

SEQUENCE LISTING

<110> HANGZHOU SUMGEN BIOTECH CO., LTD.; SUMGEN MAB (BEIJING) BIOTECH CO., LTD.

<120> CD38 PROTEIN ANTIBODY AND APPLICATION THEREOF

<130> 0070-PA-008SG

<160> 23

<170> PatentIn version 3.5

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR1

<400> 1

Arg	Ala	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ala	Phe	Ser	Tyr	Val	His
1				5					10					15

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR2

<400> 2

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 3

<211> 9

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<220>

<223> LCDR3

<400> 3

His His Ser Arg Glu Leu Pro Phe Thr
1 5

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

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<223> HCDR1

<400> 4

Leu Tyr Trp Met Asn
1 5

<210> 5
<211> 17
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<223> HCDR2

<400> 5

Lys Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 6
<211> 10
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<213> Artificial Sequence

<220>
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<400> 6

Leu Trp Ile Ala Thr Gly Gly Phe Asp Tyr
1 5 10

<210> 7
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 7

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

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

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser 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 Thr Ile His
65 70 75 80

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

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

<210> 8
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 8

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

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

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

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

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

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

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

Thr Thr Leu Thr Val Ser Ser
115

<210> 9
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized VL nucleotide

<400> 9
gagatcgtga tgacccagag ccctgccagc ctgagcgcca gcctgggcca gagggccacc 60
atcagctgca gggccagcag cagcgtgagc agcagcgcct tcagctacgt gcactggtac 120
cagcagaaga gcggccagcc tcctaagctg ctgatctacc tggccagcaa cctggagagc 180
ggcgtgcctg ccagggttcag cggcagcggc agcggcaccg acttcaccct gaccatccac 240
cctgtggaga gcgaggacgt ggccacctac tactgccacc acagcaggga gctgcctttc 300
accttcggca gcggcaccaa gctggagatc aag 333

<210> 10
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized VH nucleotide

<400> 10
caggtgcagc tgctggagag cggcggcggc ctggtgcagc ctggcggcag cctgaagctg 60
agctgcgtgg ccagcggctt cgacttcagc ctgtactgga tgaactgggt gaggcaggcc 120
cctggcaagg gcctggagtg gatcggcaag atcaaccctg acagcagcac catcaactac 180
acccctagcc tgaaggacaa gttcttcatc agcagggaca acgccaagaa caccctgtac 240
ctgcagatga ccaaggtgag gagcggaggac accgccctgt actactgcgc caggctgtgg 300
atgccaccg gcggcttcga ctactggggc cagggcacca ccctgaccgt gagcagc 357

<210> 11
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> SG003 light chain

<400> 11

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

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

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser 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 Thr Ile His
65 70 75 80

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

Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 12
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> SG003 light chain nucleotide

<400> 12
gagatcgtga tgaccagag ccctgccagc ctgagcgcca gcctgggcca gagggccacc

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 14

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> SG003 heavy chain nucleotide

<400> 14

caggtgcagc tgctggagag cggcggcggc ctggtgcagc ctggcggcag cctgaagctg	60
agctgcgtgg ccagcggctt cgacttcagc ctgtactgga tgaactgggt gaggcaggcc	120
cctggcaagg gcctggagtg gatcggcaag atcaaccctg acagcagcac catcaactac	180
acccctagcc tgaaggacaa gttcttcatc agcagggaca acgccaagaa caccctgtac	240
ctgcagatga ccaaggtgag gagcgaggac accgccctgt actactgcgc caggctgtgg	300
atcgccaccg gcggcttcga ctactggggc cagggcacca ccctgaccgt gagcagcgct	360
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac	600
atctgcaacg tgaatcaciaa gccagcaac accaaggtgg acaagaaagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg	720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag	780
gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtcaagtt caactggtac	840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaaac catctccaaa	1020
gccaaagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg	1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag	1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1320

aagagcctct ccctgtctcc gggtaaatga

1350

<210> 15
<211> 30
<212> PRT
<213> Homo sapiens

<400> 15

Pro Glu Thr Val Leu Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro
1 5 10 15

Glu Met Arg His Val Asp Cys Gln Ser Val Trp Asp Ala Phe
20 25 30

<210> 16
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated light chain 1

<400> 16

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

Gln Arg Ala Ser Ile Ser Cys Arg Ala Ser Asn Ser Val Ser Ser Ser
20 25 30

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

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

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

Pro Val Glu Ser Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg

85

90

95

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

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

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

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

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

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

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

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

<210> 17
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutated heavy chain 1

<400> 17

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Tyr Asn Phe Ser Leu Tyr

20

25

30

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

Gly Lys Ile Gln Pro Glu Ser Ser Thr Ile Gln Tyr Thr Pro Ser Leu
 50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

420

425

430

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

Lys

<210> 18
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutated light chain 2

<400> 18

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

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

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

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

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

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

Glu Leu Pro Tyr Ser Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

115

120

125

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

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

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

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

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

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

<210> 19

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated heavy chain 2

<400> 19

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

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

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

Gly Lys Ile Ser Pro Asn Ser Ser Thr Ile Asn Tyr Ser Pro Ser Leu

50

55

60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 20
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated light chain 3

<400> 20

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

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

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser 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 Thr Ile His
65 70 75 80

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

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

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

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

145 150 155 160

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

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

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

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

<210> 21
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated heavy chain 3

<400> 21

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

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

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

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

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

Leu Gln Met Thr Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys

85

90

95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 22

<211> 218

<212> PRT

<213> Artificial Sequence

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<223> Light chain formula

<220>

<221> X20

<222> (20)..(20)

<223> X20=T or S

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<221> X27

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<223> X27=S or N

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<221> X31

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<223> X31=S or T

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<221> X34

<222> (34)..(34)

<223> X34=F or Y

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<221> X57

<222> (57)..(57)

<223> X57=N or D

<220>

<221> X58

<222> (58)..(58)

<223> X58=L or I

<220>

<221> X59

<222> (59)..(59)

<223> X59=E or Q

<220>

<221> X97

<222> (97)..(97)

<223> X97=E or Q

<220>

<221> X98

<222> (98)..(98)

<223> X98=L or V

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<221> X100

<222> (100)..(100)

<223> X100=F or S

<220>

<221> X101

<222> (101)..(101)

<223> X101=T or S

<400> 22

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

Gln Arg Ala Xaa Ile Ser Cys Arg Ala Ser Xaa Ser Val Ser Xaa Ser
20 25 30

Ala Xaa Ser Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Gln Pro Pro
35 40 45

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

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

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

Xaa Xaa Pro Xaa Xaa Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 23
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain formula

<220>
<221> X27
<222> (27)..(27)
<223> X27=F or Y

<220>
<221> X28
<222> (28)..(28)
<223> X28=D or N

<220>
<221> X33
<222> (33)..(33)
<223> X33=W or Y

<220>
<221> X52
<222> (52)..(52)
<223> X52=N, Q or S

<220>
<221> X54
<222> (54)..(54)
<223> X54=D, E or N

<220>
<221> X57
<222> (57)..(57)
<223> 57=T or S

<220>
<221> X58
<222> (58)..(58)
<223> X58=I or L

<220>
<221> X59
<222> (59)..(59)
<223> X59=N or Q

<220>
<221> X61
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<223> X61=T or S

<220>
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<223> X64=L or V

<220>
<221> X100
<222> (100)..(100)
<223> X100=W or Y

<220>
<221> X102
<222> (102)..(102)
<223> X102=A or G

<220>
<221> X103
<222> (103)..(103)
<223> X103=T or S

<220>
<221> X106
<222> (106)..(106)
<223> X106=F or Y

<220>
<221> X107
<222> (107)..(107)
<223> X107=D or N

<400> 2

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Xaa Xaa Phe Ser Leu Tyr
20 25 30

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

Gly Lys Ile Xaa Pro Xaa Ser Ser Xaa Xaa Xaa Tyr Xaa Pro Ser Xaa
50 55 60

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

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

Ala Arg Leu Xaa Ile Xaa Xaa Gly Gly Xaa Xaa Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys