaccgcc 420
gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgacagtgtc ctggaactct 480
ggcgcccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540
tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt 600

```

aacgtggacc acaagccctc caacaccaag gtggacaagc gggtggaatc taagtacggc      660
cctccctgcc ccccctgccc tgcccctgaa tttctgggcg gaccttccgt gttcctgttc      720
cccccaaagc ccaaggacac cctgatgata tcccggaccc ccgaagtac ctgcgtggtg      780
gtggacgtgt cccaggaaga tcccgaggtc cagttcaatt ggtacgtgga cggcgtggaa      840
gtgcacaatg ccaagaccaa gcccagagag gaacagttca actccaccta ccgggtggtg      900
tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg      960
tccaacaagg gcctgccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc     1020
cgcgagcccc aggtgtacac cctgccccct agccaggaag agatgaccaa gaaccagggtg     1080
tccctgacct gtctgggtcaa gggcttctac ccctccgaca ttgccgtgga atgggagtcc     1140
aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggacag cgacggctcc     1200
ttcttcctgt actctcggct gaccgtggac aagtcccggg ggcaggaagg caacgtcttc     1260
tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg     1320
agcctgggca ag                                           1332

```

```

<210> 31
<211> 117
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 6470 gH36 VH

```

```

<400> 31

```

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20           25           30

```

```

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

```

Gly Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys
50 55 60

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

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

Arg Ile His Tyr Gly Asn Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 32
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH36 VH nucl.

<400> 32
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtagcac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgactcca gcaaaaacac cctgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtaatagtg gtgggttggtg gggtcagggt actctgggta ccgtctcgag c 351

<210> 33
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gH36 Heavy chain

<400> 33

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

Gly Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys
50 55 60

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

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

Arg Ile His Tyr Gly Asn Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 34
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH36 Heavy chain nucl.

<400> 34
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggaggagg cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtagcac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgactcca gcaaaaacac cctgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtaatagtg gtgggttgtg gggtcagggt actctgggta ccgtctcgag cgcttctaca 360
aagggccctt ccgtgttccc tctggcccct tgctcccggc ccacctccga gtctaccgcc 420
gctctgggct gcctgggtcaa ggactacttc cccgagcccc tgacagtgtc ctggaactct 480
ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540
tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt 600
aacgtggacc acaagccctc caacaccaag gtggacaagc ggggtggaatc taagtacggc 660
cctccctgcc ccccctgccc tgcccctgaa tttctgggcg gaccttccgt gttcctgttc 720
cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtgggtg 780
gtggacgtgt cccaggaaga tcccagggtc cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaatg ccaagaccaa gcccagagag gaacagttca actccaccta ccgggtggtg 900
tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960
tccaacaagg gcctgccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc 1020
cgcgagcccc aggtgtacac cctgccccct agccaggaag agatgaccaa gaaccaggtg 1080
tccctgacct gtctggtcaa gggcttctac ccctccgaca ttgccgtgga atgggagtcc 1140
aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggacag cgacggctcc 1200
ttcttcctgt actctcggct gaccgtggac aagtcccgtt ggcaggaagg caacgtcttc 1260
tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320
agcctgggca ag 1332

<210> 35
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gH36 VH S56N N102H

<400> 35

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

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

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

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

Arg Ile His Tyr Gly His Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 36
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH36 VH S56N N102H nucl.

<400> 36
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtataac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgactcca gcaaaaacac cctgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtcacagtg gtgggttgtg gggtcagggt actctgggta ccgtctcgag c 351

<210> 37
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 gH36 Heavy chain S56N N102H

<400> 37

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Ser His
20 25 30

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

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

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

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

Arg Ile His Tyr Gly His Ser Gly Gly Leu Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 38
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> 6470 gH36 Heavy chain S56N N102H nucl.

<400> 38
gaggttcagc tgctggagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag taagcggcat cgacctgtcc agccacgaca tgtattgggt acgtcaggca 120
ccgggtaaag gtctggaata catcggcgcc atttatgcta gtggtaatac atactacgcg 180
agctgggcga aaggccgttt caccatctcc cgtgactcca gcaaaaacac cctgtacctg 240
cagatgaact ctctgcgtgc ggaagacact gcggtttact attgcgcgcg tattcattat 300
ggtcacagtg gtgggttggtg gggtcagggt actctgggta ccgtctcgag cgcttctaca 360
aaggggcccct ccgtgttccc tctggcccct tgctcccgggt ccacctccga gtctaccgcc 420
gctctgggct gcctgggtaa ggactacttc cccgagcccg tgacagtgtc ctggaactct 480
ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540
tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt 600
aacgtggacc acaagccctc caacaccaag gtggacaagc gggtggaatc taagtacggc 660
cctccctgcc cccctgccc tgcccctgaa tttctgggcg gaccttccgt gttcctgttc 720
cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtgggtg 780
gtggacgtgt cccaggaaga tcccagggtc cagttcaatt ggtacgtgga cggcgtggaa 840
gtgcacaatg ccaagaccaa gccagagag gaacagttca actccaccta ccgggtgggtg 900
tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg 960
tccaacaagg gcctgcccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc 1020
cgcgagcccc aggtgtacac cctgccccct agccaggaag agatgaccaa gaaccagggtg 1080

tccctgacct	gtctgggtcaa	gggctttctac	ccctccgaca	ttgccgtgga	atgggagtc	1140
aacggccagc	ccgagaacaa	ctacaagacc	acccccctg	tgctggacag	cgacggctcc	1200
ttcttcctgt	actctcggct	gaccgtggac	aagtcccgg	ggcaggaagg	caacgtcttc	1260
tcctgctccg	tgatgcacga	ggccctgcac	aaccactaca	cccagaagtc	cctgtccctg	1320
agcctgggca	ag					1332

<210>	39
<211>	107
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Human IGKV1-16 JK4 acceptor framework

<400> 39

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

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

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

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

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

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

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

<210> 40
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGKV1-16 JK4 acceptor framework nucl.

<400> 40
gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgctc gggcgagtc gggcattagc aattatttag cctggtttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacag tataatagtt accctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 41
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHV3-23 JH4 acceptor framework

<400> 41

Glu Val Gln Leu Leu 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 Ser Tyr
20 25 30

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

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

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

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

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

Ser

<210> 42
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGHV3-23 JH4 acceptor framework nucl.

<400> 42
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaatacttt 300
gactactggg gccaaaggaac cctgggtcacc gtctcctca 339

<210> 43
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Fc - human 68-140 a-syn

<400> 43

Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys Thr Val Glu
1 5 10 15

Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys Lys Asp Gln
20 25 30

Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile Leu Glu Asp
35 40 45

Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu
50 55 60

Gly Tyr Gln Asp Tyr Glu Pro Glu Ala Val Glu Lys Thr Val Ala Pro
65 70 75 80

Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu Leu Leu Gly Gly
85 90 95

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
100 105 110

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp
115 120 125

Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg
130 135 140

Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg
145 150 155 160

Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys
165 170 175

Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu
180 185 190

Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr
195 200 205

Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu
210 215 220

Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp
225 230 235 240

Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val
245 250 255

Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro
260 265 270

Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His
275 280 285

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

Gly Lys
305

<210> 44
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1 X33

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Asn (N) or Arg (R)

<400> 44

Gln Ala Ser Gln Ser Val Tyr Lys Asn Xaa Tyr Leu Ala
1 5 10

<210> 45
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-H2 X56

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is Ser (S) or Asn (N)

<400> 45

Ala Ile Tyr Ala Ser Gly Xaa Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 46

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H3 X102

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is Asn (N) or His (H)

<400> 46

Ile His Tyr Gly Xaa Ser Gly Gly Leu
1 5

<210> 47

<211> 216

<212> PRT

<213> Oryctolagus cuniculus

<400> 47

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

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

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

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

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

Val Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Ala Gly Tyr Lys Gly Gly
85 90 95

Arg Asn Asp Gly Phe Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys
100 105 110

Arg Thr Pro Val Ala Pro Thr Val Leu Ile Phe Pro Pro Ala Ala Asp
115 120 125

Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val Ala Asn Lys Tyr
130 135 140

Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly Thr Thr Gln Thr
145 150 155 160

Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser Ala Asp Cys Thr
165 170 175

Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr Gln Tyr Asn Ser
180 185 190

His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr Thr Ser Val Val
195 200 205

Gln Ser Phe Asn Arg Gly Asp Cys
210 215

<210> 48

<211> 437
<212> PRT
<213> Oryctolagus cuniculus

<400> 48

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

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Ser His Asp
20 25 30

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

Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

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

Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Ile His
85 90 95

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

Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys
115 120 125

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

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

Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu
165 170 175

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

Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr
195 200 205

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

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
245 250 255

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

Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser
275 280 285

Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu
290 295 300

Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro
325 330 335

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

Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser
355 360 365

Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr
370 375 380

Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
385 390 395 400

Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser
405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser
420 425 430

Arg Ser Pro Gly Lys
435

<210> 49
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> 6470 rabbit Fab-His heavy chain

<400> 49

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

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Ser His Asp
20 25 30

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

Ala Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
50 55 60

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

Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Ile His
85 90 95

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

Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys
115 120 125

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

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

Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu
165 170 175

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

Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr
195 200 205

Val Ala Pro Ser Thr Cys Ser Lys Pro His His His His His His His
210 215 220

His His His
225