

SEQUENCE LISTING

<110> HANGZHOU SUMGEN BIOTECH CO., LTD.

<120> FUSION PROTEIN AND USE THEREOF

<130> 0070-PA-017SG

<160> 55

<170> PatentIn version 3.5

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1201 LCDR1

<400> 1

Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala
1 5 10

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1201 LCDR2

<400> 2

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1201 LCDR3

<400> 3

Gln Gln Tyr Leu Tyr His Pro Ala Thr
1 5

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 HCDR1

<400> 4

Asp Ser Trp Ile His
1 5

<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 HCDR2

<400> 5

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

Gly

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 HCDR3

<400> 6

Arg His Trp Pro Gly Gly Phe Asp Tyr
1 5

<210> 7
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 VL

<400> 7

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr 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 Leu Tyr His Pro Ala
85 90 95

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

<210> 8
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 VH

<400> 8

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 Ser
20 25 30

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

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

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

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

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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

<220>
<223> SG1201 VL nucleotide

<400> 9
gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagggtgacc 60
atcacctgca gggccagcca ggacgtgagc accgccgtgg cctggtacca gcagaagcct 120
ggcaaggccc ctaagctgct gatctacagc gccagcttcc tgtacagcgg cgtgcctagc 180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagcct 240
gaggacttcg ccacctacta ctgccagcag tacctgtacc accctgccac cttcgggccag 300
ggcaccaagg tggagatcaa g 321

<210> 10
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1201 VH nucleotide

<400> 10
gaggtgcagc tggaggagag cggcggcggc ctggtgcagc ctggcggcag cctgaggctg 60
agctgcgccg ccagcggcctt caccttcagc gacagctgga tccactgggt gaggcaggcc 120
cctggcaagg gcctggagtg ggtggcctgg atcagccctt acggcggcag cacctactac 180
gccgacagcg tgaagggcag gttcaccatc agcgccgaca ccagcaagaa caccgcctac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc caggaggcac 300
tggcctggcg gcttcgacta ctggggccag ggcaccctgg tgaccgtgag cagc 354

<210> 11
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1201 light chain

<400> 11

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr 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 Leu Tyr His Pro Ala
85 90 95

Thr Phe Gly Gln 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> 12
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1201 light chain nucleotide

<400> 12
gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagggtgacc

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

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 14

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> SG1201 heavy chain nucleotide

<400> 14

gaggtgcagc tgggtggagag cggcggcggc ctggtgcagc ctggcggcag cctgaggctg	60
agctgcgccg ccagcggcctt caccttcagc gacagctgga tccactgggt gaggcaggcc	120
cctggcaagg gcctggagtg ggtggcctgg atcagccctt acggcggcag cacctactac	180
gccgacagcg tgaagggcag gttcaccatc agcggcgaca ccagcaagaa caccgcctac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc caggaggcac	300
tggcctggcg gcttcgacta ctggggccag ggcaccctgg tgaccgtgag cagcgctagc	360
accaagggcc catcggcttt cccctggca cctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaaagtga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttcctct tcccccaaa acccaaggac accctcatga tctccggac ccctgaggtc	780
acgtgcgtgg tgggtggacgt gagccacgaa gaccccgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta cgccagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga agagatgacc	1080
aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg taaa	1344

<210> 15
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1202 LCDR1

<400> 15

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

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1202 LCDR2

<400> 16

Asp Ala Ser Ser Arg Ala Thr
1 5

<210> 17
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1202 LCDR3

<400> 17

Gln Gln Tyr Gly Ser Leu Pro Trp Thr
1 5

<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1202 HCDR1

<400> 18

Arg Tyr Trp Met Ser
1 5

<210> 19

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1202 HCDR2

<400> 19

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 20

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1202 HCDR3

<400> 20

Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr
1 5 10

<210> 21

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1202 VL

<400> 21

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 22
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> SG1202 VH

<400> 22

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 Arg Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 23
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1202 VL nucleotide

<400> 23
gagatcgtgc tgaccagtc ccctggcacc ctgtctctgt ctcccggcga gagagccacc 60
ctgtcttgcc gggcctccca gcgggtgtcc tcctcctacc tggcctggta tcagcagaaa 120
cccggacagg cccctaggct gctgatctac gacgcctcct ccagagccac cggcatccct 180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240
cctgaggact ttgccgtgta ttactgccag cagtacggct ccctgccttg gaccttcggc 300
cagggaaacca aggtggagat caaa 324

<210> 24
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1202 VH nucleotide

<400> 24
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg cctccggctt caccttctcc cggacttgga tgtcttgggt gcgccaggct	120
cctggcaagg gactggaatg ggtggccaac atcaaacagg atggctctga gaagtactac	180
gtggactccg tgaagggccg gttcaccatc tccagggaca acgccaagaa ctccctgtac	240
ctgcagatga actccctgag ggccgaggac accgccgtgt actactgtgc ccgggagggc	300
ggatggttcg gcgagctggc cttcgattac tggggccagg gcaccctggt gacagtgtcc	360
tct	363

<210> 25
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SG1202 light chain

<400> 25

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser	
20 25 30	

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 26
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1202 light chain nucleotide

<400> 26
gagatcgtgc tgacccagtc ccctggcacc ctgtctctgt ctcccggcga gagagccacc 60
ctgtcttgcc gggcctccca gcgggtgtcc tcctcctacc tggcctggta tcagcagaaa 120
cccggacagg cccctaggct gctgatctac gacgcctcct ccagagccac cggcatccct 180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240
cctgaggact ttgccgtgta ttactgccag cagtacggct ccctgccttg gaccttcggc 300
cagggaacca aggtggagat caaacgtacg gtggctgcac catctgtctt catcttcccg 360

```

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatcccagag aggccaaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtag                      648

```

```

<210> 27
<211> 451
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> SG1202 heavy chain

```

```

<400> 27

```

```

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 Arg Tyr
          20           25           30

```

```

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

```

```

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

```

```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
          100          105          110

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 28
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> SG1202 heavy chain nucleotide

<400> 28
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg cctccggctt caccttctcc cgggtactgga tgtcttgggt gcgccaggct 120

cctggcaagg gactggaatg ggtggccaac atcaaacagg atggctctga gaagtactac	180
gtggactccg tgaagggccg gttcaccatc tccagggaca acgccaagaa ctccctgtac	240
ctgcagatga actccctgag ggccgaggac accgccgtgt actactgtgc ccgggagggc	300
ggatggttcg gcgagctggc cttcgattac tggggccagg gcaccctggt gacagtgtcc	360
tctgctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca cgtgcgtggt ggtggacgtg agccacgaag accccgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
gccagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggaa	1080
gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1140
atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 29
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 29

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

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

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 30
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M1

<400> 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

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

Asn Gln Lys Lys Gly His Phe Pro Arg Val Thr Thr Leu Ser Asp Ser
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

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

<220>
<223> M5

<400> 31

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 32
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M12

<400> 32

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

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

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

Asn Gln Arg Lys Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 33
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M35

<400> 33

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

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

Asn Gln Lys Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 34
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M37

<400> 34

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

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

<220>
<223> M41

<400> 35

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 36

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> M57

<400> 36

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly

20

25

30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

Pro Asp Asp Arg Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser
 115

<210> 37
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M67

<400> 37

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
 20 25 30

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

Asn Gly Arg Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu

50

55

60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

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

Arg Ala Lys Pro Ser
 115

<210> 38
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M81

<400> 38

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
 20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser

85

90

95

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

Arg Ala Lys Pro Ser
 115

<210> 39
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M82

<400> 39

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

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

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser His Ser
 50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

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

Arg Ala Lys Pro Ser

115

<210> 40
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M84

<400> 40

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

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

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser His Ser
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 41
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> M91

<400> 41

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 42

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> M99

<400> 42

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

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

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

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Ser
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 43
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M102

<400> 43

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

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

Asn Gly Lys Gly Gly His Phe Pro Arg Val Thr Thr Val Ser Arg Ser
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 44
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M111

<400> 44

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 45
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M122

<400> 45

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

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

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 46
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M126

<400> 46

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

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

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

Asn Gln Arg Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Thr
50 55 60

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 47
<211> 117
<212> PRT

<213> Artificial Sequence

<220>

<223> M130

<400> 47

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

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

Asn Gln Arg Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
50 55 60

Thr Arg Arg Asp Asn Met Asp Phe Ser Ile Arg Ile Arg Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

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

Arg Ala Lys Pro Ser
115

<210> 48

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> M135

<400> 48

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly

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

<210> 49
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M145

<400> 49

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly	1	5	10	15
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly	20	25	30	
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Asn Leu Ile Tyr				

35

40

45

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

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

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

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

Arg Ala Lys Pro Ser
 115

<210> 50
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1-FC

<400> 50

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 35 40 45

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

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

<210> 51
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant FC

<400> 51

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

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

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

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

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 52
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker 1

<400> 52

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 53
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> SG12473 second polypeptide chain

<400> 53

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 Ser
20 25 30

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

Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

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

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Val Ile Gln

450

455

460

Pro Asp Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg
 465 470 475 480

Cys Thr Ala Thr Ser Leu Leu Pro Val Gly Pro Ile Gln Trp Phe Arg
 485 490 495

Gly Ala Gly Pro Gly Arg Gln Leu Ile Tyr Asn Gln Lys Asp Gly His
 500 505 510

Phe Pro Arg Val Thr Thr Ala Ser Asp Leu Thr Lys Arg Asn Asn Met
 515 520 525

Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr
 530 535 540

Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp Ile Glu Phe
 545 550 555 560

Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser
 565 570 575

<210> 54

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> SG12474 second polypeptide chain

<400> 54

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 Arg Tyr
 20 25 30

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

35

40

45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435

440

445

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln
 450 455 460

Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala
 465 470 475 480

Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly Pro Ile Gln
 485 490 495

Trp Phe Arg Gly Ala Gly Pro Gly Arg Gln Leu Ile Tyr Asn Gln Lys
 500 505 510

Asp Gly His Phe Pro Arg Val Thr Thr Ala Ser Asp Leu Thr Lys Arg
 515 520 525

Asn Asn Met Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr Pro Ala Asp
 530 535 540

Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp
 545 550 555 560

Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys
 565 570 575

Pro Ser

<210> 55

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> SS002M91 monomer

<400> 55

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
210 215 220

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
225 230 235 240

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
245 250 255

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
260 265 270

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
275 280 285

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
305 310 315 320

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
325 330 335

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350