

SEQUENCE LISTING

<110> F. Hoffmann-La Roche Ltd

<120> Improved antigen binding receptors

<130> P34178

<160> 130

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR H1 Kabat

<400> 1

Arg Tyr Trp Met Asn

1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR H2 Kabat

<400> 2

Glu Ile Thr Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Lys

1 5 10 15

Asp

<210> 3

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR H3 Kabat

<400> 3

Pro Tyr Asp Tyr Gly Ala Trp Phe Ala Ser
1 5 10

<210> 4

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR L1 Kabat

<400> 4

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 5

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR L2 Kabat

<400> 5

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G CDR L3 Kabat

<400> 6

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 7
<211> 433
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G-ds-scFv-CD28ATM-CD28CSD-CD3zSSD fusion pETR17096

<400> 7

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
130 135 140

Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr
145 150 155 160

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
165 170 175

Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr
180 185 190

Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile
195 200 205

Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu
210 215 220

Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
225 230 235 240

Cys Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Phe Trp Val
245 250 255

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
260 265 270

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
275 280 285

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
290 295 300

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
305 310 315 320

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
325 330 335

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
340 345 350

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
355 360 365

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
370 375 380

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
385 390 395 400

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
405 410 415

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
420 425 430

Arg

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

<220>
<223> Anti-P329G-ds VH

<400> 8

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 9

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G-ds VL

<400> 9

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe
50 55 60

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

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

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 10
<211> 248
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G-ds-scFv

<400> 10

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
130 135 140

Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr
145 150 155 160

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
165 170 175

Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr
180 185 190

Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile
195 200 205

Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu
210 215 220

Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
225 230 235 240

Cys Gly Thr Lys Leu Thr Val Leu
245

<210> 11
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> CD28ATM

<400> 11

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 12
<211> 41
<212> PRT
<213> Artificial sequence

<220>

<223> CD28CSD

<400> 12

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 13

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> CD3zSSD

<400> 13

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

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

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 14

<211> 180

<212> PRT

<213> Artificial sequence

<220>

<223> CD28ATM-CD28-CD3z

<400> 14

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
65 70 75 80

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
85 90 95

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
100 105 110

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
115 120 125

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
130 135 140

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
145 150 155 160

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
165 170 175

Leu Pro Pro Arg
180

<210> 15
<211> 238
<212> PRT
<213> Artificial sequence

<220>
<223> eGFP

<400> 15

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

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

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

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 16
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> (G4S)₄ linker

<400> 16

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

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

<220>
<223> G4S linker

<400> 17

Gly Gly Gly Gly Ser
1 5

<210> 18
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> T2A linker

<400> 18

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 19
<211> 1356
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-P329G-ds-scFv-CD28ATM-CD28CSD-CD3zSSD fusion pETR17096

<400> 19
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag 60
gtgaagctgc tggagagcgg cggcggcctg gtgcagcccg gcggcagcct gaagctgagc 120
tgcgccgcca gcggcttcga cttcagcagg tactggatga actgggtgag gcaggccccc 180
ggcaagtgtc tggagtggat cggcgagatc acccccgaca gcagcaccat caactacacc 240
cccagcctga aggacaagtt catcatcagc agggacaacg ccaagaacac cctgtacctg 300

cagatgatca aggtgaggag cgaggacacc gccctgtact actgcgtgag gccctacgac	360
tacggcgcct ggttcgccag ctggggccag ggcaccctgg tgaccgtgag cgccggaggg	420
ggcgggaagtg gtggcggggg aagcggcggg ggtggcagcg gagggggcgg atctcaggcc	480
gtggtgaccc aggagagcgc cctgaccacc agccccggcg agaccgtgac cctgacctgc	540
aggagcagca ccggcgccgt gaccaccagc aactacgcca actgggtgca ggagaagccc	600
gaccacctgt tcaccggcct gatcggcggc accaacaaga gggcccccg cgtgcccgc	660
aggttcagcg gcagcctgat cggcgacaag gccgccctga ccatcaccgg cgcccagacc	720
gaggacgagg ccatctactt ctgcgccctg tggtagca accactgggt gttcggctgt	780
ggcaccaagc tgaccgtgct gggagggggc ggatccttct gggtgctggt ggtggtgggc	840
ggcgtgctgg cctgctacag cctgctggtg accgtggcct tcatcatctt ctgggtgagg	900
agcaagagga gcaggctgct gcacagcgac tacatgaaca tgacccccag gagggccggc	960
cccaccagga agcactacca gccctacgcc cccccaggg acttcgccgc ctacaggagc	1020
agggtgaagt tcagcaggag cgccgacgcc ccgcctacc agcaggggcca gaaccagctg	1080
tataacgagc tgaacctggg caggagggag gtagtacgagc tgctggacaa gaggaggggc	1140
agggaccccg agatgggcgg caagcccagg aggaagaacc cccaggaggg cctgtataac	1200
gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg	1260
aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc	1320
tacgacgccc tgcacatgca ggccctgccc cccagg	1356

<210> 20
 <211> 357
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Anti-P329G-ds VH

<400> 20	
gaggtgaagc tgctggagag cggcggcggc ctggtgcagc ccggcggcag cctgaagctg	60
agctgcgccg ccagcggcctt cgacttcagc aggtactgga tgaactgggt gaggcaggcc	120

cccggaagt gtctggagt gatcggcgag atcaccccg acagcagcac catcaactac	180
acccccagcc tgaaggacaa gttcatcatc agcagggaca acgccaagaa caccctgtac	240
ctgcagatga tcaaggtgag gagcgaggac accgccctgt actactgcgt gaggccctac	300
gactacggcg cctggttcgc cagctggggc cagggcaccc tggtgaccgt gagcgcc	357

<210> 21
 <211> 327
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Anti-P329G-ds VL

<400> 21	
caggccgtgg tgaccagga gagcgccctg accaccagcc ccggcgagac cgtgaccctg	60
acctgcagga gcagcaccgg cgccgtgacc accagcaact acgccaactg ggtgcaggag	120
aagcccgacc acctgttcac cggcctgatc ggcggcacca acaagagggc ccccggcgtg	180
cccgccaggt tcagcggcag cctgatcggc gacaaggccg ccctgaccat caccggcgcc	240
cagaccgagg acgaggccat ctacttctgc gccctgtggt acagcaacca ctgggtgttc	300
ggctgtggca ccaagctgac cgtgctg	327

<210> 22
 <211> 799
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Anti-P329G-ds-scFv

<400> 22	
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag	60
gtgaagctgc tggagagcgg cggcggcctg gtgcagcccg gcggcagcct gaagctgagc	120
tgcgccgcca gcggcttcga cttcagcagg tactggatga actgggtgag gcaggccccc	180
ggcaagtgtc tggagtggat cggcgagatc acccccgaca gcagcaccat caactacacc	240
cccagcctga aggacaagtt catcatcagc agggacaacg ccaagaacac cctgtacctg	300

cagatgatca aggtgaggag cgaggacacc gccctgtact actgcgtgag gccctacgac	360
tacggcgccct ggttcgccag ctggggccag ggcaccctgg tgaccgtgag cgccggaggg	420
ggcgggaagtg gtggcggggg aagcggcggg ggtggcagcg gagggggcgg atctcaggcc	480
gtggtgaccc aggagagcgc cctgaccacc agccccggcg agaccgtgac cctgacctgc	540
aggagcagca ccggcgccgt gaccaccagc aactacgcca actgggtgca ggagaagccc	600
gaccacctgt tcaccggcct gatcggcggc accaacaaga gggcccccg cgtgcccgcc	660
aggttcagcg gcagcctgat cggcgacaag gccgccctga ccatcaccgg cgcccagacc	720
gaggacgagg ccatctactt ctgcgccctg tggtagcga accactgggt gttcggctgt	780
ggcaccaagc tgaccgtgc	799

<210> 23
 <211> 647
 <212> DNA
 <213> Artificial sequence

<220>
 <223> IRES EV71, internal ribosomal entry side

<400> 23	
cccgaagtaa cttagaagct gtaaataaac gatcaatagc aggtgtggca caccagtcac	60
accttgatca agcacttctg tttccccgga ctgagtatca ataggctgct cgcgcggtg	120
aaggagaaaa cgttcgttac ccgaccaact acttcgagaa gcttagtacc accatgaacg	180
aggcagggtg tttcgctcag cacaaccca gtgtagatca ggctgatgag tcaactgcaac	240
cccatgggc gaccatggca gtggctgcgt tggcggcctg cccatggaga aatccatggg	300
acgctctaata tctgacatgg tgtgaagtgc ctattgagct aactggtagt cctccggccc	360
ctgattgcgg ctaatcctaa ctgcggagca catgctcaca aaccagtggg tgggtgtgtcg	420
taacgggcaa ctctgcagcg gaaccgacta ctttgggtgt ccgtgtttcc ttttattcct	480
atattggctg cttatgggtga caatcaaaaa gttgttacca tatagctatt ggattggcca	540
tccggtgtgc aacagggcaa ctgtttacct atttattgggt tttgtaccat tatcactgaa	600
gtctgtgatc actctcaaata tcattttgac cctcaacaca atcaaac	647

<210> 24
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> CD28ATM

<400> 24
ttttgggtgc tgggtgggtg tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60
gcctttatta ttttctgggt g 81

<210> 25
<211> 123
<212> DNA
<213> Artificial sequence

<220>
<223> CD28CSD

<400> 25
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
tcc 123

<210> 26
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> CD3z SSD

<400> 26
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcaggggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gactacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggagggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 27
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> CD28ATM-CD28-CD3z

<400> 27
ttctgggtgc tgggtggtggt gggcggcgtg ctggcctgct acagcctgct ggtgaccgtg 60
gccttcatca tcttctgggt gaggagcaag aggagcaggc tgctgcacag cgactacatg 120
aacatgaccc ccaggaggcc cggccccacc aggaagcact accagcccta cgcccccccc 180
agggacttcg ccgcctacag gagcagggtg aagttcagca ggagcgccga cgcccccgcc 240
taccagcagg gccagaacca gctgtataac gagctgaacc tgggcaggag ggaggagtac 300
gacgtgctgg acaagaggag gggcagggac cccgagatgg gcggcaagcc caggaggaag 360
aacccccagg agggcctgta taacgagctg cagaaggaca agatggccga ggcctacagc 420
gagatcggca tgaagggcga gaggaggagg ggcaagggcc acgacggcct gtaccagggc 480
ctgagcaccg ccaccaagga cacctacgac gccctgcaca tgcaggccct gccccccagg 540

<210> 28
<211> 63
<212> DNA
<213> Artificial sequence

<220>
<223> T2A element

<400> 28
tccggagagg gcagaggaag tcttctaaca tgcggtgacg tggaggagaa tcccggccct 60
agg 63

<210> 29
<211> 717
<212> DNA
<213> Artificial sequence

<220>

<223> eGFP

<400> 29

gtgagcaagg gcgaggagct gttcaccggg gtggtgcca tcctggtcga gctggacggc	60
gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc	120
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc	180
gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag	240
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgac catcttcttc	300
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg	360
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag	420
ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc	480
atcaaggtga acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac	540
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac	600
ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg	660
ctggagttcg tgaccgccgc cgggatcact ctcggcatgg acgagctgta caagtga	717

<210> 30

<211> 2136

<212> DNA

<213> Artificial sequence

<220>

<223> Anti-P329G-ds-scFv-CD28ATM-CD28CSD-CD3zSSD-eGFP fusion pETR17096

<400> 30

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag	60
gtgaagctgc tggagagcgg cggcggcctg gtgcagcccg gcggcagcct gaagctgagc	120
tgcgccgcca gcggcttcga cttcagcagg tactggatga actgggtgag gcaggcccc	180
ggcaagtgtc tggagtggat cggcgagatc acccccgaca gcagcaccat caactacacc	240
cccagcctga aggacaagtt catcatcagc agggacaacg ccaagaacac cctgtacctg	300
cagatgatca aggtgaggag cgaggacacc gccctgtact actgcgtgag gccctacgac	360

tacggcgctt ggttcgccag ctggggccag ggcaccctgg tgaccgtgag cgccggaggg	420
ggcgggaagt gtggcggggg aagcggcggg ggtggcagcg gagggggcgg atctcaggcc	480
gtggtgaccc aggagagcgc cctgaccacc agccccggcg agaccgtgac cctgacctgc	540
aggagcagca ccggcgccgt gaccaccagc aactacgcca actgggtgca ggagaagccc	600
gaccacctgt tcaccggcct gatcggcggc accaacaaga gggcccccg cgtgcccgc	660
aggttcagcg gcagcctgat cggcgacaag gccgccctga ccatcaccgg cgcccagacc	720
gaggacgagg ccatctactt ctgcgccctg tggtagcga accactgggt gttcggctgt	780
ggcaccaagc tgaccgtgct gggagggggc ggatccttct gggtagctgt ggtggtgggc	840
ggcgtgctgg cctgctacag cctgtggtg accgtggcct tcatcatctt ctgggtgagg	900
agcaagagga gcaggctgct gcacagcgac tacatgaaca tgacccccag gagggccggc	960
cccaccagga agcactacca gccctacgcc cccccaggg acttcgccgc ctacaggagc	1020
agggtgaagt tcagcaggag cgccgacgcc ccgcctacc agcagggccca gaaccagctg	1080
tataacgagc tgaacctggg caggagggag gtagtagcgc tgctggacaa gaggaggggc	1140
agggaccccc agatgggcgg caagcccagg aggaagaacc cccaggaggg cctgtataac	1200
gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg	1260
aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc	1320
tacgacgccc tgcacatgca ggccctgccc cccagggtccg gagagggcag aggaagtctt	1380
ctaakatgca gtgacgtgga ggagaatccc ggccctaggg tgagcaaggg cgaggagctg	1440
ttcaccgggg tgggtcccat cctggtcgag ctggacggcg acgtaaaccg ccacaagttc	1500
agcgtgtccg gcgagggcga gggcgatgcc acctacggca agctgaccct gaagtccatc	1560
tgcaccaccg gcaagctgcc cgtgccctgg cccaccctcg tgaccaccct gacctacggc	1620
gtgcagtgtc tcagccgcta cccgaccac atgaagcagc acgacttctt caagtccgcc	1680
atgcccgaag gctacgtcca ggagcgcacc atcttcttca aggacgacgg caactacaag	1740
acccgcgccg aggtgaagtt cgagggcgac accctgggtga accgcatcga gctgaagggc	1800
atcgacttca aggaggacgg caacatcctg gggcacaagc tggagtacaa ctacaacagc	1860

cacaacgtct	atatcatggc	cgacaagcag	aagaacggca	tcaaggtgaa	cttcaagatc	1920
cgccacaaca	tcgaggacgg	cagcgtgcag	ctcgccgacc	actaccagca	gaacaccccc	1980
atcggcgacg	gccccgtgct	gctgcccgac	aaccactacc	tgagcaccca	gtccgccctg	2040
agcaaagacc	ccaacgagaa	gcgcgatcac	atggtcctgc	tggagttcgt	gaccgccgcc	2100
gggatcactc	tcggcatgga	cgagctgtac	aagtga			2136

$\langle 210 \rangle$	31
$\langle 211 \rangle$	433
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> Anti-P329G-scFv- CD28ATM-CD28CSD-CD3zSSD fusion

<400> 31

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
130 135 140

Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr
145 150 155 160

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
165 170 175

Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr
180 185 190

Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile
195 200 205

Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu
210 215 220

Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Phe Trp Val
245 250 255

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
260 265 270

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
275 280 285

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
290 295 300

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
305 310 315 320

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
325 330 335

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
340 345 350

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
355 360 365

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
370 375 380

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
385 390 395 400

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
405 410 415

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
420 425 430

Arg

<210> 32
<211> 119
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G VH

<400> 32

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 33
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G VL

<400> 33

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe
50 55 60

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

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

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 34
<211> 248
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G-scFv

<400> 34

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
130 135 140

Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr
145 150 155 160

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
165 170 175

Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr
180 185 190

Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile
195 200 205

Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu
210 215 220

Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu
245

<210> 35
<211> 1356
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-P329G-scFv-CD28ATM-CD28CSD-CD3zSSD fusion

<400> 35
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag 60

gtgaagctgc tggagagcgg cggcggcctg gtgcagcccc gcggcagcct gaagctgagc 120

tgcgcccca gcggttcga cttcagcagg tactggatga actgggtgag gcaggcccc	180
ggcaagggtc tggagtggat cggcgagatc acccccgaca gcagcaccat caactacacc	240
cccagcctga aggacaagtt catcatcagc agggacaacg ccaagaacac cctgtacctg	300
cagatgatca aggtgaggag cgaggacacc gccctgtact actgcgtgag gccctacgac	360
tacggcgctt ggttcgccag ctggggccag ggcaccctgg tgaccgtgag cgccggaggg	420
ggcggaaagt gtggcggggg aagcggcggg ggtggcagcg gagggggcgg atctcaggcc	480
gtggtgaccc aggagagcgc cctgaccacc agccccggcg agaccgtgac cctgacctgc	540
aggagcagca ccggcgccgt gaccaccagc aactacgcca actgggtgca ggagaagccc	600
gaccacctgt tcaccggcct gatcggcggc accaacaaga gggcccccg cgtgcccgcc	660
aggttcagcg gcagcctgat cggcgacaag gccgccctga ccatcaccgg cgcccagacc	720
gaggacgagg ccatctactt ctgcgccctg tggtagca accactgggt gttcggcgg	780
ggcaccaagc tgaccgtgct gggagggggc ggatccttct ggggtgctgg ggtggtgggc	840
ggcgtgctgg cctgctacag cctgctgggt accgtggcct tcatcatctt ctgggtgagg	900
agcaagagga gcaggctgct gcacagcgac tacatgaaca tgacccccag gagggccggc	960
cccaccagga agcactacca gccctacgcc cccccaggg acttcgccgc ctacaggagc	1020
agggtgaagt tcagcaggag cgccgacgcc cccgcctacc agcagggcc gaaccagctg	1080
tataacgagc tgaacctggg caggagggag gagtacgacg tgctggacaa gaggaggggc	1140
agggaccccg agatgggcgg caagcccagg aggaagaacc cccaggagg cctgtataac	1200
gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg	1260
aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc	1320
tacgacgccc tgcacatgca ggccctgccc cccagg	1356

<210> 36

<211> 357

<212> DNA

<213> Artificial sequence

<220>

<223> Anti-P329G VH

<400> 36

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gaggtgaagc tgctggagag cggcggcggc ctggtgcagc ccggcggcag cctgaagctg      60
agctgcgccg ccagcggcctt cgacttcagc aggtactgga tgaactgggt gaggcaggcc      120
cccggcaagg gtctggagtg gatcggcgag atcacccccg acagcagcac catcaactac      180
acccccagcc tgaaggacaa gttcatcatc agcagggaca acgccaagaa caccctgtac      240
ctgcagatga tcaaggtgag gagcgaggac accgccctgt actactgcgt gaggccctac      300
gactacggcg cctggttcgc cagctggggc cagggcaccc tggtgaccgt gagcgcc      357
```

<210> 37

<211> 327

<212> DNA

<213> Artificial sequence

<220>

<223> Anti-P329G VL

<400> 37

```
caggccgtgg tgacccagga gagcgccctg accaccagcc ccggcgagac cgtgaccctg      60
acctgcagga gcagcaccgg cgccgtgacc accagcaact acgccaactg ggtgcaggag      120
aagcccgacc acctgttcac cggcctgatc ggcggcacca acaagagggc ccccggcgtg      180
cccgccaggt tcagcggcag cctgatcggc gacaaggccg ccctgaccat caccggcgcc      240
cagaccgagg acgaggccat ctacttctgc gccctgtggt acagcaacca ctgggtgttc      300
ggcgggtggca ccaagctgac cgtgctg      327
```

<210> 38

<211> 2136

<212> DNA

<213> Artificial sequence

<220>

<223> Anti-P329G-scFv-CD28ATM-CD28CSD-CD3zSSD-eGFP fusion

<400> 38

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atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag      60
gtgaagctgc tggagagcgg cggcggcctg gtgcagcccc gcggcagcct gaagctgagc      120
```

tgcgccgcca gcggttcga cttcagcagg tactggatga actgggtgag gcaggcccc	180
ggcaagggtc tggagtggat cggcgagatc acccccgaca gcagcaccat caactacacc	240
cccagcctga aggacaagtt catcatcagc agggacaacg ccaagaacac cctgtacctg	300
cagatgatca aggtgaggag cgaggacacc gccctgtact actgcgtgag gccctacgac	360
tacggcgctt ggttcgccag ctggggccag ggcaccctgg tgaccgtgag cgccggaggg	420
ggcggaaagt gtggcggggg aagcggcggg ggtggcagcg gagggggcgg atctcaggcc	480
gtggtgaccc aggagagcgc cctgaccacc agccccggcg agaccgtgac cctgacctgc	540
aggagcagca ccggcgccgt gaccaccagc aactacgcca actgggtgca ggagaagccc	600
gaccacctgt tcaccggcct gatcggcggc accaacaaga gggcccccg cgtgcccgcc	660
aggttcagcg gcagcctgat cggcgacaag gccgccctga ccatcaccgg cgcccagacc	720
gaggacgagg ccatctactt ctgcgccctg tggtagca accactgggt gttcggcgg	780
ggcaccaagc tgaccgtgct gggagggggc ggatccttct ggggtgctgg ggtggtgggc	840
ggcgtgctgg cctgctacag cctgctgggt accgtggcct tcatcatctt ctgggtgagg	900
agcaagagga gcaggctgct gcacagcgac tacatgaaca tgacccccag gaggcccggc	960
cccaccagga agcactacca gccctacgcc cccccaggg acttcgccgc ctacaggagc	1020
agggtgaagt tcagcaggag cgccgacgcc cccgcctacc agcagggcc gaaccagctg	1080
tataacgagc tgaacctggg caggagggag gagtacgacg tgctggacaa gaggaggggc	1140
agggaccccg agatgggcgg caagcccagg aggaagaacc cccaggaggg cctgtataac	1200
gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg	1260
aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc	1320
tacgacgccc tgcacatgca ggccctgccc cccagggtccg gagagggcag aggaagtctt	1380
ctaakatgcg gtgacgtgga ggagaatccc ggccctaggg tgagcaaggg cgaggagctg	1440
ttcaccgggg tggtgcccac cctggtcgag ctggacggcg acgtaaacgg ccacaagtgc	1500
agcgtgtccg gcgagggcga gggcgatgcc acctacggca agctgaccct gaagttcatc	1560
tgcaccaccg gcaagctgcc cgtgccctgg cccaccctcg tgaccaccct gacctacggc	1620

```

gtgcagtgtc tcagccgcta ccccgaccac atgaagcagc acgacttctt caagtccgcc      1680
atgcccgaag gctacgtcca ggagcgcacc atcttcttca aggacgacgg caactacaag      1740
acccgcgccc aggtgaagtt cgagggcgac accctgggtga accgcatcga gctgaagggc      1800
atcgacttca aggaggacgg caacatcctg gggcacaagc tggagtacaa ctacaacagc      1860
cacaacgtct atatcatggc cgacaagcag aagaacggca tcaaggtgaa cttcaagatc      1920
cgccacaaca tcgaggacgg cagcgtgcag ctcgccgacc actaccagca gaacaccccc      1980
atcggcgacg gccccgtgct gctgcccgac aaccactacc tgagcaccca gtccgccctg      2040
agcaaagacc ccaacgagaa gcgcgatcac atggtcctgc tggagtctgt gaccgccgcc      2100
gggatcactc tcggcatgga cgagctgtac aagtga                                2136

```

```

<210> 39
<211> 407
<212> PRT
<213> Artificial sequence

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```

<220>
<223> Anti-P329G-ds-Fab- heavy chain-CD28ATM-CD28CSD-CD3zSSD fusion
      pETR17100

```

```

<400> 39

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

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

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

Thr Leu Val Thr Val Ser Ala 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 Gly Gly
210 215 220

Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
225 230 235 240

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
245 250 255

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
260 265 270

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg

275

280

285

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
 290 295 300

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 305 310 315 320

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 325 330 335

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 340 345 350

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 355 360 365

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 370 375 380

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 385 390 395 400

Met Gln Ala Leu Pro Pro Arg
 405

<210> 40

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-P329G-ds-Fab heavy chain

<400> 40

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr

20

25

30

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala 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
 210 215 220

<210> 41
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> Anti P329G-ds-Fab light chain

<400> 41

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe
50 55 60

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

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

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Arg Thr Val
100 105 110

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 42
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> CL

<400> 42

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 43
<211> 103
<212> PRT
<213> Artificial sequence

<220>
<223> CH1

<400> 43

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys
100

<210> 44
<211> 2645
<212> DNA
<213> Artificial sequence

<220>
<223> Anti-P329G-ds-Fab-heavy chain-CD28ATM-CD28CSD-CD3zSSD fusion

pETR17100

<400> 44

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gccgtgggtga cccaggagag cgccctgacc accagccccg gcgagaccgt gaccctgacc	120
tgcaggagca gcaccggcgc cgtgaccacc agcaactacg ccaactgggt gcaggagaag	180
cccgaccacc tgttcaccgg cctgatcggc ggcaccaaca agagggccccc cggcgtgccc	240
gccaggttca gcggcagcct gatcggcgac aaggccgccc tgaccatcac cggcgcccag	300
accgaggacg aggccatcta cttctgcgcc ctgtggtaca gcaaccactg ggtgttcggc	360
tgtggcacca agctgaccgt gctgcgtacg gtggctgcac catctgtctt catcttcccg	420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtagga attccccgaa	720
gtaacttaga agctgtaaat caacgatcaa tagcagggtgt ggcacaccag tcataccttg	780
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<223> CL

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pETR17100

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50 55 60

Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
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Leu Gln Met Ile Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
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Val Arg Pro Tyr Asp Tyr Gly Ala Trp Phe Ala Ser Trp Gly Gln Gly
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Thr Leu Val Thr Val Ser Ala 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
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
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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
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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 Gly Gly
210 215 220

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Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
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Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
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Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
275 280 285

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
290 295 300

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
305 310 315 320

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
325 330 335

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
340 345 350

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
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Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
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<212> PRT
<213> Artificial sequence

<220>
<223> Anti-P329G-Fab heavy chain

<400> 49

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35 40 45

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

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

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

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

Thr Leu Val Thr Val Ser Ala 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
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<210> 50

<211> 216

<212> PRT

<213> Artificial sequence

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<223> Anti-P329G-Fab light chain

<400> 50

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Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Ala Arg Phe
50 55 60

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

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

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Thr Val
100 105 110

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

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

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

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

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
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Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
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Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 51
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<212> DNA
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pETR17594

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<210> 52
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<220>
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accactacct gagcacccag tccgccctga gcaaagaccc caacgagaag cgcgatcaca	3360
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agtga	3425

<210> 53

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-AAA CDR H1 Kabat

<400> 53

Ser Tyr Gly Met Ser
1 5

<210> 54
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA CDR H2 Kabat

<400> 54

Ser Ser Gly Gly Ser Tyr
1 5

<210> 55
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA CDR H3 Kabat

<400> 55

Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp Tyr
1 5 10

<210> 56
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA CDR L1 Kabat

<400> 56

Arg Ser Ser Gln Thr Ile Val His Ser Thr Gly His Thr Tyr Leu Glu
1 5 10 15

<210> 57
<211> 7
<212> PRT
<213> Artificial sequence

<220>

<223> Anti-AAA CDR L2 Kabat

<400> 57

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 58

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-AAA CDR L3 Kabat

<400> 58

Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 59

<211> 457

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-AAA-scFv-CD28ATM-CD28CSD-CD3zSSD fusion

<400> 59

Met Asn Phe Gly Leu Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
165 170 175

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
180 185 190

Thr Gly His Thr Tyr Leu Glu Trp Phe Leu Gln Lys Pro Gly Gln Ser
195 200 205

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
210 215 220

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
245 250 255

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
260 265 270

Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu
275 280 285

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
290 295 300

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
305 310 315 320

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
325 330 335

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
340 345 350

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
355 360 365

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
370 375 380

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
385 390 395 400

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 60
<211> 272
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA-scFv

<400> 60

Met Asn Phe Gly Leu Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
165 170 175

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
180 185 190

Thr Gly His Thr Tyr Leu Glu Trp Phe Leu Gln Lys Pro Gly Gln Ser
195 200 205

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
210 215 220

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
245 250 255

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
260 265 270

<210> 61
<211> 140
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA VH

<400> 61

Met Asn Phe Gly Leu Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135 140

<210> 62
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA VL

<400> 62

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

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

Thr Gly His Thr Tyr Leu Glu Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

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

<210> 63
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA-Fab-heavy chain-CD28ATM-CD28CSD-CD3zSSD fusion

<400> 63

Met Asn Phe Gly Leu Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240

Lys Ser Cys Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly
245 250 255

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
260 265 270

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
275 280 285

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
290 295 300

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
305 310 315 320

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
325 330 335

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
340 345 350

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
355 360 365

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
370 375 380

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
385 390 395 400

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
405 410 415

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
420 425

<210> 64
<211> 243
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA-Fab heavy chain

<400> 64

Met Asn Phe Gly Leu Ser Leu Val Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Leu Gly Met Ile Thr Thr Gly Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240

Lys Ser Cys

<210> 65
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-AAA-Fab light chain

<400> 65

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

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

Thr Gly His Thr Tyr Leu Glu Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu 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> 66
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 66
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 accccggcgc cgaaaagctg cccggaacgc cattattggg cgcagggcaa actgtgctgc 120
 cagatgtgcg aaccgggcac ctttctggtg aaagattgcg atcagcatcg caaagcggcg 180
 cagtgcgatc cgtgcattcc gggcgtgagc tttagcccgg atcatcatac ccgcccgcg 240
 tgcgaaagct gccgccattg caacagcggc ctgctgggtgc gcaactgcac cattaccgcg 300
 aacgcggaat gcgcgtgccg caacggctgg cagtgccgcg ataaagaatg caccgaatgc 360
 gatccgctgc cgaacccgag cctgaccgcg cgcagcagcc aggcgctgag cccgcatccg 420
 cagccgaccc atctgccgta tgtgagcgaa atgctggaag cgcgcaccgc gggccatatg 480
 cagaccctgg cggatttttcg ccagctgccg gcgcgcaccc tgagcaccca ttggccgccg 540
 cagcgcagcc tgtgcagcag cgattttatt cgcattctgg tgatttttag cggcatgttt 600
 ctggtgttta ccctggcggg cgcgctgttt ctgcatcagc gccgcaaata tcgcagcaac 660
 aaaggcgaaa gcccgggtgga accggcggaa ccgtgccatt atagctgccc gcgcgaagaa 720

gaaggcagca ccattccgat tcaggaagat tatcgcaaac cggaaccggc gtgcagccccg

780

<210> 67

<211> 260

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
1 5 10 15

Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
20 25 30

Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
35 40 45

Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
50 55 60

Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65 70 75 80

Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
100 105 110

Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
115 120 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
130 135 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
145 150 155 160

Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
165 170 175

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
180 185 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
195 200 205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
210 215 220

Pro Val Glu Pro Ala Glu Pro Cys His Tyr Ser Cys Pro Arg Glu Glu
225 230 235 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
245 250 255

Ala Cys Ser Pro
260

<210> 68
<211> 750
<212> DNA
<213> Mus musculus

<400> 68
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accctggcgc cgaacagctg cccggataaa cattattgga ccggcggcgg cctgtgctgc 120
cgcatgtgcg aaccgggcac cttttttgtg aaagattgcg aacaggatcg caccgcggcg 180
cagtgcgatc cgtgcattcc gggcaccagc tttagcccgg attatcatat cgcgccgcat 240
tgcgaaagct gccgccattg caacagcggc tttctgattc gcaactgcac cgtgaccgcg 300
aacgcggaat gcagctgcag caaaaactgg cagtgccgcg atcaggaatg caccgaatgc 360
gatccgccgc tgaacccggc gctgaccgcg cagccgagcg aaaccccgag cccgcagccg 420
ccgccgaccc atctgccgca tggcaccgaa aaaccgagct ggccgctgca tcgccagctg 480

ccgaacagca cctgttatag ccagcgcagc agccatcgcc cgctgtgcag cagcgattgc	540
attcgcatTTt ttgtgacctt tagcagcatg tttctgattt ttgtgctggg cgcgattctg	600
ttttttcatc agcgccgcaa ccatggcccg aacgaagatc gccaggcggt gccggaagaa	660
ccgtgcccgt atagctgccc gcgcgaagaa gaaggcagcg cgattccgat tcaggaagat	720
tatcgcaaac cggaaccggc gttttatccg	750

<210> 69
 <211> 250
 <212> PRT
 <213> Mus musculus

<400> 69

Met	Ala	Trp	Pro	Pro	Pro	Tyr	Trp	Leu	Cys	Met	Leu	Gly	Thr	Leu	Val
1				5					10					15	

Gly	Leu	Ser	Ala	Thr	Leu	Ala	Pro	Asn	Ser	Cys	Pro	Asp	Lys	His	Tyr
			20					25					30		

Trp	Thr	Gly	Gly	Gly	Leu	Cys	Cys	Arg	Met	Cys	Glu	Pro	Gly	Thr	Phe
		35					40					45			

Phe	Val	Lys	Asp	Cys	Glu	Gln	Asp	Arg	Thr	Ala	Ala	Gln	Cys	Asp	Pro
	50					55					60				

Cys	Ile	Pro	Gly	Thr	Ser	Phe	Ser	Pro	Asp	Tyr	His	Thr	Arg	Pro	His
65					70					75				80	

Cys	Glu	Ser	Cys	Arg	His	Cys	Asn	Ser	Gly	Phe	Leu	Ile	Arg	Asn	Cys
				85					90					95	

Thr	Val	Thr	Ala	Asn	Ala	Glu	Cys	Ser	Cys	Ser	Lys	Asn	Trp	Gln	Cys
			100					105					110		

Arg	Asp	Gln	Glu	Cys	Thr	Glu	Cys	Asp	Pro	Pro	Leu	Asn	Pro	Ala	Leu
		115					120					125			

Thr Arg Gln Pro Ser Glu Thr Pro Ser Pro Gln Pro Pro Pro Thr His
130 135 140

Leu Pro His Gly Thr Glu Lys Pro Ser Trp Pro Leu His Arg Gln Leu
145 150 155 160

Pro Asn Ser Thr Val Tyr Ser Gln Arg Ser Ser His Arg Pro Leu Cys
165 170 175

Ser Ser Asp Cys Ile Arg Ile Phe Val Thr Phe Ser Ser Met Phe Leu
180 185 190

Ile Phe Val Leu Gly Ala Ile Leu Phe Phe His Gln Arg Arg Asn His
195 200 205

Gly Pro Asn Glu Asp Arg Gln Ala Val Pro Glu Glu Pro Cys Pro Tyr
210 215 220

Ser Cys Pro Arg Glu Glu Glu Gly Ser Ala Ile Pro Ile Gln Glu Asp
225 230 235 240

Tyr Arg Lys Pro Glu Pro Ala Phe Tyr Pro
245 250

<210> 70

<211> 660

<212> DNA

<213> Homo sapiens

<400> 70

atgctgcgcc tgctgctggc gctgaacctg tttccgagca ttcaggtgac cggcaacaaa 60

attctggtga aacagagccc gatgctggtg gcgtatgata acgcggtgaa cctgagctgc 120

aaatatagct ataacctgtt tagccgcgaa tttcgcgcga gcctgcataa aggcctggat 180

agcgcggtgg aagtgtgctg ggtgtatggc aactatagcc agcagctgca ggtgtatagc 240

aaaaccggct ttaactgcga tggcaaaactg ggcaacgaaa gcgtgacctt ttatctgcag 300

aacctgtatg tgaaccagac cgatatttat ttttgcaaaa ttgaagtgat gtatccgccg 360

ccgtatctgg ataacgaaaa aagcaacggc accattattc atgtgaaagg caaacatctg	420
tgcccagagcc cgctgtttcc gggcccgagc aaaccgtttt gggtgctggg ggtgggtgggc	480
ggcgtgctgg cgtgctatag cctgctgggtg accgtggcgt ttattatattt ttgggtgcgc	540
agcaaacgca gccgcctgct gcatagcgat tatatgaaca tgaccccgcg ccgcccgggc	600
ccgacccgca aacattatca gccgtatgcg ccgccgcgcg attttgcggc gtatcgcagc	660

<210> 71
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 71

Met	Leu	Arg	Leu	Leu	Leu	Ala	Leu	Asn	Leu	Phe	Pro	Ser	Ile	Gln	Val
1			5					10						15	

Thr	Gly	Asn	Lys	Ile	Leu	Val	Lys	Gln	Ser	Pro	Met	Leu	Val	Ala	Tyr
		20					25					30			

Asp	Asn	Ala	Val	Asn	Leu	Ser	Cys	Lys	Tyr	Ser	Tyr	Asn	Leu	Phe	Ser
		35					40					45			

Arg	Glu	Phe	Arg	Ala	Ser	Leu	His	Lys	Gly	Leu	Asp	Ser	Ala	Val	Glu
	50					55					60				

Val	Cys	Val	Val	Tyr	Gly	Asn	Tyr	Ser	Gln	Gln	Leu	Gln	Val	Tyr	Ser
65					70				75					80	

Lys	Thr	Gly	Phe	Asn	Cys	Asp	Gly	Lys	Leu	Gly	Asn	Glu	Ser	Val	Thr
			85					90						95	

Phe	Tyr	Leu	Gln	Asn	Leu	Tyr	Val	Asn	Gln	Thr	Asp	Ile	Tyr	Phe	Cys
		100						105					110		

Lys	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser
		115					120					125			

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 72
 <211> 654
 <212> DNA
 <213> Mus musculus

<400> 72
 atgacctgc gcctgctgtt tctggcgctg aactttttta gcgtgcaggt gaccgaaaac 60
 aaaattctgg tgaaacagag cccgctgctg gtggtggata gcaacgaagt gagcctgagc 120
 tgccgctata gctataacct gctggcgaaa gaatttcgcg cgagcctgta taaaggcgtg 180
 aacagcgatg tggaagtgtg cgtgggcaac ggcaacttta cctatcagcc gcagtttcgc 240
 agcaacgcgg aatttaactg cgatggcgat ttgataacg aaaccgtgac ctttcgcctg 300
 tggaacctgc atgtgaacca taccgatatt tatttttgca aaattgaatt tatgtatccg 360
 ccgccgtatc tggataacga acgcagcaac ggaccatta ttcataataa agaaaaacat 420
 ctgtgccata ccagagcag cccgaaactg ttttgggcgc tggtggtggt ggcgggcgtg 480
 ctgttttgct atggcctgct ggtgaccgtg gcgctgtgcg tgatttggac caacagccgc 540
 cgcaaccgcc tgctgcagag cgattatatg aacatgaccc cgcgccgcc ggcctgacc 600

cgcaaaccgt atcagccgta tgcgccggcg cgcgattttg cggcgtatcg cccg

654

<210> 73

<211> 218

<212> PRT

<213> Mus musculus

<400> 73

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

<210> 74
<211> 768
<212> DNA
<213> Homo sapiens

<400> 74
atgggaaaca gctgttacaa catagtagcc actctgttgc tggtcctcaa ctttgagagg 60
acaagatcat tgcaggatcc ttgtagtaac tgcccagctg gtacattctg tgataataac 120
aggaatcaga tttgcagtcc ctgtcctcca aatagtttct ccagcgcagg tggacaaagg 180
acctgtgaca tatgcaggca gtgtaaaggt gttttcagga ccaggaagga gtgttcctcc 240
accagcaatg cagagtgtga ctgcactcca gggtttact gcctgggggc aggatgcagc 300
atgtgtgaac aggattgtaa acaagggtcaa gaactgacaa aaaaagggtg taaagactgt 360
tgctttggga catttaacga tcagaaacgt ggcatctgtc gaccctggac aaactgttct 420
ttggatggaa agtctgtgct tgtgaatggg acgaaggaga gggacgtggt ctgtggacca 480
tctccagccg acctctctcc gggagcatcc tctgtgaccc cgcctgcccc tgcgagagag 540
ccaggacact ctccgcagat catctccttc tttcttgccg tgacgtcgac tgcgttgctc 600
ttcctgctgt tcttcctcac gctccgtttc tctgttggtta aacggggcag aaagaaactc 660
ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 720
tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgtga 768

<210> 75

<211> 255
<212> PRT
<213> Homo sapiens

<400> 75

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
35 40 45

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

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

<210> 76
<211> 768
<212> DNA
<213> Mus musculus

<400> 76
atgggcaaca actgctataa cgtggtggtg attgtgctgc tgctggtggg ctgcgaaaaa 60
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aaccgggtgt gcaaaaagctg cccgccgagc accttttagca gcattggcgg ccagccgaac 180
tgcaacattt gccgcgtgtg cgcgggctat tttcgttta aaaaattttg cagcagcacc 240
cataacgcgg aatgcgaatg cattgaaggc tttcattgcc tgggcccgc gtgcacccgc 300
tgcgaaaaag attgccgcc gggccaggaa ctgaccaaac agggctgcaa aacctgcagc 360
ctgggcacct ttaacgatca gaacggcacc ggctgtgcc gcccgtggac caactgcagc 420
ctggatggcc gcagcgtgct gaaaaccggc accaccgaaa aagatgtggt gtgcggcccg 480
ccggtggtga gctttagccc gagcaccacc attagcgtga ccccggaagg cggcccgggc 540
ggccatagcc tgcaaggctg gacctgttt ctggcgctga ccagcgcgt gctgctggcg 600
ctgattttta ttacctgct gtttagcgtg ctgaaatgga ttcgcaaaaa atttccgcat 660
atttttaaac agccgtttaa aaaaaccacc ggcgcggcgc aggaagaaga tgcgtgcagc 720

tgccgctgcc cgcaggaaga agaaggcggc ggcggcggct atgaactg

768

<210> 77

<211> 256

<212> PRT

<213> Mus musculus

<400> 77

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140

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

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
180 185 190

Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
195 200 205

Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
210 215 220

Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
225 230 235 240

Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu
245 250 255

<210> 78
<211> 831
<212> DNA
<213> Homo sapiens

<400> 78
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ctgggcctga gcaccgtgac cggcctgcat tgcgtgggcg atacctatcc gagcaacgat 120
cgctgctgcc atgaatgccg cccgggcaac ggcatggtga gccgctgcag ccgcagccag 180
aacaccgtgt gccgcccgtg cggcccgggc ttttataacg atgtggtgag cagcaaaccg 240
tgcaaaccgt gcacctggtg caacctgcgc agcggcagcg aacgcaaaca gctgtgcacc 300
gcgacccagg ataccgtgtg ccgctgccgc gcgggcaccc agccgctgga tagctataaa 360
ccgggcgtgg attgcgcgcc gtgcccgcgc ggccatttta gcccgggcga taaccaggcg 420
tgcaaaccgt ggaccaactg caccctggcg ggcaaacata ccctgcagcc ggcgagcaac 480
agcagcgatg cgatttgcga agatcgcgat ccgccggcga cccagccgca ggaaacccag 540
ggcccgcggc gcgcgccgat taccgtgcag ccgaccgaag cgtggccgcg caccagccag 600

ggcccagca cccgcccggg ggaagtgccg ggcggccgcg cggtaggcggc gattctgggc 660
ctgggcctgg tgctgggcct gctgggcccg ctggcgattc tgctggcgct gtatctgctg 720
cgccgcgatc agcgccctgcc gccggatgcg cataaaccgc cgggcggcgg cagctttcgc 780
accccgattc aggaagaaca ggcggatgcg catagcaccc tggcgaaaat t 831

<210> 79
<211> 277
<212> PRT
<213> Homo sapiens

<400> 79

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
1 5 10 15

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

Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110

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

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
 145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
 165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
 180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
 195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
 210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
 225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
 245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
 260 265 270

Thr Leu Ala Lys Ile
 275

<210> 80

<211> 816

<212> DNA

<213> Mus musculus

<400> 80

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accgcgcgcc gcctgaactg cgtgaaacat acctatccga gcggccataa atgctgccgc 120

gaatgccagc cgggccatgg catggtgagc cgctgcgatc ataccgcga taccctgtgc 180

catccgtgcg aaaccggctt ttataacgaa gcggtgaact atgatacctg caaacagtgc	240
acccagtgc accatcgag cggcagcgaa ctgaaacaga actgcacccc gaccaggat	300
accgtgtgcc gctgccgccc gggcacccag ccgcgccagg atagcggcta taaactgggc	360
gtggattgcg tgccgtgccc gccgggcat tttagcccgg gcaacaacca ggcgtgcaaa	420
ccgtggacca actgcaccct gagcggcaaa cagaccgcc atccggcgag cgatagcctg	480
gatgcggtgt gcgaagatcg cagcctgctg gcgaccctgc tgtgggaaac ccagcgccc	540
acctttcgcc cgaccaccgt gcagagcacc accgtgtggc cgcgaccag cgaactgccg	600
agcccgccga ccctggtgac cccggaaggc ccggcgtttg cggctgtgct gggcctgggc	660
ctgggcctgc tggcgccgct gaccgtgctg ctggcgctgt atctgctgcg caaagcgtgg	720
cgctgccga acaccccgaa accgtgctgg ggcaacagct ttcgcacccc gattcaggaa	780
gaacataccg atgcgcattt taccctggcg aaaatt	816

<210> 81
 <211> 272
 <212> PRT
 <213> Mus musculus

<400> 81

Met	Tyr	Val	Trp	Val	Gln	Gln	Pro	Thr	Ala	Leu	Leu	Leu	Leu	Ala	Leu
1				5					10					15	

Thr	Leu	Gly	Val	Thr	Ala	Arg	Arg	Leu	Asn	Cys	Val	Lys	His	Thr	Tyr
			20					25					30		

Pro	Ser	Gly	His	Lys	Cys	Cys	Arg	Glu	Cys	Gln	Pro	Gly	His	Gly	Met
		35					40					45			

Val	Ser	Arg	Cys	Asp	His	Thr	Arg	Asp	Thr	Leu	Cys	His	Pro	Cys	Glu
	50					55					60				

Thr	Gly	Phe	Tyr	Asn	Glu	Ala	Val	Asn	Tyr	Asp	Thr	Cys	Lys	Gln	Cys
65					70					75					80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr
85 90 95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg
100 105 110

Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro
115 120 125

Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn
130 135 140

Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu
145 150 155 160

Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu
165 170 175

Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val
180 185 190

Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro
195 200 205

Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu
210 215 220

Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp
225 230 235 240

Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr
245 250 255

Pro Ile Gln Glu Glu His Thr Asp Ala His Phe Thr Leu Ala Lys Ile
260 265 270

<210> 82
<211> 597

<212> DNA

<213> Homo sapiens

<400> 82

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atgaaaagcg gcctgtggta ttttttctg ttttgcctgc gcattaaagt gctgaccggc      60
gaaattaacg gcagcgcgaa ctatgaaatg tttatttttc ataacggcgg cgtgcagatt      120
ctgtgcaa atccggatat tgtgcagcag tttaaaatgc agctgctgaa aggcggccag      180
attctgtgcg atctgaccaa aaccaaaggc agcggcaaca ccgtgagcat taaaagcctg      240
aaattttgcc atagccagct gagcaacaac agcgtgagct tttttctgta taacctggat      300
catagccatg cgaactatta tttttgcaac ctgagcattt ttgatccgcc gccgtttaaa      360
gtgaccctga ccggcggcta tctgcatatt tatgaaagcc agctgtgctg ccagctgaaa      420
ttttggctgc cgattggctg cgcggcgttt gtggtggtgt gcattctggg ctgcattctg      480
atttgctggc tgaccaaaaa aaaatatagc agcagcgtgc atgatccgaa cggcgaatat      540
atgtttatgc gcgcggtgaa caccgcgaaa aaaagccgcc tgaccgatgt gaccctg      597
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<210> 83

<211> 199

<212> PRT

<213> Homo sapiens

<400> 83

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Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1           5           10          15
```

```
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
          20          25          30
```

```
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
          35          40          45
```

```
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
          50          55          60
```

```
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65          70          75          80
```

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 84
<211> 600
<212> DNA
<213> Mus musculus

<400> 84
atgaaaccgt atttttgccg cgtgtttgtg ttttgctttc tgattcgcct gctgaccggc 60
gaaattaacg gcagcgcgga tcatcgcatt ttttagctttc ataacggcgg cgtgcagatt 120
agctgcaaat atccggaaac cgtgcagcag ctgaaaatgc gcctgtttcg cgaacgcgaa 180
gtgctgtgcg aactgaccaa aaccaaaggc agcggcaacg cggtgagcat taaaaacccg 240
atgctgtgcc tgtatcatct gagcaacaac agcgtgagct tttttctgaa caaccggat 300

agcagccagg gcagctatta tttttgcagc ctgagcattt ttgatccgcc gccgtttcag	360
gaacgcaacc tgagcggcgg ctatctgcat atttatgaaa gccagctgtg ctgccagctg	420
aaactgtggc tgccgggtggg ctgcgcggcg tttgtggtgg tgctgctgtt tggctgcatt	480
ctgattatit ggtttagcaa aaaaaaatat ggcagcagcg tgcattgatcc gaacagcgaa	540
tatatgttta tggcggcggg gaacaccaac aaaaaagcc gcctggcggg cgtgaccagc	600

<210> 85
 <211> 200
 <212> PRT
 <213> Mus musculus

 <400> 85

Met	Lys	Pro	Tyr	Phe	Cys	Arg	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Arg
1				5					10					15	

Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser
			20					25					30		

Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val
		35					40					45			

Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu
	50					55					60				

Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro
65					70					75				80	

Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85					90					95	

Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser
			100					105					110		

Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr
		115					120					125			

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 86
<211> 279
<212> DNA
<213> Homo sapiens

<400> 86
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accccgggcg aacgcagcag cctgccggcg ttttatccgg gcaccagcgg cagctgcagc 120
ggctgcggca gcctgagcct gccgctgctg gcgggcctgg tggcggcgga tgcggtggcg 180
agcctgctga ttgtgggcgc ggtgtttctg tgcgcgcgcc cgcgccgcag cccggcgcag 240
gaagatggca aagtgtatat taacatgccg ggccgcggc 279

<210> 87
<211> 93
<212> PRT
<213> Homo sapiens

<400> 87

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
1 5 10 15

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
20 25 30

Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
35 40 45

Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
50 55 60

Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
65 70 75 80

Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
85 90

<210> 88
<211> 237
<212> DNA
<213> Mus musculus

<400> 88
atggatccgc cgggctatct gctgtttctg ctgctgctgc cgggtggcggc gagccagacc 60
agcgcgggca gctgcagcgg ctgcggcacc ctgagcctgc cgctgctggc gggcctgggtg 120
gcggcgggatg cggtgatgag cctgctgatt gtgggcgtgg tgtttgtgtg catgcgcccg 180
catggccgcc cggcgcagga agatggccgc gtgtatatta acatgccggg ccgcggc 237

<210> 89
<211> 79
<212> PRT
<213> Mus musculus

<400> 89

Met Asp Pro Pro Gly Tyr Leu Leu Phe Leu Leu Leu Leu Pro Val Ala
1 5 10 15

Ala Ser Gln Thr Ser Ala Gly Ser Cys Ser Gly Cys Gly Thr Leu Ser
20 25 30

Leu Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Met Ser Leu
35 40 45

Leu Ile Val Gly Val Val Phe Val Cys Met Arg Pro His Gly Arg Pro
50 55 60

Ala Gln Glu Asp Gly Arg Val Tyr Ile Asn Met Pro Gly Arg Gly
65 70 75

<210> 90
<211> 342
<212> DNA
<213> Homo sapiens

<400> 90
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ggtctccgtc ctgtccaggc ccaggcccag agcgattgca gttgctctac ggtgagcccg 120
ggcgtgctgg cagggatcgt gatgggagac ctggtgctga cagtgctcat tgccctggcc 180
gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240
aaacagcgta tcaactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300
gtctacagcg acctcaacac acagaggccg tattacaaat ga 342

<210> 91
<211> 113
<212> PRT
<213> Homo sapiens

<400> 91

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
85 90 95

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
100 105 110

Lys

<210> 92
<211> 345
<212> DNA
<213> Mus musculus

<400> 92
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agccctgggtg tactggctgg gattgttctg ggtgacttgg tgttgactct gctgattgcc 180
ctggctgtgt actctctggg ccgcctggtc tcccagggtc aaggacagc ggaaggacc 240
cggaacaac acattgctga gactgagtcg cttatcagg agcttcaggg tcagagacca 300
gaagtataca gtgacctcaa cacacagagg caatattaca gatga 345

<210> 93
<211> 114
<212> PRT
<213> Mus musculus

<400> 93

Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu
1 5 10 15

Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe
20 25 30

Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile
35 40 45

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

Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr
65 70 75 80

Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln
85 90 95

Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr
100 105 110

Tyr Arg

<210> 94
<211> 164
<212> PRT
<213> Homo sapiens

<400> 94

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
1 5 10 15

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg

65	70	75	80
Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met			
	85	90	95
Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn			
	100	105	110
Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met			
	115	120	125
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly			
	130	135	140
Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala			
145	150	155	160

Leu Pro Pro Arg

<210> 95
 <211> 492
 <212> DNA
 <213> Homo sapiens

<400> 95	
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atctatggtg tcattctcac tgccttgttc ctgagagtga agttcagcag gagcgcagag	180
ccccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga	240
gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg	300
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag	360
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt	420
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ccccctcgct aa	492

<210> 96
<211> 164
<212> PRT
<213> Mus musculus

<400> 96

Met Lys Trp Lys Val Ser Val Leu Ala Cys Ile Leu His Val Arg Phe
1 5 10 15

Pro Gly Ala Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Ile Thr Ala
35 40 45

Leu Tyr Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala Asn
50 55 60

Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65 70 75 80

Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu Met
85 90 95

Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr Asn
100 105 110

Ala Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Thr
115 120 125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
130 135 140

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Thr
145 150 155 160

Leu Ala Pro Arg

<210> 97
<211> 495
<212> DNA
<213> Mus musculus

<400> 97
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atctacggag tcatcatcac agccctgtac ctgagagcaa aattcagcag gagtgcagag 180
actgctgcca acctgcagga cccaaccag ctctacaatg agctcaatct agggcgaaga 240
gaggaatatg acgtcttggga gaagaagcgg gctcgggatac cagagatggg aggcaaacag 300
cagaggagga ggaaccccca ggaaggcgta tacaatgcac tgcagaaaga caagatggca 360
gaagcctaca gtgagatcgg cacaaaaggc gagaggcgga gaggcaaggg gcacgatggc 420
ctttaccagg gtctcagcac tgccaccaag gacacctatg atgccctgca tatgcagacc 480
ctggcccctc gctaa 495

<210> 98
<211> 254
<212> PRT
<213> Homo sapiens

<400> 98

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

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

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

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

<211> 762
<212> DNA
<213> Homo sapiens

<400> 99
atgtggcagc tgctgctgcc gaccgcgctg ctgctgctgg tgagcgcggg catgcgcacc 60
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gatagcgtga ccctgaaatg ccagggcgcg tatagcccgg aagataacag caccagtggt 180
tttcataacg aaagcctgat tagcagccag gcgagcagct attttattga tgcggcgacc 240
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cagctggaag tgcatattgg ctggctgctg ctgcaggcgc cgcgctgggt gtttaaagaa 360
gaagatccga ttcattctgcg ctgccatagc tggaaaaaca ccgcgctgca taaagtgacc 420
tatctgcaga acggcaaagg ccgcaaatat tttcatcata acagcgattt ttatattccg 480
aaagcgaccc tgaaagatag cggcagctat ttttgccgcg gcctgtttgg cagcaaaaac 540
gtgagcagcg aaaccgtgaa cattaccatt acccagggcc tggcggtgag caccattagc 600
agcttttttc cgccgggcta tcaggtgagc ttttgcctgg tgatgggtgct gctgtttgcg 660
gtggataccg gcctgtatatt tagcgtgaaa accaacattc gcagcagcac ccgcgattgg 720
aaagatcata aatttaaatg gcgcaaagat ccgcaggata aa 762

<210> 100
<211> 261
<212> PRT
<213> Mus musculus

<400> 100

Met Phe Gln Asn Ala His Ser Gly Ser Gln Trp Leu Leu Pro Pro Leu
1 5 10 15

Thr Ile Leu Leu Leu Phe Ala Phe Ala Asp Arg Gln Ser Ala Ala Leu
20 25 30

Pro Lys Ala Val Val Lys Leu Asp Pro Pro Trp Ile Gln Val Leu Lys
35 40 45

Glu Asp Met Val Thr Leu Met Cys Glu Gly Thr His Asn Pro Gly Asn
50 55 60

Ser Ser Thr Gln Trp Phe His Asn Gly Arg Ser Ile Arg Ser Gln Val
65 70 75 80

Gln Ala Ser Tyr Thr Phe Lys Ala Thr Val Asn Asp Ser Gly Glu Tyr
85 90 95

Arg Cys Gln Met Glu Gln Thr Arg Leu Ser Asp Pro Val Asp Leu Gly
100 105 110

Val Ile Ser Asp Trp Leu Leu Leu Gln Thr Pro Gln Arg Val Phe Leu
115 120 125

Glu Gly Glu Thr Ile Thr Leu Arg Cys His Ser Trp Arg Asn Lys Leu
130 135 140

Leu Asn Arg Ile Ser Phe Phe His Asn Glu Lys Ser Val Arg Tyr His
145 150 155 160

His Tyr Lys Ser Asn Phe Ser Ile Pro Lys Ala Asn His Ser His Ser
165 170 175

Gly Asp Tyr Tyr Cys Lys Gly Ser Leu Gly Ser Thr Gln His Gln Ser
180 185 190

Lys Pro Val Thr Ile Thr Val Gln Asp Pro Ala Thr Thr Ser Ser Ile
195 200 205

Ser Leu Val Trp Tyr His Thr Ala Phe Ser Leu Val Met Cys Leu Leu
210 215 220

Phe Ala Val Asp Thr Gly Leu Tyr Phe Tyr Val Arg Arg Asn Leu Gln
225 230 235 240

Thr Pro Arg Glu Tyr Trp Arg Lys Ser Leu Ser Ile Arg Lys His Gln

245

250

255

Ala Pro Gln Asp Lys
260

<210> 101

<211> 786

<212> DNA

<213> Mus musculus

<400> 101

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cccccatgga tccaggtgct caaggaagac atggtgacac tgatgtgcga agggacccac      180
aaccctggga actcttctac ccagtgggtc cacaacggga ggtccatccg gagccaggtc      240
caagccagtt acacgtttta ggccacagtc aatgacagtg gagaatatcg gtgtcaaatg      300
gagcagaccc gcctcagcga ccctgtagat ctgggagtga tttctgactg gctgctgctc      360
cagaccccctc agcgggtggt tctggaaggg gaaaccatca cgctaagggtg ccatagctgg      420
aggaacaaac tactgaacag gatctcattc ttccataatg aaaaatccgt gaggtatcat      480
cactacaaaa gtaatttctc tatcccaaaa gccaacacac gtcacagtgg ggactactac      540
tgcaaaggaa gtctaggaag tacacagcac cagtccaagc ctgtcaccat cactgtccaa      600
gatccagcaa ctacatcctc catctctcta gtctgggtacc aactgctttt ctccctagtg      660
atgtgcctcc tgtttgcagt ggacacgggc ctttatttct acgtacggag aaatcttcaa      720
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<210> 102

<211> 216

<212> PRT

<213> Homo sapiens

<400> 102

Met Gly Trp Ile Arg Gly Arg Arg Ser Arg His Ser Trp Glu Met Ser

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

Tyr Ile Cys Met Gln Arg Thr Val
210 215

<210> 103
<211> 648
<212> DNA
<213> Homo sapiens

<400> 103
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gtggtgaaaa gcaaatgccg cgaaaacgcg agcccgtttt ttttttgctg ctttattgcg 180
gtggcgatgg gcattcgctt tattattatg gtggcgattt ggagcgcggt gtttctgaac 240
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aaaaactgga tttgctataa aaacaactgc tatcagtttt ttgatgaaag caaaaactgg 360
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gaagatcagg atctgctgaa actggtgaaa agctatcatt ggatgggcct ggtgcatatt 480
ccgaccaacg gcagctggca gtgggaagat ggcagcattc tgagcccgaa cctgctgacc 540
attattgaaa tgcagaaagg cgattgcgcg ctgtatgcga gcagctttaa aggctatatt 600
gaaaactgca gcaccccgaa cacctatatt tgcatgcagc gcaccgtg 648

<210> 104
<211> 232
<212> PRT
<213> Mus musculus

<400> 104

Met Ala Leu Ile Arg Asp Arg Lys Ser His His Ser Glu Met Ser Lys
1 5 10 15

Cys His Asn Tyr Asp Leu Lys Pro Ala Lys Trp Asp Thr Ser Gln Glu
20 25 30

Gln Gln Lys Gln Arg Leu Ala Leu Thr Thr Ser Gln Pro Gly Glu Asn

35

40

45

Gly Ile Ile Arg Gly Arg Tyr Pro Ile Glu Lys Leu Lys Ile Ser Pro
 50 55 60

Met Phe Val Val Arg Val Leu Ala Ile Ala Leu Ala Ile Arg Phe Thr
 65 70 75 80

Leu Asn Thr Leu Met Trp Leu Ala Ile Phe Lys Glu Thr Phe Gln Pro
 85 90 95

Val Leu Cys Asn Lys Glu Val Pro Val Ser Ser Arg Glu Gly Tyr Cys
 100 105 110

Gly Pro Cys Pro Asn Asn Trp Ile Cys His Arg Asn Asn Cys Tyr Gln
 115 120 125

Phe Phe Asn Glu Glu Lys Thr Trp Asn Gln Ser Gln Ala Ser Cys Leu
 130 135 140

Ser Gln Asn Ser Ser Leu Leu Lys Ile Tyr Ser Lys Glu Glu Gln Asp
 145 150 155 160

Phe Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val Gln Ile
 165 170 175

Pro Ala Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ser Leu Ser Tyr
 180 185 190

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

Gly Ser Ser Phe Lys Ala Tyr Thr Glu Asp Cys Ala Asn Leu Asn Thr
 210 215 220

Tyr Ile Cys Met Lys Arg Ala Val
 225 230

<210> 105
<211> 696
<212> DNA
<213> Mus musculus

<400> 105
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gatctgaaac cggcgaaatg ggataccagc caggaacagc agaaacagcg cctggcgctg 120
accaccagcc agccggggcga aaacggcatt attcgcggcc gctatccgat tgaaaaactg 180
aaaattagcc cgatgtttgt ggtgcgcgtg ctggcgattg cgctggcgat tcgctttacc 240
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aaagaagtgc cgggtgagcag ccgcgaaggc tattgcggcc cgtgcccga caactggatt 360
tgccatcgca acaactgcta tcagTTTTT aacgaagaaa aaacctggaa ccagagccag 420
gcgagctgcc tgagccagaa cagcagcctg ctgaaaattt atagcaaaga agaacaggat 480
tttctgaaac tggtgaaaag ctatcattgg atgggcctgg tgcagattcc ggcgaaacggc 540
agctggcagt gggaagatgg cagcagcctg agctataacc agctgaccct ggtggaaatt 600
ccgaaaggca gctgcgcggt gtatggcagc agctttaaaag cgtataaccga agattgcgcg 660
aacctgaaca cctatatTTTg catgaaacgc gcggtg 696

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

<220>
<223> CD28 YNMN

<400> 106

Tyr Met Asn Met
1

<210> 107
<211> 4
<212> PRT
<213> Artificial sequence

<220>

<223> CD28 PYAP

<400> 107

Pro Tyr Ala Pro

1

<210> 108

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> CD28 FMNM

<400> 108

Phe Met Asn Met

1

<210> 109

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> CD28 AYAA

<400> 109

Ala Tyr Ala Ala

1

<210> 110

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> Signal peptide

<400> 110

Ala Thr Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala

1

5

10

15

Thr Gly Val His Ser
20

<210> 111
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Signal peptide DNA sequence

<400> 111
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcactcc 57

<210> 112
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CD20 (GA101) heavy chain

<400> 112

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

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

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

Gly Arg Ile Phe Pro Gly Asp Gly Asp Thr Asp Tyr Asn Gly Lys Phe
50 55 60

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

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

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

Thr Leu Val 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> 113

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-CD20 (GA101) light chain

<400> 113

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

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

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

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

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

Leu Glu Leu Pro Tyr Thr 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> 114
<211> 447
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-FAP(4B9) PGLALA heavy chain

<400> 114

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 115

<211> 215

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-FAP(4B9) light chain

<400> 115

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 Ser Val Thr 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 Asn Val Gly Ser Arg 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 Gly Ile Met Leu Pro
85 90 95

Pro 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> 116

<211> 451

<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CEA (A5B7) PGLALA heavy chain

<400> 116

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

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

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

Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala
50 55 60

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

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

Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr 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 Ala Ala 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 Asn 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 Gly 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 Asp Glu Leu 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> 117
<211> 223
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CEA (A5B7) light chain

<400> 117

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

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

Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr
35 40 45

Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val
50 55 60

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

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys
100 105 110

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

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

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
165 170 175

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

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
195 200 205

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 118

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-CEA (T84.66LCHA) PGLALA heavy chain

<400> 118

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

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

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

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

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

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

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala 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 Ala Ala 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 Asn 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 Gly 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 Asp Glu Leu 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> 119
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CEA (T84.66LCHA) light chain

<400> 119

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

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

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

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

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln 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> 120

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-CEA (CH1A1A98/992F1) PGLALA heavy chain

<400> 120

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

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

Gln Gly Thr Thr 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 Ala Ala 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 Asn 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 Gly 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

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

Leu Ser Cys Ala 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 Val 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> 121
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CEA (CH1A1A98/992F1) light chain

<400> 121

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

Phe Thr Phe Gly Gln Gly Thr Lys Leu 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> 122

<211> 449

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-CEA (hMN14) PGLALA heavy chain

<400> 122

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

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

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

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Pro Val 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 Ala Ala 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 Gly 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> 123
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-CEA (hMN14) light chain

<400> 123

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 124
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-TNC (2B10) PGLALA heavy chain

<400> 124

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr 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 Ala Ala 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 Asn 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 Gly 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

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

Leu Ser Cys Ala 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 Val 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> 125

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-TNC (2B10) light chain

<400> 125

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 Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln 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> 126
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-HER2 (PER) PG LALA heavy chain 1

<400> 126

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 Thr Asp Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val 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 Ala Ala 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 Gly 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> 127
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-HER2 (PER) light chain 1

<400> 127

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 Lys Ala Ser Gln Asp Val Ser Ile Gly
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 Tyr Arg Tyr Thr 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 Tyr Ile Tyr Pro Tyr
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> 128
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> Anti-HER2 (PER) PG LALA heavy chain 2

<400> 128

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 Thr Asp Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val 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 Ala Ala 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 Gly 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> 129

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Anti-HER2 (PER) light chain 2

<400> 129

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 Lys Ala Ser Gln Asp Val Ser Ile Gly
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 Tyr Arg Tyr Thr 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 Tyr Ile Tyr Pro Tyr
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> 130

<211> 330

<212> PRT

<213> Homo sapiens

<400> 130

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

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

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330