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<110> Roche Glycart AG

<120> Bispecific T cell activating antigen binding molecules

<130> 30598

<150> EP 11178370.0
<151> 2011-08-23

<150> EP 12168192.8
<151> 2012-05-16

<160> 266

<170> PatentIn version 3.5

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<212> PRT
<213> Artificial Sequence

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<223> V9 (scFab)-Fc(hole) P329G LALA

<400> 1

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
                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
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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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430
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eolf-seql

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Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
465                 470                 475                 480

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
                485                 490                 495

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            500                 505                 510

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        515                 520                 525

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    530                 535                 540

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
545                 550                 555                 560

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                565                 570                 575

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            580                 585                 590

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
        595                 600                 605

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
    610                 615                 620

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
625                 630                 635                 640

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                645                 650                 655

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            660                 665                 670

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        675                 680                 685

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    690                 695                 700
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<213> Artificial Sequence

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<223> V9 (scFab)-Fc(hole) P329G LALA

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ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttccccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

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cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccatc ggtcttcccc 1140

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aacaccaagg tggacaagaa agttgagccc aaatcttgtg acaaaactca cacatgccca 1440

ccgtgcccag cacctgaagc tgcaggggga ccgtcagtct tcctcttccc cccaaaaccc 1500

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 1560

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tga 2103

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1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

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

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

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

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
        355                 360                 365

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
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<211> 1329
<212> DNA
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tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac 180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac 300

tactggggcc aaggcaccac tctcacagtc tcctcagcta gcaccaaggg cccatcggtc 360

ttcccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa gacccacacc 660

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aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtcgat 780

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac 840

aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 960

aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1020

ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg 1080

tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaataa 1329

<210> 5
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 (VL-CL)

<400> 5

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Trp
                85                  90                  95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
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<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (VL-CL)

<400> 6

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gatggaactg ttaaactcct gatctattac acatcaagtt tacactcagg agtcccatca      180
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aggttcagtg gcagtgggtc tgggacagat tattctctca ccatcagcaa cctggaacct 240

gaagatattg ccacttacta ttgtcagcag tatagtaagc ttccttggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

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<211> 704
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 (scFab)-Fc(hole) P329G LALA

<400> 7

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu 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

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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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Gln Glu Ser Gly
                245                 250                 255

Pro Gly Leu Val Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val
            260                 265                 270

Thr Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln
        275                 280                 285

Phe Pro Gly Asn Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly
    290                 295                 300

Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg
305                 310                 315                 320

Asp Thr Ser Lys Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr
                325                 330                 335

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln
            340                 345                 350

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        355                 360                 365

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    370                 375                 380

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                405                 410                 415

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            420                 425                 430
```

eolf-seql

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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        435                 440                 445

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    450                 455                 460

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ala Gln Asp Lys Thr
465                 470                 475                 480

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
                485                 490                 495

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            500                 505                 510

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        515                 520                 525

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    530                 535                 540

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
545                 550                 555                 560

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                565                 570                 575

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            580                 585                 590

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
        595                 600                 605

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
    610                 615                 620

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
625                 630                 635                 640

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                645                 650                 655

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
            660                 665                 670

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        675                 680                 685

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    690                 695                 700
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<210> 8
<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (scFab)-Fc(hole) P329G LALA

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gacggcacag tgaagctgct gatctactac accagcagcc tgcacagcgg cgtgccaagc 180

agattcagcg gcagcggctc cggcacagac tacagcctga ccatctccaa cctggaaccc 240

gaggatatcg ccacctacta ctgccagcag tacagcaagc tgccctggac cttcggcgga 300

ggcaccaagc tggaaatcaa gcggaccgtg gccgctccca gcgtgttcat cttcccaccc 360

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ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

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aagccaagcc agagtctgag cctgacctgc agcgtgaccg gctacagcat taccagcggc 840

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acctacgacg gcagcaacaa ctacaacccc agcctgaaga accggatcag catcacccgg 960

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aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1980

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<210> 9
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (VH-CH1) -Fc(knob) LALA

<400> 9

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ala Gln Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
```

eolf-seql

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 10
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (VH-CH1) -Fc(knob) LALA

<400> 10
gaggtgcagc tggtcgagag cggaggcggc ctggtgcagc ctggcggcag cctgagactg 60

agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggca 120

cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gagcacctac 180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc 300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcaccct cgtgaccgtg 360

tctagcgcta gcaccaaggg cccctccgtg ttccccctgg ccccagcag caagagcacc 420

agcggcggca cagccgctct gggctgcctg gtcaaggact acttccccga gcccgtgacc 480

gtgtcctgga acagcggagc cctgacctcc ggcgtgcaca ccttccccgc cgtgctgcag 540

agttctggcc tgtatagcct gagcagcgtg gtcaccgtgc cttctagcag cctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660

gagcccaaga gctgcgacgg cggtggtggc tccggaggcg gtggatccgg agctcaggac 720

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 1140

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380

tccctgtctc cgggtaaatg a 1401

<210> 11
<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (VL-CL)

<400> 11

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 12
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (VL-CL)

<400> 12
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tgccctggac cttcggccag 300

ggcacaaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 13
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) wt

<400> 13

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
                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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400
```

```
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
                485                 490                 495

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser
            500                 505                 510

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
        515                 520                 525

Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr
    530                 535                 540

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
545                 550                 555                 560

Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala
                565                 570                 575

Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            580                 585                 590

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        595                 600                 605

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    610                 615                 620

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
625                 630                 635                 640

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                645                 650                 655

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            660                 665                 670
```

```
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        675                 680                 685

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    690                 695                 700

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
705                 710                 715                 720

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                725                 730                 735

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            740                 745                 750

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        755                 760                 765

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    770                 775                 780

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
785                 790                 795                 800

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                805                 810                 815

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            820                 825                 830

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        835                 840                 845

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    850                 855                 860

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
865                 870                 875                 880

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                885                 890                 895

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            900                 905                 910

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        915                 920                 925
```

<210> 14
<211> 2781

<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) wt

<400> 14
gacatccaga tgacccagag cccctctagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttccccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

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gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggcggtggat ctgaagtgca gctgcaggaa agcggccctg gcctggtcaa gcccagccag 1500

agcctgagcc tgacctgtag cgtgaccggc tactccatca cctccggcta ctactggaat 1560

tggattcggc agttccccgg caacaagctg gaatggatgg gctacatcac ctacgacggc 1620

agcaacaact acaaccccag cctgaagaac cggatcagca tcacccggga caccagcaag 1680

aaccagttct tcctgaagtt gaattctgtg actactgagg acacagctac atattactgt 1740

gcggactttg actactgggg ccaaggcacc actctcacag tctcctcagc tagcaccaag 1800

ggcccatcgg tcttcccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1860

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1920

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1980

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 2040

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 2100

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 2160

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gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 2340

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 2400

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 2460

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 2520

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2580

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2640

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 2700

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2760

tccctgtctc cgggtaaatg a 2781

<210> 15
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) wt

<400> 15

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

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

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

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

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

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
        355                 360                 365
```

eolf-seql

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

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

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 16
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) wt

<400> 16

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gaggtccagc tgcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc       60

acctgctctg tcactggcta ctccatcacc agtggttatt actggaactg gatccggcag      120

tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac      180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc      240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac      300

tactggggcc aaggcaccac tctcacagtc tcctcagcta gcaccaaggg cccaagcgtg      360

ttccctctgg cccccagcag caagagcaca agcggcggaa cagccgccct gggctgcctg      420

gtcaaggact acttccccga gcccgtgaca gtgtcctgga acagcggagc cctgaccagc      480

ggcgtgcaca cctttccagc cgtgctgcag agcagcggcc tgtacagcct gagcagcgtg      540

gtcacagtgc ctagcagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag      600

cccagcaaca ccaaggtgga caagaaggtg gagcccaaga gctgcgacaa gacccacacc      660

tgtccccctt gtcctgcccc tgagctgctg ggcggaccca gcgtgttcct gttccccccа      720

aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggac      780

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaggtgcac      840

aatgccaaga ccaagccccg ggaggaacag tacaacagca cctaccgggt ggtgtccgtg      900

ctgaccgtgc tgcaccagga ctggctgaac ggcaaagagt acaagtgcaa ggtctccaac      960

aaggccctgc ctgccccat cgagaaaacc atcagcaagg ccaagggcca gcccagagaa     1020

ccccaggtgt gcaccctgcc ccccagcaga gatgagctga ccaagaacca ggtgtccctg     1080

agctgtgccg tcaagggctt ctaccccagc gatatcgccg tggagtggga gagcaacggc     1140

cagcctgaga acaactacaa gaccaccccc cctgtgctgg acagcgacgg cagcttcttc     1200
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ctggtgtcca aactgaccgt ggacaagagc cggtggcagc agggcaacgt gttcagctgc 1260

agcgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgag cctgagcccc 1320

ggcaagtga 1329

<210> 17
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) LALA

<400> 17

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
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

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Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480
```

```
Gly Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
                485                 490                 495

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser
            500                 505                 510

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
        515                 520                 525

Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr
    530                 535                 540

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
545                 550                 555                 560

Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala
                565                 570                 575

Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            580                 585                 590

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        595                 600                 605

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    610                 615                 620

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
625                 630                 635                 640

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                645                 650                 655

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            660                 665                 670

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        675                 680                 685

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    690                 695                 700

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
705                 710                 715                 720

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                725                 730                 735

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            740                 745                 750
```

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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        755                 760                 765

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    770                 775                 780

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
785                 790                 795                 800

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                805                 810                 815

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            820                 825                 830

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        835                 840                 845

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    850                 855                 860

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
865                 870                 875                 880

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                885                 890                 895

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            900                 905                 910

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        915                 920                 925


<210>  18
<211>  2781
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  V9 (scFab)-LC007 (VH-CH1)-Fc(knob) LALA

<400>  18
gacatccaga tgacccagag cccctctagc ctgagcgcca gcgtgggcga cagagtgacc       60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc      120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc      180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc      240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag      300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccccccc      360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac      420
```

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccctc cgtgttcccc 1140

ctggccccca gcagcaagag caccagcggc ggcacagccg ccctcggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggcggtggat ctgaagtgca gctgcaggaa agcggccctg gcctggtcaa gcccagccag 1500

agcctgagcc tgacctgtag cgtgaccggc tactccatca cctccggcta ctactggaat 1560

tggattcggc agttccccgg caacaagctg gaatggatgg gctacatcac ctacgacggc 1620

agcaacaact acaaccccag cctgaagaac cggatcagca tcacccggga caccagcaag 1680

aaccagttct tcctgaagtt gaattctgtg actactgagg acacagctac atattactgt 1740

gcggactttg actactgggg ccaaggcacc actctcacag tctcctcagc tagcaccaag 1800

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1860

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1920

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1980

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 2040

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 2100

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 2160

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 2220

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 2280

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 2340

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 2400

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 2460

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 2520

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2580

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2640

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 2700

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2760

tccctgtctc cgggtaaatg a 2781

<210> 19
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) LALA

<400> 19

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

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

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

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

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

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
        355                 360                 365

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

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

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 20
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) LALA

<400> 20
gaggtccagc tgcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60

acctgctctg tcactggcta ctccatcacc agtggttatt actggaactg gatccggcag 120

tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac 180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac 300

tactggggcc aaggcaccac tctcacagtc tcctcagcta gcaccaaggg cccatcggtc 360

ttcccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa aactcacaca 660

tgcccaccgt gcccagcacc tgaagctgca gggggaccgt cagtcttcct cttccccca 720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 960

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1020

ccacaggtgt gcaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctc 1080

tcgtgcgcag tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctcgtgagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaatga 1329

<210> 21
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) P329G LALA

<400> 21

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
                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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285
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Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
                485                 490                 495

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser
            500                 505                 510

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
        515                 520                 525

Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr
    530                 535                 540

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
545                 550                 555                 560
```

```
Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala
                565                 570                 575

Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            580                 585                 590

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        595                 600                 605

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    610                 615                 620

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
625                 630                 635                 640

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                645                 650                 655

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            660                 665                 670

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        675                 680                 685

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    690                 695                 700

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
705                 710                 715                 720

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                725                 730                 735

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            740                 745                 750

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        755                 760                 765

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    770                 775                 780

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
785                 790                 795                 800

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                805                 810                 815

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            820                 825                 830
```

```
Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        835                 840                 845

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    850                 855                 860

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
865                 870                 875                 880

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                885                 890                 895

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            900                 905                 910

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        915                 920                 925
```

<210> 22
<211> 2781
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) P329G LALA

<400> 22

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atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc      120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc      180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc      240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag      300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccccc       360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac      420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag      480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc      540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc      600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga      660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt      720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg      780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac      840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac      900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg      960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc     1020
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gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccctc cgtgttcccc 1140

ctggccccca gcagcaagag caccagcggc ggcacagccg ccctcggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggcggtggat ctgaagtgca gctgcaggaa agcggccctg gcctggtcaa gcccagccag 1500

agcctgagcc tgacctgtag cgtgaccggc tactccatca cctccggcta ctactggaat 1560

tggattcggc agttccccgg caacaagctg gaatggatgg gctacatcac ctacgacggc 1620

agcaacaact acaaccccag cctgaagaac cggatcagca tcacccggga caccagcaag 1680

aaccagttct tcctgaagtt gaattctgtg actactgagg acacagctac atattactgt 1740

gcggactttg actactgggg ccaaggcacc actctcacag tctcctcagc tagcaccaag 1800

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1860

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1920

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1980

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 2040

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 2100

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 2160

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 2220

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 2280

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 2340

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 2400

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 2460

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 2520

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2580

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2640

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 2700

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2760

tccctgtctc cgggtaaatg a 2781

<210> 23
<211> 442
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql

<223> LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 23

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
260 265 270

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

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

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

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

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
340 345 350

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
355 360 365

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

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

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
405 410 415

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 24
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 24
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acctgctctg tcactggcta ctccatcacc agtggttatt actggaactg gatccggcag 120

tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac 180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac 300

tactggggcc aaggcaccac tctcacagtc tcctcagcta gcaccaaggg cccatcggtc 360

ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa aactcacaca 660

tgcccaccgt gcccagcacc tgaagctgca gggggaccgt cagtcttcct cttccccca 720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 960

aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1020

ccacaggtgt gcaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctc 1080

tcgtgcgcag tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctcgtgagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaatga 1329

<210> 25
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) P329G LALA N297D

<400> 25

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365
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Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
                485                 490                 495

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser
            500                 505                 510

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
        515                 520                 525

Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr
    530                 535                 540

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
545                 550                 555                 560

Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala
                565                 570                 575

Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            580                 585                 590

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        595                 600                 605

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    610                 615                 620

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
625                 630                 635                 640
```

```
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                645                 650                 655

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            660                 665                 670

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        675                 680                 685

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    690                 695                 700

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
705                 710                 715                 720

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                725                 730                 735

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            740                 745                 750

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        755                 760                 765

Lys Pro Arg Glu Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val
    770                 775                 780

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
785                 790                 795                 800

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                805                 810                 815

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            820                 825                 830

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        835                 840                 845

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    850                 855                 860

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
865                 870                 875                 880

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                885                 890                 895

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            900                 905                 910
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
915 920 925

<210> 26
<211> 2781
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (scFab)-LC007 (VH-CH1)-Fc(knob) P329G LALA N297D

<400> 26
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atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccctc cgtgttcccc 1140

ctggccccca gcagcaagag caccagcggc ggcacagccg ccctcggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggcggtggat ctgaagtgca gctgcaggaa agcggccctg gcctggtcaa gcccagccag 1500

agcctgagcc tgacctgtag cgtgaccggc tactccatca cctccggcta ctactggaat 1560

tggattcggc agttccccgg caacaagctg gaatggatgg gctacatcac ctacgacggc 1620

agcaacaact acaaccccag cctgaagaac cggatcagca tcacccggga caccagcaag 1680

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ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1920

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1980

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 2040

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 2100

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 2160

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 2220

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 2280

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacgacag cacgtaccgt 2340

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 2400

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 2460

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 2520

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2580

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2640

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 2700

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2760

tccctgtctc cgggtaaatg a 2781

<210> 27
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) P329G LALA N297D

<400> 27

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

```
Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

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

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

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

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

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

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

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

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

Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

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

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

eolf-seql

```
Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
        355                 360                 365

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

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

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
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<210> 28
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 (VH-CH1)-Fc(hole) P329G LALA N297D

<400> 28

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gaggtccagc tgcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc       60

acctgctctg tcactggcta ctccatcacc agtggttatt actggaactg gatccggcag      120

tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac      180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc      240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac      300

tactggggcc aaggcaccac tctcacagtc tcctcagcta gcaccaaggg cccatcggtc      360

ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg      420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg      540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa aactcacaca      660

tgcccaccgt gcccagcacc tgaagctgca gggggaccgt cagtcttcct cttccccca       720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac      780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat      840

aatgccaaga caaagccgcg ggaggagcag tacgacagca cgtaccgtgt ggtcagcgtc      900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac      960
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aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1020

ccacaggtgt gcaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctc 1080

tcgtgcgcag tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctcgtgagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

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ggtaaatga 1329

<210> 29
<211> 664
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 29

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

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

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

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

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

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

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

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

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

```
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
            180                 185                 190

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
        195                 200                 205

Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
    210                 215                 220

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser Leu
225                 230                 235                 240

Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
                245                 250                 255

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
            260                 265                 270

Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
        275                 280                 285

Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu Lys
    290                 295                 300

Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Asp
305                 310                 315                 320

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser
                325                 330                 335

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
            340                 345                 350

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        355                 360                 365

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
    370                 375                 380

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
385                 390                 395                 400

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                405                 410                 415

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            420                 425                 430

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        435                 440                 445
```

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
450 455 460

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
465 470 475 480

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
485 490 495

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
500 505 510

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
515 520 525

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
530 535 540

Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
545 550 555 560

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
565 570 575

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
580 585 590

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
595 600 605

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
610 615 620

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
625 630 635 640

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
645 650 655

Ser Leu Ser Leu Ser Pro Gly Lys
660

<210> 30
<211> 1995
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 30
gatatccaga tgacccagag ccccagctct ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctactac accagcagac tggaaagcgg cgtgccctcc 180
agattttccg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240
gaggatttcg ccacatatta ctgccagcag ggcaataccc tgccctggac cttcggacag 300
ggcacaaaag tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg 360
gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat 420
tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat 480
actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg 540
cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac 600
accaaggtgg acaagaaggt ggaacccaag tcttgtggcg gaggcggatc cggcggaggg 660
ggatctgagg tgcagctgca ggaaagcggc cctggcctgg tgaaacccag ccagagcctg 720
agcctgacct gcagcgtgac cggctacagc atcaccagcg gctactactg gaactggatc 780
agacagttcc ccggcaacaa gctggaatgg atgggctaca tcacctacga cggcagcaac 840
aactacaacc ccagcctgaa gaacagaatc agcatcaccc gggacaccag caagaaccag 900
ttcttcctga agctgaacag cgtgaccacc gaggacaccg ccacctacta ctgcgccgac 960
ttcgactact ggggccaggg caccaccctg accgtgtcct ccgcctctac caagggcccc 1020
agcgtgttcc ccctggcacc cagcagcaag agcacatctg gcggaacagc cgctctgggc 1080
tgtctggtga aagactactt ccccgagccc gtgaccgtgt cttggaactc tggcgccctg 1140
accagcggcg tgcacacctt ccagccgtg ctgcagagca gcggcctgta ctccctgtcc 1200
tccgtggtca ccgtgccctc tagctccctg ggaacacaga catatatctg taatgtcaat 1260
cacaagcctt ccaacaccaa agtcgataag aaagtcgagc ccaagagctg cgacaaaact 1320
cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 1380
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1440
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1500
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1560
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1620
tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1680
cgagaaccac aggtgtgcac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1740
agcctctcgt gcgcagtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1800
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1860
ttcttcctcg tgagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1920
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1980
tctccgggta aatga 1995

<210> 31
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc(knob) wt

<400> 31

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

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

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

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

Pro Gly Lys Ser Gly
225
```

<210> 32
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc(knob) wt

<400> 32
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 420

aaccaggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa atccggatga 690

<210> 33
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (VH-CL)

<400> 33

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
    130                 135                 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145                 150                 155                 160

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
            180                 185                 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
        195                 200                 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
    210                 215                 220

Asn Arg Gly Glu Cys
225
```

<210> 34
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (VH-CL)

<400> 34

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gaggtgcagc tggtcgagag cggaggcggc ctggtgcagc ctggcggcag cctgagactg       60

agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggca      120

cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gagcacctac      180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat      240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc      300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcaccct cgtgaccgtg      360

tctagcgcta gcgtggctgc accatctgtc ttcatcttcc cgccatctga tgagcagttg      420

aaatctggaa ctgcctctgt tgtgtgcctg ctgaataact tctatcccag agaggccaaa      480

gtacagtgga aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag      540

caggacagca aggacagcac ctacagcctc agcagcaccc tgacgctgag caaagcagac      600

tacgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc      660
```

acaaagagct tcaacagggg agagtgttga 690

<210> 35
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> FN18 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 35

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Asn Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
85 90 95

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

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

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

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

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

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

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

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly
210 215 220

```
Gly Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
225                 230                 235                 240

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser
                245                 250                 255

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
            260                 265                 270

Lys Leu Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr
        275                 280                 285

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
    290                 295                 300

Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala
305                 310                 315                 320

Thr Tyr Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
                325                 330                 335

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
            340                 345                 350

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
        355                 360                 365

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

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
385                 390                 395                 400

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
                405                 410                 415

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
            420                 425                 430

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
        435                 440                 445

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
    450                 455                 460

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
465                 470                 475                 480

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                485                 490                 495
```

```
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            500                 505                 510

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        515                 520                 525

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    530                 535                 540

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
545                 550                 555                 560

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
            580                 585                 590

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        595                 600                 605

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    610                 615                 620

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
625                 630                 635                 640

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                645                 650                 655

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            660                 665                 670


<210>  36
<211>  2013
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FN18 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400>  36
gacatcgtga tgagccagag ccccagcagc ctggccgtgt ccgtgggcga gaaagtgacc       60

atgagctgca agagcagcca gagcctgctg tactcctcta accagaagaa ctacctggcc      120

tggtatcagc agaagcccgg ccagtccccc aagctgctga tcaactgggc cagcacccgc      180

gagagcggcg tgcccgatag attcacaggc agcggcagcc ggaccgactt caccctgacc      240

atcagcagcg tgaaggccga ggatctggcc gtgtacttct gccagcagtt ctacagctac      300

ccccccacct tcggcggagg cacgaagctg gaaatcaaga gcagcgcttc caccaaaggc      360

ccttccgtgt ttcctctggc tcctagctcc aagtccacct ctggaggcac cgctgctctc      420
```

ggatgcctcg tgaaggatta ttttcctgag cctgtgacag tgtcctggaa tagcggagca 480

ctgacctctg gagtgcatac tttccccgct gtgctgcagt cctctggact gtacagcctg 540

agcagcgtgg tgacagtgcc cagcagcagc ctgggcaccc agacctacat ctgcaacgtg 600

aaccacaagc ccagcaacac caaggtggac aagaaggtgg aacccaagtc ttgtggcgga 660

ggcggatccg gcggaggggg atctgaggtg cagctgcagg aaagcggccc tggcctggtg 720

aaacccagcc agagcctgag cctgacctgc agcgtgaccg gctacagcat caccagcggc 780

tactactgga actggatcag acagttcccc ggcaacaagc tggaatggat gggctacatc 840

acctacgacg gcagcaacaa ctacaacccc agcctgaaga acagaatcag catcacccgg 900

gacaccagca agaaccagtt cttcctgaag ctgaacagcg tgaccaccga ggacaccgcc 960

acctactact gcgccgactt cgactactgg ggccagggca ccaccctgac cgtgtcctcc 1020

gcctctacca agggccccag cgtgttcccc ctggcaccca gcagcaagag cacatctggc 1080

ggaacagccg ctctgggctg tctggtgaaa gactacttcc ccgagcccgt gaccgtgtct 1140

tggaactctg gcgccctgac cagcggcgtg cacacctttc cagccgtgct gcagagcagc 1200

ggcctgtact ccctgtcctc cgtggtcacc gtgccctcta gctccctggg aacacagaca 1260

tatatctgta atgtcaatca caagccttcc aacaccaaag tcgataagaa agtcgagccc 1320

aagagctgcg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 1380

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 1440

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1500

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 1560

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1620

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1680

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1740

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1800

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1860

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1920

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1980

cagaagagcc tctccctgtc tccgggtaaa tga 2013

<210> 37
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> FN18 (VH-CL)

<400> 37

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

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

Thr Ile His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Asp Trp Ile
35 40 45

Gly Tyr Phe Asn Pro Ser Ser Glu Ser Thr Glu Tyr Asn Arg Lys Phe
50 55 60

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

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

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

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
180 185 190

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
210 215 220

Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 38
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> FN18 (VH-CL)

<400> 38
caggtgcagc tgcagcagag cgaggccgag ctggctagac ctggagccag cgtgaagatg 60

agctgcaagg ccagcggcta caccttcacc gactacacca tccactggct gaagcagcgg 120

cctggacagg gcctggactg gatcggctac ttcaacccca gcagcgagag caccgagtac 180

aaccggaagt tcaaggaccg gaccatcctg accgccgaca gaagcagcac caccgcctac 240

atgcagctga gcagcctgac cagcgaggac agcgccgtgt actactgcag ccggaagggc 300

gagaagctgc tgggcaacag atactggtac ttcgacgtgt ggggagccgg caccagcgtg 360

accgtgtcta gcgctagcgt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420

cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480

gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540

acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac gctgagcaaa 600

gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660

cccgtcacaa agagcttcaa caggggagag tgttga 696

<210> 39
<211> 664
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 39

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

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

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

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

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

Glu Asp Ile Gly Ser Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp
85 90 95

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

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

```
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145                 150                 155                 160

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

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
        195                 200                 205

Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
    210                 215                 220

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser Leu
225                 230                 235                 240

Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
                245                 250                 255

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
            260                 265                 270

Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
        275                 280                 285

Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu Lys
    290                 295                 300

Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Asp
305                 310                 315                 320

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser
                325                 330                 335

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
            340                 345                 350

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        355                 360                 365

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
    370                 375                 380

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
385                 390                 395                 400

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                405                 410                 415
```

```
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            420                 425                 430

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        435                 440                 445

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    450                 455                 460

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
465                 470                 475                 480

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                485                 490                 495

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            500                 505                 510

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        515                 520                 525

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    530                 535                 540

Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
545                 550                 555                 560

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                565                 570                 575

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
            580                 585                 590

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        595                 600                 605

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
    610                 615                 620

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
625                 630                 635                 640

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                645                 650                 655

Ser Leu Ser Leu Ser Pro Gly Lys
            660
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<210> 40
<211> 1995

<212> DNA
<213> Artificial Sequence

<220>
<223> 2C11 (VL-CH1)-LC007 (VH-CH1)-Fc(hole) P329G LALA

<400> 40
gacatccaga tgacccagag ccccagcagc ctgcctgcca gcctgggcga cagagtgacc 60

atcaactgcc aggccagcca ggacatcagc aactacctga actggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctactac accaacaagc tggccgacgg cgtgcccagc 180

agattcagcg gcagcggctc cggcagagac agcagcttca ccatctccag cctggaaagc 240

gaggacatcg gcagctacta ctgccagcag tactacaact acccctggac cttcggccct 300

ggcaccaagc tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg 360

gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat 420

tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat 480

actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg 540

cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac 600

accaaggtgg acaagaaggt ggaacccaag tcttgtggcg gaggcggatc cggcggaggg 660

ggatctgagg tgcagctgca ggaaagcggc cctggcctgg tgaaacccag ccagagcctg 720

agcctgacct gcagcgtgac cggctacagc atcaccagcg gctactactg gaactggatc 780

agacagttcc ccggcaacaa gctggaatgg atgggctaca tcacctacga cggcagcaac 840

aactacaacc ccagcctgaa gaacagaatc agcatcaccc gggacaccag caagaaccag 900

ttcttcctga agctgaacag cgtgaccacc gaggacaccg ccacctacta ctgcgccgac 960

ttcgactact ggggccaggg caccaccctg accgtgtcct ccgcctctac caagggcccc 1020

agcgtgttcc ccctggcacc cagcagcaag agcacatctg gcggaacagc cgctctgggc 1080

tgtctggtga aagactactt ccccgagccc gtgaccgtgt cttggaactc tggcgccctg 1140

accagcggcg tgcacacctt ccagccgtg ctgcagagca gcggcctgta ctccctgtcc 1200

tccgtggtca ccgtgccctc tagctccctg ggaacacaga catatatctg taatgtcaat 1260

cacaagcctt ccaacaccaa agtcgataag aaagtcgagc ccaagagctg cgacaaaact 1320

cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 1380

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1440

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1500

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1560

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1620

tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1680

cgagaaccac aggtgtgcac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1740

agcctctcgt gcgcagtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1800

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1860

ttcttcctcg tgagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1920

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1980

tctccgggta aatga 1995

<210> 41
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 (VH-CL)

<400> 41

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

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

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

Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
50 55 60

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

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

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

Thr Val Ser Ser Ala Ser 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> 42
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> 2C11 (VH-CL)

<400> 42
gaggtgcagc tggtggaaag cggcggaggc ctggtgcagc ccggcaagag cctgaagctg 60

agctgcgagg ccagcggctt caccttcagc ggctacggca tgcactgggt gagacaggcc 120

cctggcagag gactggaaag cgtggcctac atcaccagca gcagcatcaa cattaagtac 180

gccgacgccg tgaagggccg gttcaccgtg tccagggata acgccaagaa cctgctgttc 240

ctgcagatga acatcctgaa gtccgaggac accgctatgt attactgcgc cagattcgac 300

tgggacaaga actactgggg ccagggcacc atggtcacag tgtctagcgc tagcgtggct 360

gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 420

gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 480

aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 540

acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 600

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 660

ggagagtgtt ga 672

<210> 43
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-Fc(knob) P329G LALA

<400> 43

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

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

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

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

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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
                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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350
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Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
465                 470                 475                 480

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
                485                 490                 495

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            500                 505                 510

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        515                 520                 525

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    530                 535                 540

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
545                 550                 555                 560

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                565                 570                 575

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            580                 585                 590

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
        595                 600                 605

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
    610                 615                 620
```

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
625 630 635 640

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
645 650 655

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
660 665 670

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
675 680 685

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
690 695 700

<210> 44
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (scFab)-Fc(knob) P329G LALA

<400> 44
gacatccaga tgacccagag cccctctagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggccctag cgtgttccct 1140

ctggccccta gcagcaagag cacaagtgga ggaacagccg ccctgggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaattctg gcgccctgac aagcggcgtg 1260

cacacatttc cagccgtgct gcagagcagc ggcctgtact ctctgagcag cgtcgtgacc 1320

gtgccctcta gctctctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aacaccaaag tggacaagaa ggtggaaccc aagagctgcg acaagaccca cacctgtccc 1440

ccttgccctg cccctgaagc tgctggtggc ccttccgtgt tcctgttccc cccaaagccc 1500

aaggacaccc tgatgatcag ccggaccccc gaagtgacct gcgtggtggt cgatgtgtcc 1560

cacgaggacc ctgaagtgaa gttcaattgg tacgtggacg gcgtggaagt gcacaatgcc 1620

aagaccaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1680

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1740

ctcggcgccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1800

gtgtacaccc tgccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc 1860

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1920

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1980

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 2040

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 2100

taa 2103

<210> 45
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 (VH-CH1)-Fc(hole) P329G LALA

<400> 45

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 Thr Phe Thr Asp Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
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<210> 46
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 (VH-CH1)-Fc(hole) P329G LALA

<400> 46

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caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cctctggttt cacattcact gactacaaga tacactgggt gcgacaggcc      120

cctggacaag ggctcgagtg gatgggatat ttcaacccta acagcggtta tagtacctac      180

gcacagaagt tccagggcag ggtcaccatt accgcggaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagactatcc      300

ccaggcggtt actatgttat ggatgcctgg ggccaaggga ccaccgtgac cgtctcctca      360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc      600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga      720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct      780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac      900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
```

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa tga 1353

<210> 47
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 (VL-CL)

<400> 47

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 Asn Asn Tyr
20 25 30

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

Tyr Asn Thr Asn Asn Leu Gln Thr 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 His Asn Ser Phe Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu 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

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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> 48
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 (VL-CL)

<400> 48
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60

atcacctgcc gggcaagtca gggcattaac aattacttaa attggtacca gcagaagcca 120

gggaaagccc ctaagcgcct gatctataat accaacaact tgcagacagg cgtcccatca 180

aggttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gaagattttg ccacctatta ctgcttgcag cataatagtt ttcccacgtt tggccagggc 300

accaagctcg agatcaagcg tacggtggct gcaccatctg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgtt ag 642

<210> 49
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 (scFab)-Fc(knob) P329G LALA

<400> 49

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 Asn Asn Tyr
20 25 30

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

Tyr Asn Thr Asn Asn Leu Gln Thr 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 His Asn Ser Phe Pro Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu 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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly
    210                 215                 220

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
225                 230                 235                 240

Gly Ser Gly Gly Gly Ser Gly Gln Val Gln Leu Val Gln Ser Gly Ala
                245                 250                 255

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
            260                 265                 270

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

Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro Asn Ser Gly Tyr
    290                 295                 300

Ser Thr Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
305                 310                 315                 320

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
                325                 330                 335
```

```
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Ser Pro Gly Gly Tyr Tyr
            340                 345                 350

Val Met Asp Ala Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        355                 360                 365

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    370                 375                 380

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                405                 410                 415

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            420                 425                 430

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        435                 440                 445

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    450                 455                 460

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
465                 470                 475                 480

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                485                 490                 495

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            500                 505                 510

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        515                 520                 525

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    530                 535                 540

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
545                 550                 555                 560

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                565                 570                 575

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            580                 585                 590

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
        595                 600                 605
```

```
Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
    610                 615                 620

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
625                 630                 635                 640

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                645                 650                 655

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            660                 665                 670

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        675                 680                 685

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    690                 695
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<210> 50
<211> 2094
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 (scFab)-Fc(knob) P329G LALA

<400> 50

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atcacctgcc gggcaagtca gggcattaac aattacttaa attggtacca gcagaagcca      120

gggaaagccc ctaagcgcct gatctataat accaacaact tgcagacagg cgtcccatca      180

aggttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cctgcagcct      240

gaagattttg ccacctatta ctgcttgcag cataatagtt ttcccacgtt tggccagggc      300

accaagctcg agatcaagcg tacggtggcc gctcccagcg tgttcatctt ccccccccagc     360

gacgagcagc tgaaatctgg caccgccagc gtcgtgtgcc tgctgaacaa cttctacccc      420

cgggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggaa      480

agcgtcaccg agcaggacag caaggactcc acctatagcc tgtccagcac cctgaccctg      540

agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg      600

agcagccccg tgaccaagag cttcaaccgg ggcgagtgca gcggcggagg tagcggaggc      660

ggctctgagg gcggaggaag cgagggcgga ggctccgaag gcggcggaag cgaaggtggc      720

ggctctggcg gcggatccgg ccaggtgcag ctggtgcagt ctggggctga ggtgaagaag      780

cctgggtcct cggtgaaggt ctcctgcaag gcctctggtt tcacattcac tgactacaag      840

atacactggg tgcgacaggc ccctggacaa gggctcgagt ggatgggata tttcaaccct      900

aacagcggtt atagtaccta cgcacagaag ttccagggca gggtcaccat taccgcggac      960

aaatccacga gcacagccta catggagctg agcagcctga gatctgagga cacggccgtg     1020
```

tattactgtg cgagactatc cccaggcggt tactatgtta tggatgcctg gggccaaggg 1080

accaccgtga ccgtctcctc agctagcacc aagggcccta gcgtgttccc tctggccccct 1140

agcagcaaga gcacaagtgg aggaacagcc gccctgggct gcctggtcaa ggactacttc 1200

cccgagcccg tgaccgtgtc ctggaattct ggcgccctga caagcggcgt gcacacattt 1260

ccagccgtgc tgcagagcag cggcctgtac tctctgagca gcgtcgtgac cgtgccctct 1320

agctctctgg gcacccagac ctacatctgc aacgtgaacc acaagcccag caacaccaaa 1380

gtggacaaga aggtggaacc caagagctgc gacaagaccc acacctgtcc cccttgccct 1440

gcccctgaag ctgctggtgg cccttccgtg ttcctgttcc ccccaaagcc caaggacacc 1500

ctgatgatca gccggacccc cgaagtgacc tgcgtggtgg tcgatgtgtc ccacgaggac 1560

cctgaagtga agttcaattg gtacgtggac ggcgtggaag tgcacaatgc caagaccaag 1620

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1680

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcggcgcc 1740

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1800

ctgcccccat gccgggatga gctgaccaag aaccaggtca gcctgtggtg cctggtcaaa 1860

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1920

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1980

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 2040

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ataa 2094

<210> 51
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (VH-CH1)-Fc(hole) P329G LALA

<400> 51

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 52
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (VH-CH1)-Fc(hole) P329G LALA

<400> 52
gaggtgcagc tggtcgagag cggaggcggc ctggtgcagc ctggcggcag cctgagactg 60

agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggca 120

cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gagcacctac 180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc 300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcaccct cgtgaccgtg 360

tctagcgcta gcaccaaggg cccctccgtg ttccccctgg ccccagcag caagagcacc 420

agcggcggca cagccgctct gggctgcctg gtcaaggact acttccccga gcccgtgacc 480

gtgtcctgga acagcggagc cctgacctcc ggcgtgcaca ccttccccgc cgtgctgcag 540

agttctggcc tgtatagcct gagcagcgtg gtcaccgtgc cttctagcag cctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660

gagcccaaga gctgcgacaa aactcacaca tgcccaccgt gcccagcacc tgaagctgca 720

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcg gcgcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt gcaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctc tcgtgcgcag tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctcgtgagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1359

<210> 53
<211> 934
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-GA201 (VH-CH1)-Fc(knob) P329G LALA

<400> 53

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445
```

```
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
                485                 490                 495

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr
            500                 505                 510

Phe Thr Asp Tyr Lys Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly
        515                 520                 525

Leu Glu Trp Met Gly Tyr Phe Asn Pro Asn Ser Gly Tyr Ser Thr Tyr
    530                 535                 540

Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
545                 550                 555                 560

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
                565                 570                 575

Val Tyr Tyr Cys Ala Arg Leu Ser Pro Gly Gly Tyr Tyr Val Met Asp
            580                 585                 590

Ala Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
        595                 600                 605

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    610                 615                 620

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
625                 630                 635                 640

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                645                 650                 655

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            660                 665                 670

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        675                 680                 685

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    690                 695                 700

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
705                 710                 715                 720
```

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
725 730 735

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
740 745 750

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
755 760 765

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
770 775 780

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
785 790 795 800

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
805 810 815

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
820 825 830

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
835 840 845

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
850 855 860

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
865 870 875 880

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
885 890 895

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
900 905 910

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
915 920 925

Ser Leu Ser Pro Gly Lys
930

<210> 54
<211> 2805
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 (scFab)-GA201 (VH-CH1)-Fc(knob) P329G LALA

<400> 54
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atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttccccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccctc cgtgttcccc 1140

ctggccccca gcagcaagag caccagcggc ggcacagccg ccctcggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggcggtggat ctcaggtgca gctggtgcag tctggggctg aggtgaagaa gcctgggtcc 1500

tcggtgaagg tctcctgcaa ggcctctggt ttcacattca ctgactacaa gatacactgg 1560

gtgcgacagg cccctggaca agggctcgag tggatgggat atttcaaccc taacagcggt 1620

tatagtacct acgcacagaa gttccagggc agggtcacca ttaccgcgga caaatccacg 1680

agcacagcct acatggagct gagcagcctg agatctgagg acacggccgt gtattactgt 1740

gcgagactat ccccaggcgg ttactatgtt atggatgcct ggggccaagg gaccaccgtg 1800

accgtctcct cagctagcac caagggcccc tccgtgttcc ccctggcccc cagcagcaag 1860

agcaccagcg gcggcacagc cgctctgggc tgcctggtca aggactactt ccccgagccc 1920

gtgaccgtgt cctggaacag cggagccctg acctccggcg tgcacacctt ccccgccgtg 1980

ctgcagagtt ctggcctgta tagcctgagc agcgtggtca ccgtgccttc tagcagcctg 2040

ggcacccaga cctacatctg caacgtgaac cacaagccca gcaacaccaa ggtggacaag 2100

aaggtggagc ccaagagctg cgacaaaact cacacatgcc caccgtgccc agcacctgaa 2160

gctgcagggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 2220

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 2280

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 2340

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 2400

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcggcgc ccccatcgag 2460

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 2520

tgccgggatg agctgaccaa gaaccaggtc agcctgtggt gcctggtcaa aggcttctat 2580

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 2640

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 2700

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2760

aaccactaca cgcagaagag cctctccctg tctccgggta aatga 2805

<210> 55
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 (scFab)-Fc(knob) P329G LALA

<400> 55

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 Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Glu Val Gln Leu Leu Glu Ser Gly Gly
                245                 250                 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
            260                 265                 270

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
        275                 280                 285

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
    290                 295                 300

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
305                 310                 315                 320

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
                325                 330                 335

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn
            340                 345                 350

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
        355                 360                 365

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    370                 375                 380

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
385                 390                 395                 400
```

```
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                405                 410                 415

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            420                 425                 430

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        435                 440                 445

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    450                 455                 460

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
                565                 570                 575

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
        595                 600                 605

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    610                 615                 620

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625                 630                 635                 640

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                645                 650                 655

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            660                 665                 670
```

eolf-seql

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
675 680 685

Ser Leu Ser Pro Gly Lys
690

<210> 56
<211> 2085
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 (scFab)-Fc(knob) P329G LALA

<400> 56
gagatcgtgc tgacacagag ccccggaacc ctgtctctga gccctggcga aagagccacc 60

ctgagctgta gagccagcca gagcgtgacc agcagctacc tggcctggta tcagcagaag 120

cctggacagg cccccagact gctgatcaat gtgggcagca gacgggccac cggcatccct 180

gatagatttt ctggcagcgg cagcggcacc gacttcaccc tgaccatcag cagactggaa 240

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgccccc tacatttggc 300

cagggcacca aggtggaaat caagcgtacg gtggccgctc ccagcgtgtt catcttccca 360

cctagcgacg agcagctgaa gtctggcaca gccagcgtcg tgtgcctgct gaacaacttc 420

taccccgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagag cggcaacagc 480

caggaaagcg tcaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg 540

accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag 600

ggcctgtcta gccccgtgac caagagcttc aaccggggag aatgtggcgg cggaggatct 660

ggtggcggag gtagtggtgg tggtggatct ggcggaggcg gatccggcgg aggtggaagc 720

ggaggtggtg gaagtggggg agaagtgcag ctgctggaaa gtggcggagg cctggtgcag 780

cctggcggat ctctgagact gagctgtgcc gccagcggct tcacctttag cagctacgcc 840

atgagctggg tccgacaggc ccctggaaag ggactggaat gggtgtccgc catctctggc 900

tctggcggca gcacctacta cgccgatagc gtgaagggcc ggttcaccat cagccgggac 960

aacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga taccgccgtg 1020

tattattgcg ccaagggatg gttcggcggc ttcaactatt ggggccaggg aaccctggtc 1080

accgtgtcta gtgctagcac caagggccct agcgtgttcc ctctggcccc tagcagcaag 1140

agcacaagtg gaggaacagc cgccctgggc tgcctggtca aggactactt ccccgagccc 1200

gtgaccgtgt cctggaattc tggcgccctg acaagcggcg tgcacacatt tccagccgtg 1260

ctgcagagca gcggcctgta ctctctgagc agcgtcgtga ccgtgccctc tagctctctg 1320

ggcacccaga cctacatctg caacgtgaac cacaagccca gcaacaccaa agtggacaag 1380

aaggtggaac ccaagagctg cgacaagacc cacacctgtc ccccttgccc tgcccctgaa 1440

gctgctggtg gcccttccgt gttcctgttc cccccaaagc ccaaggacac cctgatgatc 1500

agccggaccc ccgaagtgac ctgcgtggtg gtcgatgtgt cccacgagga ccctgaagtg 1560

aagttcaatt ggtacgtgga cggcgtggaa gtgcacaatg ccaagaccaa gccgcgggag 1620

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1680

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcggcgc ccccatcgag 1740

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1800

tgccgggatg agctgaccaa gaaccaggtc agcctgtggt gcctggtcaa aggcttctat 1860

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1920

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1980

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2040

aaccactaca cgcagaagag cctctccctg tctccgggta aataa 2085

<210> 57
<211> 931
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 (scFab)-3F2 (VH-CH1)-Fc(knob) P329G LALA

<400> 57

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
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

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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 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
    210                 215                 220

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Gly Glu Val Gln Leu Val Glu Ser Gly
                245                 250                 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
            260                 265                 270

Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala
        275                 280                 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly
    290                 295                 300

Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val
305                 310                 315                 320

Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
                325                 330                 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
            340                 345                 350

Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        355                 360                 365

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    370                 375                 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
385                 390                 395                 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                405                 410                 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
            420                 425                 430
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Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
        435                 440                 445

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
    450                 455                 460

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
                485                 490                 495

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
            500                 505                 510

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
        515                 520                 525

Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr
    530                 535                 540

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
545                 550                 555                 560

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
                565                 570                 575

Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly
            580                 585                 590

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        595                 600                 605

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    610                 615                 620

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
625                 630                 635                 640

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                645                 650                 655

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            660                 665                 670

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        675                 680                 685

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    690                 695                 700
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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
705                 710                 715                 720

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                725                 730                 735

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            740                 745                 750

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        755                 760                 765

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    770                 775                 780

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
785                 790                 795                 800

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                805                 810                 815

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            820                 825                 830

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        835                 840                 845

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    850                 855                 860

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
865                 870                 875                 880

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                885                 890                 895

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            900                 905                 910

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        915                 920                 925

Pro Gly Lys
    930
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<210> 58
<211> 2796
<212> DNA
<213> Artificial Sequence

<220>

<223> V9 (scFab)-3F2 (VH-CH1)-Fc(knob) P329G LALA

<400> 58
gacatccaga tgacccagag cccctctagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccccc 360

agcgacgagc agctgaagtc cggcaccgcc agcgtcgtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480

gaaagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac cggggcgagt gcagcggcgg aggctctgga 660

ggcggctctg aaggcggagg aagtgagggc ggaggctcag aaggcggcgg aagcgaaggt 720

ggcggctctg gcggcggatc cggcgaggtg cagctggtcg agtccggcgg aggcctggtg 780

cagcctggcg gcagcctgag actgagctgc gccgccagcg gctacagctt caccggctac 840

accatgaact gggtccggca ggctcctggc aagggcctcg aatgggtggc cctgatcaac 900

ccctacaagg gcgtgagcac ctacaaccag aagttcaagg accggttcac catcagcgtg 960

gacaagagca agaacaccgc ctatctgcag atgaacagcc tgcgggccga ggacaccgcc 1020

gtgtactact gcgccagaag cggctactac ggcgacagcg actggtactt cgacgtgtgg 1080

ggccagggca cactggtcac cgtgtccagc gctagcacca agggcccctc cgtgttcccc 1140

ctggccccca gcagcaagag caccagcggc ggcacagccg ccctcggctg cctggtcaag 1200

gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg 1260

cacaccttcc ccgccgtgct gcagagcagc ggcctgtaca gcctgtccag cgtggtcacc 1320

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 1380

aataccaagg tggacaagaa ggtggagccc aagagctgcg acggcggtgg tggctccgga 1440

ggaggaggca gcgaggtgca gctgctggaa tctggaggcg gcctggtgca gcctggcggc 1500

agcctgagac tgtcttgcgc cgccagcggc ttcaccttca gcagctacgc catgagctgg 1560

gtccgacagg ctcctggcaa gggactggaa tgggtgtccg ccatctccgg cagcggaggc 1620

agcacctact acgccgacag cgtgaagggc cggttcacca tcagcagaga caacagcaag 1680

aacaccctgt acctgcagat gaacagcctg cgggccgagg ataccgccgt gtattattgc 1740

gccaagggat ggttcggcgg cttcaactac tggggccagg gaaccctggt gacagtgtcc 1800

agcgccagca ccaagggccc ctccgtgttt cctctggccc ccagcagcaa gagcacctct 1860

ggcggaacag ccgccctggg ctgcctggtg aaagactact tccccgagcc cgtgaccgtg 1920

tcctggaact ctggcgccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc 1980

agcggcctgt actccctgag cagcgtggtg acagtgccct ccagcagcct gggcacccag 2040

acctacatct gcaacgtgaa ccacaagccc agcaacacca aagtggacaa gaaggtggaa 2100

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 2160

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 2220

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 2280

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 2340

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 2400

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 2460

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atgccgggat 2520

gagctgacca agaaccaggt cagcctgtgg tgcctggtca aaggcttcta tcccagcgac 2580

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 2640

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 2700

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 2760

acgcagaaga gcctctccct gtctccgggt aaatga 2796

<210> 59
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 (VH-CH1)-Fc(hole) P329G LALA

<400> 59

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

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

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

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

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

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

Ala Lys 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 Cys Thr Leu Pro
            340                 345                 350

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

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

eolf-seql

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 Val 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> 60
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 (VH-CH1)-Fc(hole) P329G LALA

<400> 60
gaggtgcagc tgctggaatc tggaggcggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgacaggct 120

cctggcaagg gactggaatg ggtgtccgcc atctccggca gcggaggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agcagagaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggat accgccgtgt attattgcgc caagggatgg 300

ttcggcggct tcaactactg gggccaggga accctggtga cagtgtccag cgccagcacc 360

aagggcccct ccgtgtttcc tctggccccc agcagcaaga gcacctctgg cggaacagcc 420

gccctgggct gcctggtgaa agactacttc cccgagcccg tgaccgtgtc ctggaactct 480

ggcgccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac 540

tccctgagca gcgtggtgac agtgccctcc agcagcctgg gcacccagac ctacatctgc 600

aacgtgaacc acaagcccag caacaccaaa gtggacaaga aggtggaacc caagagctgc 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

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ctctccctgt ctccgggtaa atga 1344

<210> 61
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 (VL-CL)

<400> 61

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> 62
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 (VL-CL)

<400> 62
gagatcgtgc tgacccagtc tcccggcacc ctgagcctga gccctggcga gagagccacc 60

ctgagctgca gagccagcca gagcgtgacc agcagctacc tggcctggta tcagcagaag 120

cccggccagg cccccagact gctgatcaac gtgggcagca gacgggccac cggcatcccc 180

gatagattca gcggcagcgg ctccggcacc gacttcaccc tgaccatcag ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgccccc caccttcggc 300

cagggcacca aggtggaaat caagcggacc gtggccgctc ccagcgtgtt catcttccca 360

cccagcgacg agcagctgaa gtccggcaca gccagcgtgg tgtgcctgct gaacaacttc 420

taccccgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagag cggcaacagc 480

caggaatccg tgaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg 540

accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag 600

ggcctgtcca gccccgtgac caagagcttc aaccggggcg agtgctga 648

<210> 63
<211> 673
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (VH-CH1)- V9 (VL-CH1)-Fc(knob) P329G LALA

<400> 63

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr 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

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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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
225                 230                 235                 240

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                245                 250                 255

Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln
            260                 265                 270

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu
        275                 280                 285

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    290                 295                 300

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
305                 310                 315                 320

Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr
                325                 330                 335

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
        355                 360                 365
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
    370                 375                 380

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
385                 390                 395                 400

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                405                 410                 415

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
            420                 425                 430

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
        435                 440                 445

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
    450                 455                 460

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
465                 470                 475                 480

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
                485                 490                 495

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
            500                 505                 510

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
        515                 520                 525

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
    530                 535                 540

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
545                 550                 555                 560

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                565                 570                 575

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
            580                 585                 590

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
        595                 600                 605

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
    610                 615                 620

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
625                 630                 635                 640
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eolf-seql

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
645 650 655

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
660 665 670

Lys

<210> 64
<211> 2022
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A (VH-CH1)- V9 (VL-CH1)-Fc(knob) P329G LALA

<400> 64
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cctggacagg gcctggaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accaccgaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctact atgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agtgctagca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctggtc aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtggtc accgtgccta gctctagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcggcggagg cggatccgga ggcggaggat ctgatatcca gatgacccag 720

agccccagca gcctgtctgc cagcgtgggc gacagagtga ccattacctg cagagccagc 780

caggacatca gaaactacct gaactggtat cagcagaagc ccggcaaggc ccccaagctg 840

ctgatctact acaccagcag actggaatcc ggcgtgccca gcagattttc cggcagcggc 900

tctggcaccg actacaccct gacaatcagc agcctgcagc ccgaggactt cgccacctac 960

tactgccagc agggcaacac cctgccctgg acatttggac agggcacaaa ggtggaaatc 1020

aagagcagcg cctccaccaa gggcccttcc gtgtttccac tggccccag ctctaagagc 1080

accagcggag gaacagctgc tctgggatgt ctcgtgaagg attacttccc cgaacctgtg 1140

accgtcagct ggaacagcgg cgctctgaca tctggggtgc acacattccc cgctgtcctg 1200

cagtcctccg gcctgtacag tctgtccagc gtcgtgacag tgcctagcag ctccctggga 1260

acacagacat atatctgtaa tgtcaatcac aagccctcta ataccaaggt cgacaaaaaa 1320

gtcgagccca agtcctgcga caagacccac acctgtcccc cttgtcctgc ccctgaagct 1380

gctggcggcc cttctgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 1440

cggacccccg aagtgacctg cgtggtggtg gatgtgtccc acgaggaccc tgaagtgaag 1500

ttcaattggt acgtggacgg cgtggaagtg cacaacgcca agacaaagcc gcgggaggag 1560

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1620

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcggcgcccc catcgagaaa 1680

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatgc 1740

cgggatgagc tgaccaagaa ccaggtcagc ctgtggtgcc tggtcaaagg cttctatccc 1800

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1860

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1920

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1980

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 2022

<210> 65
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (VH-CH1)-Fc(hole) P329G LALA

<400> 65

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
```

eolf-seql

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> 66
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A (VH-CH1)-Fc(hole) P329G LALA

<400> 66
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agcgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420

ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480

tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540

tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaatga 1356

<210> 67
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (VL-CL)

<400> 67

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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
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<210> 68
<211> 648

<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A (VL-CL)

<400> 68
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atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 69
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 HCDR1

<400> 69

Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 70
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 HCDR1

<400> 70
ggctactcca tcaccagtgg ttattactgg aac 33

<210> 71
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 HCDR2

<400> 71

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

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 HCDR2

<400> 72
tacataacct acgacggtag caataactac aacccatctc tcaaaaat 48

<210> 73
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 HCDR3

<400> 73

Phe Asp Tyr
1

<210> 74
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 HCDR3

<400> 74
tttgactac 9

<210> 75
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 VH

<400> 75

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

<210> 76
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 VH

<400> 76
gaggtccagc tgcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60

acctgctctg tcactggcta ctccatcacc agtggttatt actggaactg gatccggcag 120

tttccaggaa acaagctgga atggatgggc tacataacct acgacggtag caataactac 180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240

ctgaagttga attctgtgac tactgaggac acagctacat attactgtgc ggactttgac 300

tactggggcc aaggcaccac tctcacagtc tcctca 336

<210> 77
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 LCDR1

<400> 77

Ser Ala Ser Gln Gly Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 78
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 LCDR1

<400> 78
agtgcaagtc agggcattag aaattattta aac 33

<210> 79
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 LCDR2

<400> 79

Tyr Thr Ser Ser Leu His Ser
1 5

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 LCDR2

<400> 80
tacacatcaa gtttacactc a 21

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 LCDR3

<400> 81

Gln Gln Tyr Ser Lys Leu Pro Trp Thr
1 5

<210> 82
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 LCDR3

<400> 82
cagcagtata gtaagcttcc ttggacg 27

<210> 83
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007 VL

<400> 83

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

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

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

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

eolf-seql

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Trp
85 90 95

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

<210> 84
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007 VL

<400> 84
gatattgtgc tcacacagtc tccatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atcagttgca gtgcaagtca gggcattaga aattatttaa actggtatca gcagagacca 120

gatggaactg ttaaactcct gatctattac acatcaagtt tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tgggacagat tattctctca ccatcagcaa cctggaacct 240

gaagatattg ccacttacta ttgtcagcag tatagtaagc ttccttggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 85
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 HCDR1

<400> 85

Asp Tyr Lys Ile His
1 5

<210> 86
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 HCDR1

<400> 86
gactacaaga tacac 15

<210> 87
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 HCDR2

<400> 87

Tyr Phe Asn Pro Asn Ser Gly Tyr Ser Thr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 88
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 HCDR2

<400> 88
tatttcaacc ctaacagcgg ttatagtacc tacgcacaga agttccaggg c 51

<210> 89
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 HCDR3

<400> 89

Leu Ser Pro Gly Gly Tyr Tyr Val Met Asp Ala
1 5 10

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 HCDR3

<400> 90
ctatccccag gcggttacta tgttatggat gcc 33

<210> 91
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 VH

<400> 91

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 Thr Phe Thr Asp Tyr
20 25 30

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 92
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 VH

<400> 92
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctctggttt cacattcact gactacaaga tacactgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggatat ttcaacccta acagcggtta tagtacctac 180

gcacagaagt tccagggcag ggtcaccatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagactatcc 300

ccaggcggtt actatgttat ggatgcctgg ggccaaggga ccaccgtgac cgtctcctca 360

<210> 93
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 LCDR1

<400> 93

Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Asn
1 5 10

<210> 94
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 LCDR1

<400> 94
cgggcaagtc agggcattaa caattactta aat 33

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 LCDR2

<400> 95

Asn Thr Asn Asn Leu Gln Thr
1 5

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 LCDR2

<400> 96
aataccaaca acttgcagac a 21

<210> 97
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 LCDR3

<400> 97

Leu Gln His Asn Ser Phe Pro Thr
1 5

<210> 98
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 LCDR3

<400> 98
ttgcagcata atagttttcc cacg 24

<210> 99
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> GA201 VL

<400> 99

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

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

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

Tyr Asn Thr Asn Asn Leu Gln Thr 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 His Asn Ser Phe Pro Thr
85 90 95

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

<210> 100
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> GA201 VL

<400> 100
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60

atcacctgcc gggcaagtca gggcattaac aattacttaa attggtacca gcagaagcca 120

gggaaagccc ctaagcgcct gatctataat accaacaact tgcagacagg cgtcccatca 180

aggttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gaagattttg ccacctatta ctgcttgcag cataatagtt ttcccacgtt tggccagggc 300

accaagctcg agatcaag 318

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 HCDR1

<400> 101

Ser Tyr Ala Met Ser
1 5

<210> 102
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 HCDR1

<400> 102
agctacgcca tgagc 15

<210> 103
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 HCDR2

<400> 103

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

<210> 104
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 HCDR2

<400> 104
gccatctccg gcagcggagg cagcacctac tacgccgaca gcgtgaag 48

<210> 105
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 HCDR3

<400> 105

Tyr Cys Ala Lys Gly Trp Phe Gly
1 5

<210> 106
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 HCDR3

<400> 106
tattgcgcca agggatggtt cggc 24

<210> 107
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 VH

<400> 107

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

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

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
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<210> 108
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 VH

<400> 108

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gaggtgcagc tgctggaatc tggaggcggc ctggtgcagc ctggcggcag cctgagactg       60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgacaggct      120

cctggcaagg gactggaatg ggtgtccgcc atctccggca gcggaggcag cacctactac      180

gccgacagcg tgaagggccg gttcaccatc agcagagaca acagcaagaa caccctgtac      240

ctgcagatga acagcctgcg ggccgaggat accgccgtgt attattgcgc caagggatgg      300

ttcggcggct tcaactactg gggccaggga accctggtga cagtgtccag c               351
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<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 LCDR1

<400> 109

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Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu
1               5                   10
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<210> 110
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 LCDR1

<400> 110
agagccagcc agagcgtgac cagcagctac ctg 33

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

<220>
<223> 3F2 LCDR2

<400> 111

Asn Val Gly Ser Arg Arg Ala
1 5

<210> 112
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 LCDR2

<400> 112
aacgtgggca gcagacgggc c 21

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2 LCDR3

<400> 113

Cys Gln Gln Gly Ile Met Leu Pro Pro
1 5

<210> 114
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 LCDR3

<400> 114
tgccagcagg gcatcatgct gcccccc 27

<210> 115
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> 3F2 VL

<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
100 105

<210> 116
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 VL

<400> 116
gagatcgtgc tgacccagtc tcccggcacc ctgagcctga gccctggcga gagagccacc 60

ctgagctgca gagccagcca gagcgtgacc agcagctacc tggcctggta tcagcagaag 120

cccggccagg cccccagact gctgatcaac gtgggcagca gacgggccac cggcatcccc 180

gatagattca gcggcagcgg ctccggcacc gacttcaccc tgaccatcag ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgccccc caccttcggc 300

cagggcacca aggtggaaat caag 324

<210> 117
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR1

<400> 117

Glu Phe Gly Met Asn
1 5

<210> 118
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR1

<400> 118
gagttcggca tgaac 15

<210> 119
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR2

<400> 119

Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe Lys
1 5 10 15

Gly

<210> 120
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR2

<400> 120
tggatcaaca ccaagaccgg cgaggccacc tacgtggaag agttcaaggg c 51

<210> 121
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR3

<400> 121

Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 122
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A HCDR3

<400> 122
tgggacttcg cctattacgt ggaagccatg gactac 36

<210> 123
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A VH

<400> 123

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
115 120

<210> 124
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A VH

<400> 124
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 125
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR1

<400> 125

Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala
1 5 10

<210> 126
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR1

<400> 126
aaggccagtg cggctgtggg tacgtatgtt gcg 33

<210> 127
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR2

<400> 127

Ser Ala Ser Tyr Arg Lys Arg
1 5

<210> 128
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR2

<400> 128
tcggcatcct accgcaaaag g 21

<210> 129
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR3

<400> 129

His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr
1 5 10

<210> 130
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A LCDR3

<400> 130
caccaatatt acacctatcc tctattcacg 30

<210> 131
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A VL

<400> 131

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
100 105

<210> 132
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A VL

<400> 132
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caag 324

<210> 133
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR1

<400> 133

Gly Tyr Thr Ile Thr Asp Ser Asn Ile His
1 5 10

<210> 134
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR1

<400> 134
ggctacacca tcaccgacag caacatccac 30

<210> 135
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR2

<400> 135

Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Asp Tyr Asn Gln
1 5 10

<210> 136
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR2

<400> 136
tacatctacc cctacaacgg cggcaccgac tacaaccag 39

<210> 137
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR3

<400> 137

Gly Asn Pro Trp Leu Ala Tyr
1 5

<210> 138
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 HCDR3

<400> 138
ggcaacccct ggctggccta t 21

<210> 139
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 VH

<400> 139

Glu 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 Thr Ile Thr Asp Ser
20 25 30

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

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

Lys Asn Arg Ala Thr Leu Thr Val Asp Asn Pro Thr Asn Thr Ala Tyr
65 70 75 80

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

Val Asn Gly Asn Pro Trp Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 140
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 VH

<400> 140
gaagtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg ccagcggcta caccatcacc gacagcaaca tccactgggt ccgacaggcc 120

cctgggcaga gcctggaatg gatcggctac atctacccct acaacggcgg caccgactac 180

aaccagaagt tcaagaaccg ggccaccctg accgtggaca accccaccaa caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccttct actactgcgt gaacggcaac 300

ccctggctgg cctattgggg ccagggaacc ctggtcaccg tgtctagc 348

<210> 141
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR1

<400> 141

Arg Ala Ser Glu Ser Leu Asp Asn Tyr Gly Ile Arg Phe Leu Thr
1 5 10 15

<210> 142
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR1

<400> 142
cgggccagcg agagcctgga caactacggc atccggtttc tgacc 45

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR2

<400> 143

Ala Ala Ser Asn Gln Gly Ser
1 5

<210> 144
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR2

<400> 144
gccgccagca accagggcag c 21

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR3

<400> 145

Gln Gln Thr Lys Glu Val Pro Trp Ser
1 5

<210> 146
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 LCDR3

<400> 146
cagcagacca aagaggtgcc ctggtcc 27

<210> 147
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD33 VL

<400> 147

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Leu Asp Asn Tyr
20 25 30

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

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

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

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

Glu Val Pro Trp Ser Phe Gly Gln Gly Thr Lys Val Glu Val Lys
100 105 110

<210> 148
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD33 VL

<400> 148
gacatccagc tgacccagag ccccagcacc ctgtctgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcga gagcctggac aactacggca tccggtttct gacctggttc 120

cagcagaagc ccggcaaggc ccccaagctg ctgatgtacg ccgccagcaa ccagggcagc 180

ggcgtgccaa gcagattcag cggcagcggc tccggcaccg agttcaccct gaccatcagc 240

agcctgcagc ccgacgactt cgccacctac tactgccagc agaccaaaga ggtgccctgg 300

tccttcggcc agggcaccaa ggtggaagtg aag 333

<210> 149
<211> 227
<212> PRT
<213> Homo sapiens

<400> 149

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

eolf-seql
210 215 220

Pro Gly Lys
225

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 150

Glu Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 151

Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 152
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 152

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

<210> 153
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 153

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

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly

eolf-seql

20 25 30

Ser Gly

<210> 154
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader 1

<400> 154

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 155
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 1

<400> 155
atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 156
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 1

<400> 156
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 157
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader 2

<400> 157

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Gly Ala Arg Cys
20

<210> 158

<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 2

<400> 158
atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt cccaggtgcc 60

aggtgt 66

<210> 159
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader 3

<400> 159

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 160
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 3

<400> 160
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattcc 57

<210> 161
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 3

<400> 161
atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 162
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader 3

<400> 162
atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 163

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

<220>
<223> V9 HCDR1

<400> 163

Gly Tyr Thr Met Asn
1 5

<210> 164
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 HCDR1

<400> 164
ggctacacca tgaac 15

<210> 165
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 HCDR2

<400> 165

Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 166
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 HCDR2

<400> 166
ctgatcaacc cctacaaggg cgtgagcacc tacaaccaga agttcaagga c 51

<210> 167
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 HCDR3

<400> 167

Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val
1 5 10

<210> 168
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 HCDR3

<400> 168
agcggctact acggcgacag cgactggtac ttcgacgtg 39

<210> 169
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 VH

<400> 169

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 170
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 VH

<400> 170
gaggtgcagc tggtcgagtc cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggct 120

cctggcaagg gcctcgaatg ggtggccctg atcaacccct acaagggcgt gagcacctac 180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc 300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcacact ggtcaccgtg 360

tccagc 366

<210> 171
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 LCDR1

<400> 171

Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 172
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 LCDR1

<400> 172
cgggccagcc aggacatcag aaactacctg aac 33

<210> 173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 LCDR2

<400> 173

Tyr Thr Ser Arg Leu Glu Ser
1 5

<210> 174
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 LCDR2

<400> 174
tacacctcta gactggaaag c 21

<210> 175
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 LCDR3

<400> 175

Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 176
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 LCDR3

<400> 176
cagcagggca acacactccc ctggacc 27

<210> 177
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V9 VL

<400> 177

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

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

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

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

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

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

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

<210> 178
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> V9 VL

<400> 178

gacatccaga tgacccagag cccctctagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac acctctagac tggaaagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag ggcaacacac tcccctggac cttcggccag 300

ggcaccaagg tggagatcaa g 321

<210> 179
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-LC007(VL-CL)

<400> 179

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
130 135 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145 150 155 160

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

```
            180                 185                 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
        195                 200                 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
    210                 215                 220

Asn Arg Gly Glu Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225                 230                 235                 240

Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
                245                 250                 255

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Arg Asn Tyr
            260                 265                 270

Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val Lys Leu Leu Ile
        275                 280                 285

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    290                 295                 300

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
305                 310                 315                 320

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Trp
                325                 330                 335

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            340                 345                 350

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        355                 360                 365

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    370                 375                 380

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
385                 390                 395                 400

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            420                 425                 430

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        435                 440                 445

Phe Asn Arg Gly Glu Cys
```

450

<210> 180
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-LC007(VL-CL)

<400> 180
gaggtgcagc tggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt gcgccaggcc 120

cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gtccacctac 180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actattgtgc cagaagcggc 300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcacact cgtgaccgtg 360

tcaagcgcta gcgtggccgc tcccagcgtg ttcatcttcc cacctagcga cgagcagctg 420

aagtccggca cagcctctgt cgtgtgcctg ctgaacaact tctacccccg cgaggccaag 480

gtgcagtgga aggtggacaa tgccctgcag agcggcaaca gccaggaaag cgtgaccgag 540

caggacagca aggatagcac ctacagcctg agcagcaccc tgaccctgag caaggccgac 600

tacgagaagc acaaggtgta cgcctgcgaa gtgacccacc agggcctgtc tagccccgtg 660

accaagagct tcaaccgggg cgagtgtgat ggcggaggcg gatccggggg aggcggctct 720

gatattgtgc tgacccagag ccccagcagc ctgtctgcct ctctgggcga cagagtgacc 780

atcagctgta gcgcctctca gggcatccgg aactacctga actggtatca gcagcggccc 840

gacggcaccg tgaagctgct gatctactac accagctccc tgcactccgg cgtgcccagc 900

agattttctg gcagcggctc cggcaccgac tactccctga ccatctccaa cctggaaccc 960

gaggatatcg ccacctacta ctgccagcag tactccaagc tgccctggac ctttggaggc 1020

ggcaccaagc tggaaatcaa gcgtacggtg gctgcccccc ccgtgtttat ctttccccca 1080

tccgatgaac agctgaaaag cggcaccgcc agcgtcgtgt gtctgctgaa caatttttac 1140

cctagggaag ctaaagtgca gtggaaagtg gataacgcac tgcagtccgg caactcccag 1200

gaatctgtga cagaacagga ctctaaggac agcacatact ccctgtcctc caccctgaca 1260

ctgtctaagg ctgattatga gaaacacaaa gtgtatgctt gtgaagtgac acatcaggga 1320

ctgagcagcc ctgtgacaaa gtccttcaac agaggcgagt gc 1362

<210> 181
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc(knob) P329G LALA

<400> 181

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

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

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

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

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

Pro Gly Lys
225
```

<210> 182
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc(knob) P329G LALA

<400> 182
gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 420

aaccaggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 183
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)

<400> 183

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

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

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

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

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

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

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

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

```
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
    130                 135                 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145                 150                 155                 160

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

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
        195                 200                 205

Pro Lys Ser Cys
    210
```

<210> 184
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)

<400> 184

```
gatattcaga tgacccagag ccccagctct ctgagcgcca gcgtgggcga cagagtgacc       60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc      120

ggcaaggccc ccaagctgct gatctactac accagcagac tggaaagcgg cgtgccctcc      180

agattttccg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc      240

gaggatttcg ccacatatta ctgccagcag ggcaataccc tgccctggac cttcggacag      300

ggcacaaaag tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg      360

gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat      420

tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat      480

actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg      540

cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac      600

accaaggtgg acaagaaggt ggaacccaag tcttgt                                636
```

<210> 185
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-Fc(knob) P329G LALA

<400> 185

```
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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
130 135 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145 150 155 160

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
180 185 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
195 200 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
210 215 220

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

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
245 250 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
260 265 270

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

eolf-seql

```
        275                 280                 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305                 310                 315                 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                325                 330                 335

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
        355                 360                 365

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385                 390                 395                 400

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            420                 425                 430

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

Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 186
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-Fc(knob) P329G LALA

<400> 186

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gaggtgcagc tggtcgagag cggaggcggc ctggtgcagc ctggcggcag cctgagactg       60

agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggca      120

cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gagcacctac      180

aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat      240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc      300

tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcaccct cgtgaccgtg      360
```

tctagcgcta gcgtggccgc tccctccgtg tttatctttc ccccatccga tgaacagctg 420

aaaagcggca ccgcctccgt cgtgtgtctg ctgaacaatt tttaccctag ggaagctaaa 480

gtgcagtgga aagtggataa cgcactgcag tccggcaact cccaggaatc tgtgacagaa 540

caggactcca aggacagcac ctactccctg tcctccaccc tgacactgtc taaggctgat 600

tatgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc 660

acaaagagct tcaacagggg agagtgtgac aagacccaca cctgtccccc ttgtcctgcc 720

cctgaagctg ctggcggccc ttctgtgttc ctgttccccc caaagcccaa ggacaccctg 780

atgatcagcc ggacccccga agtgacctgc gtggtggtgg atgtgtccca cgaggaccct 840

gaagtgaagt tcaattggta cgtggacggc gtggaagtgc acaacgccaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cggcgccccc 1020

atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080

cccccatgcc gggatgagct gaccaagaac caggtcagcc tgtggtgcct ggtcaaaggc 1140

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1260

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1320

ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa 1368

<210> 187
<211> 682
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007(VH-CH1)-V9(VH-CL)-Fc(knob) P329G LALA

<400> 187

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
225                 230                 235                 240

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Thr
                245                 250                 255

Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            260                 265                 270

Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln
        275                 280                 285

Lys Phe Lys Asp Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr
    290                 295                 300

Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
305                 310                 315                 320

Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp
                325                 330                 335

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala
            340                 345                 350

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        355                 360                 365
```

```
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    370                 375                 380

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
385                 390                 395                 400

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

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            420                 425                 430

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        435                 440                 445

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys
    450                 455                 460

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
465                 470                 475                 480

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                485                 490                 495

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            500                 505                 510

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        515                 520                 525

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    530                 535                 540

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
545                 550                 555                 560

Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                565                 570                 575

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
            580                 585                 590

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
        595                 600                 605

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    610                 615                 620

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
625                 630                 635                 640
```

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
645 650 655

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
660 665 670

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 188
<211> 2046
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007(VH-CH1)- V9(VH-CL)-Fc(knob) P329G LALA

<400> 188
gaggtgcagc tgcaggaatc tggccctggc ctggtcaagc caagccagag tctgagcctg 60

acctgcagcg tgaccggcta cagcattacc agcggctact actggaactg gattcggcag 120

ttccccggca ataagctgga atggatgggc tacatcacct acgacggcag caacaactac 180

aaccccagcc tgaagaaccg gatcagcatc acccgggaca ccagcaagaa ccagttcttc 240

ctgaagctga acagcgtgac caccgaggac accgccacat actattgcgc cgacttcgac 300

tactggggcc agggcaccac cctgaccgtg tccagcgcca gcacaaaggg ccctagcgtg 360

ttccctctgg cccccagcag caagagcaca agcggcggaa cagccgccct gggctgcctc 420

gtgaaggact acttccccga gcccgtgaca gtgtcttgga acagcggagc cctgacaagc 480

ggcgtgcaca ccttccctgc cgtgctgcag agcagcggcc tgtactccct gagcagcgtg 540

gtcaccgtgc ctagcagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag 600

cccagcaaca ccaaagtgga caagaaggtg gagcccaaga gctgtgatgg cggaggaggg 660

tccggaggcg gaggatccga agtgcagctg gtggaatctg gcggaggcct ggtgcagcct 720

ggcggatctc tgagactgag ctgtgccgcc agcggctaca gcttcaccgg ctacaccatg 780

aactgggtgc gccaggcccc tggcaaggga ctggaatggg tggccctgat caacccctac 840

aagggcgtgt ccacatacaa ccagaagttc aaggaccggt tcaccatcag cgtggacaag 900

agcaagaaca ccgcctacct gcagatgaac agcctgcggg ccgaggacac cgccgtgtac 960

tattgtgcca gaagcggcta ctacggcgac agcgactggt acttcgacgt gtggggccag 1020

ggcacactcg tgaccgtgtc aagcgctagc gtggccgctc cctccgtgtt tatctttccc 1080

ccatccgatg aacagctgaa aagcggcacc gcctccgtcg tgtgtctgct gaacaatttt 1140

taccctaggg aagctaaagt gcagtggaaa gtggataacg cactgcagtc cggcaactcc 1200

caggaatctg tgacagaaca ggactccaag gacagcacct actccctgtc ctccaccctg 1260

acactgtcta aggctgatta tgagaaacac aaagtctacg cctgcgaagt cacccatcag 1320

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtgacaa gacccacacc 1380

tgtccccctt gtcctgcccc tgaagctgct ggcggccctt ctgtgttcct gttccccca 1440

aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggat 1500

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac 1560

aacgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1620

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1680

aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1740

ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg 1800

tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1860

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1920

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1980

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 2040

ggtaaa 2046

<210> 189
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2(VL-CL)

<400> 189

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 Tyr
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Trp
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

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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> 190
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2(VL-CL)

<400> 190
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgcc gggccagcca gggcatccgg aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagcc tgcacagcgg cgtgcctagc 180

cggtttagcg gcagcggctc cggcaccgac ttcaccctga ccattagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacagcaagc tgccctggac cttcggccag 300

ggaacaaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 191
<211> 664
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA

<400> 191

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

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

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

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

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

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

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

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
    130                 135                 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145                 150                 155                 160

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

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
        195                 200                 205

Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
    210                 215                 220

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu
225                 230                 235                 240

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly Tyr Tyr
                245                 250                 255

Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
            260                 265                 270

Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Ser
        275                 280                 285
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Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
    290                 295                 300

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Asp
305                 310                 315                 320

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
                325                 330                 335

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
            340                 345                 350

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        355                 360                 365

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
    370                 375                 380

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
385                 390                 395                 400

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                405                 410                 415

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            420                 425                 430

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        435                 440                 445

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    450                 455                 460

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
465                 470                 475                 480

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                485                 490                 495

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            500                 505                 510

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        515                 520                 525

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    530                 535                 540

Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
545                 550                 555                 560
```

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
565 570 575

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
580 585 590

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
595 600 605

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
610 615 620

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
625 630 635 640

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
645 650 655

Ser Leu Ser Leu Ser Pro Gly Lys
660

<210> 192
<211> 1992
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA (DNA)

<400> 192
gatatccaga tgacccagag ccccagctct ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagac tggaaagcgg cgtgccctcc 180

agattttccg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggatttcg ccacatatta ctgccagcag ggcaataccc tgccctggac cttcggacag 300

ggcacaaaag tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg 360

gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat 420

tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat 480

actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg 540

cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac 600

accaaggtgg acaagaaggt ggaacccaag tcttgtggcg gaggcggatc cggcggaggg 660

ggatctcagg tgcagctgca ggaaagcggc cctggcctgg tcaagcccag ccagaccctg 720

agcctgacct gcaccgtgtc cggcggcagc atcaccagcg gctactactg gaactggatt 780

cggcagcacc ccggcaaggg cctggaatgg atcggctaca tcacctacga cggcagcaac 840

aactacaacc ccagcctgaa gtccagagtg accatcagcc gggacaccag caagaaccag 900

ttcagcctga agctgtccag cgtgacagcc gccgacaccg ccgtgtacta ctgcgccgac 960

ttcgactact ggggccaggg caccctggtc accgtgtcca gcgctagcac caagggcccc 1020

agcgtgttcc ccctggcacc cagcagcaag agcacatctg gcggaacagc cgctctgggc 1080

tgtctggtga aagactactt ccccgagccc gtgaccgtgt cttggaactc tggcgccctg 1140

accagcggcg tgcacacctt ccagccgtg ctgcagagca gcggcctgta ctccctgtcc 1200

tccgtggtca ccgtgccctc tagctccctg ggaacacaga catatatctg taatgtcaat 1260

cacaagcctt ccaacaccaa agtcgataag aaagtcgagc ccaagagctg cgacaaaact 1320

cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 1380

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1440

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1500

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1560

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1620

tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1680

cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc 1740

agcctgtggt gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1800

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1860

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1920

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1980

tctccgggta aa 1992

<210> 193
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2(VH-CH1)-Fc(hole) P329G LALA

<400> 193

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

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

Tyr Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

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

```
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

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

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

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

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

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

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

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

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

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

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

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350
```

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Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
        355                 360                 365

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

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

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 194
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2(VH-CH1)-Fc(hole) P329G LALA

<400> 194

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caggtgcagc tgcaggaaag cggccctggc ctggtcaagc ccagccagac cctgagcctg       60

acctgcaccg tgtccggcgg cagcatcacc agcggctact actggaactg gatccggcag      120

caccccggca agggcctgga atggatcggc tacatcacct acgacggcag caacaactac      180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc      240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac      300

tactggggcc agggcaccct ggtcaccgtg tccagcgcta gcaccaaggg cccctccgtg      360

ttccccctgg cccccagcag caagagcacc agcggcggca cagccgctct gggctgcctg      420

gtcaaggact acttccccga gcccgtgacc gtgtcctgga acagcggagc cctgacctcc      480

ggcgtgcaca ccttccccgc cgtgctgcag agttctggcc tgtatagcct gagcagcgtg      540

gtcaccgtgc cttctagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag      600

cccagcaaca ccaaggtgga caagaaggtg gagcccaaga gctgcgacaa aactcacaca      660

tgcccaccgt gcccagcacc tgaagctgca gggggaccgt cagtcttcct cttccccccа      720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac      780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat      840

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc      900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac      960

aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa     1020
```

ccacaggtgt gcaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctc 1080

tcgtgcgcag tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctcgtgagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaa 1326

<210> 195
<211> 681
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA

<400> 195

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 Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

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

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

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
130 135 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145 150 155 160

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

```
            180                 185                 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
        195                 200                 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
    210                 215                 220

Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
225                 230                 235                 240

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr
                245                 250                 255

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

Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile
        275                 280                 285

Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys
    290                 295                 300

Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu
305                 310                 315                 320

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                325                 330                 335

Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
            340                 345                 350

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
        355                 360                 365

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
385                 390                 395                 400

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
                405                 410                 415

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
            420                 425                 430

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
        435                 440                 445

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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    450                 455                 460

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
465                 470                 475                 480

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                485                 490                 495

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
            500                 505                 510

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        515                 520                 525

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    530                 535                 540

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
545                 550                 555                 560

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                565                 570                 575

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
            580                 585                 590

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
        595                 600                 605

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    610                 615                 620

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
625                 630                 635                 640

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
                645                 650                 655

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            660                 665                 670

Lys Ser Leu Ser Leu Ser Pro Gly Lys
        675                 680
```

<210> 196
<211> 2043
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VH-CL)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA (DNA)

<400> 196

```
gaggtgcagc tggtcgagag cggaggcggc ctggtgcagc ctggcggcag cctgagactg       60
agctgcgccg ccagcggcta cagcttcacc ggctacacca tgaactgggt ccggcaggca      120
cctggcaagg gactggaatg ggtggccctg atcaacccct acaagggcgt gagcacctac      180
aaccagaagt tcaaggaccg gttcaccatc agcgtggaca agagcaagaa caccgcctat      240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagaagcggc      300
tactacggcg acagcgactg gtacttcgac gtgtggggcc agggcaccct cgtgaccgtg      360
tctagcgcta gcgtggctgc accatctgtc ttcatcttcc cgccatctga tgagcagttg      420
aaatctggaa ctgcctctgt tgtgtgcctg ctgaataact tctatcccag agaggccaaa      480
gtacagtgga aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag      540
caggacagca aggacagcac ctacagcctc agcagcaccc tgacgctgag caaagcagac      600
tacgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc      660
acaaagagct tcaacagggg agagtgtggc ggaggcggat ccggcggagg gggatctcag      720
gtgcagctgc aggaaagcgg ccctggcctg gtcaagccca gccagaccct gagcctgacc      780
tgcaccgtgt ccggcggcag catcaccagc ggctactact ggaactggat tcggcagcac      840
cccggcaagg gcctggaatg gatcggctac atcacctacg acggcagcaa caactacaac      900
cccagcctga agtccagagt gaccatcagc cgggacacca gcaagaacca gttcagcctg      960
aagctgtcca gcgtgacagc cgccgacacc gccgtgtact actgcgccga cttcgactac     1020
tggggccagg gcaccctggt caccgtgtcc agcgctagca ccaagggccc cagcgtgttc     1080
cccctggcac ccagcagcaa gagcacatct ggcggaacag ccgctctggg ctgtctggtg     1140
aaagactact tccccgagcc cgtgaccgtg tcttggaact ctggcgccct gaccagcggc     1200
gtgcacacct ttccagccgt gctgcagagc agcggcctgt actccctgtc ctccgtggtc     1260
accgtgccct ctagctccct gggaacacag acatatatct gtaatgtcaa tcacaagcct     1320
tccaacacca aagtcgataa gaaagtcgag cccaagagct gcgacaaaac tcacacatgc     1380
ccaccgtgcc cagcacctga agctgcaggg ggaccgtcag tcttcctctt ccccccaaaa     1440
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg     1500
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat     1560
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc     1620
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa     1680
gccctcggcg cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca     1740
caggtgtaca ccctgccccc atgccgggat gagctgacca agaaccaggt cagcctgtgg     1800
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag     1860
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc     1920
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc     1980
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt     2040
```

<210> 197
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A(VH-CH1)- V9(VH-CL)-Fc(knob) P329G LALA

<400> 197

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

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
225                 230                 235                 240

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                245                 250                 255

Ala Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg
            260                 265                 270

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr
        275                 280                 285

Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile
    290                 295                 300

Ser Val Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
305                 310                 315                 320

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr
                325                 330                 335

Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro
        355                 360                 365

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
    370                 375                 380

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
385                 390                 395                 400

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                405                 410                 415

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
            420                 425                 430

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
        435                 440                 445

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
    450                 455                 460

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
465                 470                 475                 480

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                485                 490                 495
```

```
Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
            500                 505                 510

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        515                 520                 525

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    530                 535                 540

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
545                 550                 555                 560

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                565                 570                 575

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            580                 585                 590

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        595                 600                 605

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    610                 615                 620

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
625                 630                 635                 640

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                645                 650                 655

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            660                 665                 670

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        675                 680                 685

Gly Lys
    690
```

<210> 198
<211> 2070
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A(VH-CH1)-V9(VH-CL)-Fc(knob) P329G LALA

<400> 198

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caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgccag cgtgaaggtg       60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggcc      120

cctggacagg gcctggaatg gatgggctgg atcaacacca agaccggcga ggccacctac      180
```

gtggaagagt tcaagggcag agtgaccttc accaccgaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctact atgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agtgctagca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctggtc aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtggtc accgtgccta gctctagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcggcggagg cggatccgga ggcggaggat ccgaagtgca gctggtggaa 720

tctggcggag gcctggtgca gcctggcgga tctctgagac tgagctgtgc cgccagcggc 780

tacagcttca ccggctacac catgaactgg gtgcgccagg cccctggcaa gggactggaa 840

tgggtggccc tgatcaaccc ctacaagggc gtgtccacat acaaccagaa gttcaaggac 900

cggttcacca tcagcgtgga caagagcaag aacaccgcct acctgcagat gaacagcctg 960

cgggccgagg acaccgccgt gtactattgt gccagaagcg gctactacgg cgacagcgac 1020

tggtacttcg acgtgtgggg ccagggcaca ctcgtgaccg tgtcaagcgc tagcgtggcc 1080

gctccctccg tgtttatctt tcccccatcc gatgaacagc tgaaaagcgg caccgcctcc 1140

gtcgtgtgtc tgctgaacaa tttttaccct agggaagcta aagtgcagtg gaaagtggat 1200

aacgcactgc agtccggcaa ctcccaggaa tctgtgacag aacaggactc caaggacagc 1260

acctactccc tgtcctccac cctgacactg tctaaggctg attatgagaa acacaaagtc 1320

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1380

ggagagtgtg acaagaccca cacctgtccc ccttgtcctg cccctgaagc tgctggcggc 1440

ccttctgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 1500

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 1560

tacgtggacg gcgtggaagt gcacaacgcc aagacaaagc cgcgggagga gcagtacaac 1620

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1680

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1740

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccccatg ccgggatgag 1800

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc 1860

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1920

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1980

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 2040

cagaagagcc tctccctgtc tccgggtaaa 2070

<210> 199
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> H2C(VL-CH1)

<400> 199

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

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

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

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65                  70                  75                  80

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

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala
            100                 105                 110

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

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

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

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

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

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
        195                 200                 205

Val Glu Pro Lys Ser Cys
    210
```

<210> 200
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> H2C(VL-CH1)

<400> 200
cagaccgtgg tgacacagga acccagcctg accgtctccc ctggcggcac cgtgaccctg 60

acctgtggaa gcagcacagg cgccgtgacc agcggctact accccaactg ggtgcagcag 120

aagcccggcc aggcccctag aggactgatc ggcggcacca agtttctggc ccctggcacc 180

cccgccagat tctctggctc tctgctgggc ggcaaggccg ccctgacact gtctggcgtg 240

cagcctgagg acgaggccga gtactactgc gccctgtggt acagcaacag atgggtgttc 300

ggcggaggca ccaagctgac cgtgctgagc agcgcttcca ccaaaggccc ttccgtgttt 360

cctctggctc ctagctccaa gtccacctct ggaggcaccg ctgctctcgg atgcctcgtg 420

aaggattatt ttcctgagcc tgtgacagtg tcctggaata gcggagcact gacctctgga 480

gtgcatactt tccccgctgt gctgcagtcc tctggactgt acagcctgag cagcgtggtg 540

acagtgccca gcagcagcct gggcacccag acctacatct gcaacgtgaa ccacaagccc 600

agcaacacca aggtggacaa gaaggtggaa cccaagtctt gt 642

<210> 201
<211> 684
<212> PRT
<213> Artificial Sequence

<220>
<223> H2C(VH-CL)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA

<400> 201

Glu Val Gln Leu Val 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 Thr Phe Asn Lys Tyr
20 25 30

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val
115 120 125

```
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
    130                 135                 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145                 150                 155                 160

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

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
            180                 185                 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
        195                 200                 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
    210                 215                 220

Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly
225                 230                 235                 240

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
                245                 250                 255

Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr
            260                 265                 270

Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu
        275                 280                 285

Glu Trp Ile Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro
    290                 295                 300

Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln
305                 310                 315                 320

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                325                 330                 335

Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            340                 345                 350

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
        355                 360                 365

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    370                 375                 380

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
385                 390                 395                 400
```

```
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                405                 410                 415

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            420                 425                 430

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
        435                 440                 445

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    450                 455                 460

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
465                 470                 475                 480

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                485                 490                 495

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            500                 505                 510

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        515                 520                 525

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    530                 535                 540

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
545                 550                 555                 560

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                565                 570                 575

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
            580                 585                 590

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
        595                 600                 605

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    610                 615                 620

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
625                 630                 635                 640

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                645                 650                 655

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            660                 665                 670
```

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
675 680

<210> 202
<211> 2052
<212> DNA
<213> Artificial Sequence

<220>
<223> H2C(VH-CL)-M4-3 ML2(VH-CH1)-Fc(knob) P329G LALA

<400> 202
gaggtgcagc tggtggaaag cggcggagga ctggtgcagc ctggcggaag cctgaagctg 60

tcttgcgccg ccagcggctt caccttcaac aaatacgcca tgaactgggt gcgccaggcc 120

cctggcaagg gactggaatg ggtggcccgg atcagaagca agtacaacaa ctacgccacc 180

tactacgccg acagcgtgaa ggaccggttc accatcagcc gggacgacag caagaacacc 240

gcctacctgc agatgaacaa cctgaaaacc gaggacaccg ccgtgtacta ctgcgtgcgg 300

cacggcaact tcggcaacag ctacatcagc tactgggcct actggggaca gggcaccctg 360

gtgacagtgt ccagcgctag cgtggctgca ccatctgtct tcatcttccc gccatctgat 420

gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga 480

gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 540

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 600

aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 660

tcgcccgtca caaagagctt caacagggga gagtgtggcg gaggcggatc cggcggaggg 720

ggatctcagg tgcagctgca ggaaagcggc cctggcctgg tcaagcccag ccagaccctg 780

agcctgacct gcaccgtgtc cggcggcagc atcaccagcg gctactactg gaactggatt 840

cggcagcacc ccggcaaggg cctggaatgg atcggctaca tcacctacga cggcagcaac 900

aactacaacc ccagcctgaa gtccagagtg accatcagcc gggacaccag caagaaccag 960

ttcagcctga agctgtccag cgtgacagcc gccgacaccg ccgtgtacta ctgcgccgac 1020

ttcgactact ggggccaggg caccctggtc accgtgtcca gcgctagcac caagggcccc 1080

agcgtgttcc ccctggcacc cagcagcaag agcacatctg gcggaacagc cgctctgggc 1140

tgtctggtga aagactactt ccccgagccc gtgaccgtgt cttggaactc tggcgccctg 1200

accagcggcg tgcacacctt ccagccgtg ctgcagagca gcggcctgta ctccctgtcc 1260

tccgtggtca ccgtgccctc tagctccctg ggaacacaga catatatctg taatgtcaat 1320

cacaagcctt ccaacaccaa agtcgataag aaagtcgagc ccaagagctg cgacaaaact 1380

cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 1440

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1500

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1560

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1620

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1680

tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1740

cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc 1800

agcctgtggt gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1860

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1920

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1980

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 2040

tctccgggta aa 2052

<210> 203
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> 431/26(VL-CL)

<400> 203

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 Ser Thr Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr Phe
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
100 105 110

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

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

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

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr

eolf-seql

165 170 175

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

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 204
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> 431/26(VL-CL)

<400> 204
gacatccaga tgacccagag ccccagcagc ctgtctgcca gcgtgggcga cagagtgacc 60

atcacctgta gcaccagcag cagcgtgtcc tacatgcact ggtatcagca gaagcccggc 120

aaggccccca agctgctgat ctacagcacc tccaatctgg ccagcggcgt gcccagcaga 180

ttttctggca gcggctccgg caccgacttc accttcacca tcagctccct gcagcccgag 240

gatatcgcca cctactactg ccaccagtgg tccagctacc ccacctttgg ccagggcacc 300

aaggtggaaa tcaagcgtac ggtggctgca ccatctgtct tcatcttccc gccatctgat 360

gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga 420

gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 480

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 540

aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 600

tcgcccgtca caaagagctt caacagggga gagtgt 636

<210> 205
<211> 689
<212> PRT
<213> Artificial Sequence

<220>
<223> 431/26(VH-CH1)-V9(VH-CL)-Fc(knob) P329G LALA

<400> 205

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
20 25 30

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

```
Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

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

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

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
225                 230                 235                 240

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
                245                 250                 255

Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln
            260                 265                 270

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys
        275                 280                 285

Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser
    290                 295                 300

Val Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg
305                 310                 315                 320
```

```
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly
                325                 330                 335

Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
            340                 345                 350

Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
        355                 360                 365

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
    370                 375                 380

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
385                 390                 395                 400

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
                405                 410                 415

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
            420                 425                 430

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
        435                 440                 445

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys
    450                 455                 460

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
465                 470                 475                 480

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                485                 490                 495

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            500                 505                 510

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        515                 520                 525

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    530                 535                 540

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
545                 550                 555                 560

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                565                 570                 575

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            580                 585                 590
```

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
595 600 605

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
610 615 620

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
625 630 635 640

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
645 650 655

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
660 665 670

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
675 680 685

Lys

<210> 206
<211> 2067
<212> DNA
<213> Artificial Sequence

<220>
<223> 431/26(VH-CH1)-V9(VH-CL)-Fc(knob) P329G LALA

<400> 206
caggtgcagc tgcaggaatc tggccctgga ctcgtgcggc ctagccagac actgagcctg 60

acctgtaccg tgtccggctt caccatcagc agcggctaca gctggcattg ggtgcgccag 120

ccacctggca gaggcctgga atggatcggc tacatccagt acagcggcat caccaactac 180

aaccccagcc tgaagtccag agtgaccatg ctggtggaca cctccaagaa ccagttcagc 240

ctgcggctga gcagcgtgac agccgccgat acagccgtgt actactgcgc cagagaggac 300

tacgactacc actggtactt cgacgtgtgg ggccagggct ctctcgtgac cgtgtcaagc 360

gctagcacaa agggccccag cgtgttccct ctggccccta gcagcaagag cacatctggc 420

ggaacagccg ccctgggctg cctggtcaag gactactttc ccgagcccgt gacagtgtcc 480

tggaactctg gcgccctgac aagcggcgtg cacacctttc cagccgtgct gcagagcagc 540

ggcctgtact ctctgagcag cgtggtcacc gtgcctagct ctagcctggg cacccagacc 600

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggaaccc 660

aagagctgcg gcggaggcgg atccggaggc ggaggatccg aagtgcagct ggtggaatct 720

ggcggaggcc tggtgcagcc tggcggatct ctgagactga gctgtgccgc cagcggctac 780

agcttcaccg gctacaccat gaactgggtg cgccaggccc ctggcaaggg actggaatgg 840

gtggccctga tcaaccccta caagggcgtg tccacataca accagaagtt caaggaccgg 900

ttcaccatca gcgtggacaa gagcaagaac accgcctacc tgcagatgaa cagcctgcgg 960

gccgaggaca ccgccgtgta ctattgtgcc agaagcggct actacggcga cagcgactgg 1020

tacttcgacg tgtggggcca gggcacactc gtgaccgtgt caagcgctag cgtggccgct 1080

ccctccgtgt ttatctttcc cccatccgat gaacagctga aaagcggcac cgcctccgtc 1140

gtgtgtctgc tgaacaattt ttaccctagg gaagctaaag tgcagtggaa agtggataac 1200

gcactgcagt ccggcaactc ccaggaatct gtgacagaac aggactccaa ggacagcacc 1260

tactccctgt cctccaccct gacactgtct aaggctgatt atgagaaaca caaagtctac 1320

gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 1380

gagtgtgaca agacccacac ctgtcccccc tgtcctgccc ctgaagctgc tggcggccct 1440

tctgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa 1500

gtgacctgcg tggtggtgga tgtgtcccac gaggaccctg aagtgaagtt caattggtac 1560

gtggacggcg tggaagtgca caacgccaag acaaagccgc gggaggagca gtacaacagc 1620

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1680

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1740

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatgccg ggatgagctg 1800

accaagaacc aggtcagcct gtggtgcctg gtcaaaggct tctatcccag cgacatcgcc 1860

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1920

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1980

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 2040

aagagcctct ccctgtctcc gggtaaa 2067

<210> 207
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 431/26(VH-CH1)-Fc(hole) P329G LALA

<400> 207

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
20 25 30

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

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser

65 70 75 80

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

Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys

eolf-seql

```
            340                 345                 350

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

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

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

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

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

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

Gly Lys
    450
```

<210> 208
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 431/26(VH-CH1)-Fc(hole) P329G LALA

<400> 208

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caggtgcagc tgcaggaatc tggccctgga ctcgtgcggc ctagccagac actgagcctg       60

acctgtaccg tgtccggctt caccatcagc agcggctaca gctggcattg ggtgcgccag      120

ccacctggca gaggcctgga atggatcggc tacatccagt acagcggcat caccaactac      180

aaccccagcc tgaagtccag agtgaccatg ctggtggaca cctccaagaa ccagttcagc      240

ctgcggctga gcagcgtgac agccgccgat acagccgtgt actactgcgc cagagaggac      300

tacgactacc actggtactt cgacgtgtgg ggccagggct ctctcgtgac cgtgtcaagc      360

gctagcacca agggcccctc cgtgttcccc ctggccccca gcagcaagag caccagcggc      420

ggcacagccg ctctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc      480

tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagttct      540

ggcctgtata gcctgagcag cgtggtcacc gtgccttcta gcagcctggg cacccagacc      600

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc      660

aagagctgcg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga      720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct      780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
```

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 209
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A(VL-CL)-V9 (VH-CL)

<400> 209

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 Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
225                 230                 235                 240

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
                245                 250                 255

Cys Ala Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val
            260                 265                 270

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Asn Pro
        275                 280                 285

Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr
    290                 295                 300

Ile Ser Val Asp Lys Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser
305                 310                 315                 320

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr
                325                 330                 335

Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
            340                 345                 350

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
        355                 360                 365

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
    370                 375                 380

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
385                 390                 395                 400

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
                405                 410                 415

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
            420                 425                 430
```

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
435 440 445

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
450 455 460

<210> 210
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A(VL-CL)-V9 (VH-CL)

<400> 210
gatatccaga tgacccagag ccccagcagc ctgtctgcca gcgtgggcga cagagtgacc 60

atcacatgca aggcctctgc cgccgtgggc acatacgtgg cctggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctacagc gccagctacc ggaagagagg cgtgcccagc 180

agattttccg gcagcggctc tggcaccgac ttcaccctga ccatcagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccaccag tactacacct acccccctgtt caccttcggc 300

cagggcacca agctcgagat caagcgtacg gtggccgctc ccagcgtgtt catcttccca 360

cctagcgacg agcagctgaa gtccggcaca gcctctgtcg tgtgcctgct gaacaacttc 420

taccccgcg aggccaaggt gcagtggaag gtggacaatg ccctgcagag cggcaacagc 480

caggaaagcg tgaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg 540

acactgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag 600

ggcctgtcta gccccgtgac caagagcttc aaccggggcg aatgtggcgg cggaggatcc 660

ggcggaggcg gctccggagg cggaggaagt ggcggagggg gatctgaagt gcagctggtg 720

gaatctggcg gaggcctggt gcagcctggc ggatctctga gactgagctg tgccgccagc 780

ggctacagct tcaccggcta caccatgaac tgggtgcgcc aggcccctgg caagggactg 840

gaatgggtgg ccctgatcaa cccctacaag ggcgtgtcca catacaacca gaagttcaag 900

gaccggttca ccatcagcgt ggacaagagc aagaacaccg cctacctgca gatgaacagc 960

ctgcgggccg aggacaccgc cgtgtactac tgtgccagaa gcggctacta cggcgacagc 1020

gactggtact tcgacgtgtg gggccaggga accctcgtga ccgtgtcaag cgctagcgtg 1080

gccgcaccct ctgtgtttat ctttccaccc tctgacgaac agctgaaaag cggcaccgcc 1140

agcgtcgtgt gtctgctgaa caatttttac cctagggaag ctaaagtgca gtggaaagtg 1200

gataacgcac tgcagtccgg caactcccag gaatctgtga cagaacagga ctccaaggac 1260

agcacatact ccctgtccag cacactgacc ctgtctaagg ccgattatga gaaacacaaa 1320

gtgtatgctt gtgaagtgac acatcaggga ctgagcagcc ctgtgacaaa gtccttcaac 1380

agaggcgagt gt 1392

<210> 211

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

<220>
<223> CH1A1A(VH-CH1)-Fc(knob) P329G LALA

<400> 211

```
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

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

Leu Trp 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>  212
<211>  1353
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  CH1A1A(VH-CH1)-Fc(knob) P329G LALA

<400>  212
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg       60
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tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agcgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atgccgggat 1080

gagctgacca agaaccaggt cagcctgtgg tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

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

<220>
<223> Fc(hole) P329G LALA

<400> 213

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

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50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

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

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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

Pro Gly Lys
225

<210> 214
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc(hole) P329G LALA

<400> 214
gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 420

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 215
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2527(VL-CH1)

<400> 215

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

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

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

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

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

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

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr

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180 185 190

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
195 200 205

Val Glu Pro Lys Ser Cys
210

<210> 216
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> CH2527(VL-CH1)

<400> 216
caggccgtcg tgacccagga aagcgccctg acaacaagcc ctggcgagac agtgaccctg 60

acctgcagat ctagcacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccgacc acctgttcac cggcctgatc ggcggcacca acaaaagggc tccaggcgtg 180

ccagccagat tcagcggcag cctgattggc gataaggccg ccctgaccat cactggcgcc 240

cagacagagg acgaggccat ctacttttgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtgctgagc agcgcttcca ccaaaggccc ttccgtgttt 360

cctctggctc ctagctccaa gtccacctct ggaggcaccg ctgctctcgg atgcctcgtg 420

aaggattatt ttcctgagcc tgtgacagtg tcctggaata gcggagcact gacctctgga 480

gtgcatactt tccccgctgt gctgcagtcc tctggactgt acagcctgag cagcgtggtg 540

acagtgccca gcagcagcct gggcacccag acctacatct gcaacgtgaa ccacaagccc 600

agcaacacca aggtggacaa gaaggtggaa cccaagtctt gt 642

<210> 217
<211> 684
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2527(VH-CL)-LC007(VH-CH1)-Fc(knob) P329G LALA

<400> 217

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Val
        115                 120                 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
    130                 135                 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145                 150                 155                 160

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

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
            180                 185                 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
        195                 200                 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
    210                 215                 220

Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly
225                 230                 235                 240

Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
                245                 250                 255

Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
            260                 265                 270

Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
        275                 280                 285

Glu Trp Met Gly Tyr Ile Thr Tyr Asp Gly Ser Asn Asn Tyr Asn Pro
    290                 295                 300

Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
305                 310                 315                 320

Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
                325                 330                 335
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Tyr Cys Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
            340                 345                 350

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
        355                 360                 365

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    370                 375                 380

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
385                 390                 395                 400

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                405                 410                 415

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            420                 425                 430

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
        435                 440                 445

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    450                 455                 460

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
465                 470                 475                 480

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                485                 490                 495

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            500                 505                 510

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        515                 520                 525

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    530                 535                 540

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
545                 550                 555                 560

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                565                 570                 575

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
            580                 585                 590

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
        595                 600                 605
```

```
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    610                 615                 620

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
625                 630                 635                 640

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                645                 650                 655

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            660                 665                 670

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        675                 680
```

<210> 218
<211> 2052
<212> DNA
<213> Artificial Sequence

<220>
<223> CH2527(VH-CL)-LC007(VH-CH1)-Fc(knob) P329G LALA

<400> 218

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gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctaagggctc tctgaagctg       60

agctgtgccg ccagcggctt caccttcaac acctacgcca tgaactgggt gcgccaggcc      120

cctggcaaag gcctggaatg ggtggcccgg atcagaagca agtacaacaa ttacgccacc      180

tactacgccg acagcgtgaa ggaccggttc accatcagcc gggacgacag ccagagcatc      240

ctgtacctgc agatgaacaa cctgaaaacc gaggacaccg ccatgtacta ctgcgtgcgg      300

cacggcaact tcggcaacag ctatgtgtct tggtttgcct actggggcca gggcaccctc      360

gtgacagtgt ctgctgctag cgtggctgca ccatctgtct tcatcttccc gccatctgat      420

gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga      480

gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt      540

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc      600

aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc      660

tcgcccgtca caaagagctt caacagggga gagtgtggcg gaggcggatc cggcggaggg      720

ggatctgagg tccagctgca ggagtcagga cctggcctcg tgaaaccttc tcagtctctg      780

tctctcacct gctctgtcac tggctactcc atcaccagtg gttattactg gaactggatt      840

cggcagtttc caggaaacaa gctggaatgg atgggctaca taacctacga cggtagcaat      900

aactacaacc catctctcaa aaatcgaatc tccattactc gtgacacatc taagaaccag      960

tttttcctga agttgaattc tgtgactact gaggacacag ctacatatta ctgtgcggac     1020

tttgactact ggggccaagg caccactctc acagtctcca gcgctagcac caagggcccc     1080

agcgtgttcc ccctggcacc cagcagcaag agcacatctg gcggaacagc cgctctgggc     1140
```

tgtctggtga aagactactt ccccgagccc gtgaccgtgt cttggaactc tggcgccctg 1200

accagcggcg tgcacacctt tccagccgtg ctgcagagca gcggcctgta ctccctgtcc 1260

tccgtggtca ccgtgccctc tagctccctg ggaacacaga catatatctg taatgtcaat 1320

cacaagcctt ccaacaccaa agtcgataag aaagtcgagc ccaagagctg cgacaaaact 1380

cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 1440

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 1500

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1560

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1620

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1680

tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1740

cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc 1800

agcctgtggt gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1860

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1920

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1980

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 2040

tctccgggta aa 2052

<210> 219
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> LC007(VH-CH1)-CH2527(VH-CL)-Fc(knob) P329G LALA

<400> 219

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

```
            100                 105                 110

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
225                 230                 235                 240

Lys Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
                245                 250                 255

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            260                 265                 270

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
        275                 280                 285

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Gln
    290                 295                 300

Ser Ile Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
305                 310                 315                 320

Met Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
                325                 330                 335

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala
            340                 345                 350

Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        355                 360                 365

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

370 375 380

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
385 390 395 400

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
405 410 415

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
420 425 430

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
435 440 445

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys
450 455 460

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
465 470 475 480

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
485 490 495

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
500 505 510

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
515 520 525

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
530 535 540

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
545 550 555 560

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
580 585 590

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
595 600 605

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
610 615 620

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
625 630 635 640

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

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645 650 655

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
660 665 670

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
675 680 685

<210> 220
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> LC007(VH-CH1)-CH2527(VH-CL)-Fc(knob) P329G LALA

<400> 220
gaggtgcagc tgcaggaatc tggccctggc ctggtcaagc caagccagag tctgagcctg 60

acctgcagcg tgaccggcta cagcattacc agcggctact actggaactg gattcggcag 120

ttccccggca ataagctgga atggatgggc tacatcacct acgacggcag caacaactac 180

aaccccagcc tgaagaaccg gatcagcatc acccgggaca ccagcaagaa ccagttcttc 240

ctgaagctga acagcgtgac caccgaggac accgccacat actattgcgc cgacttcgac 300

tactggggcc agggcaccac cctgaccgtg tccagcgcca gcacaaaggg ccctagcgtg 360

ttccctctgg cccccagcag caagagcaca agcggcggaa cagccgccct gggctgcctc 420

gtgaaggact acttccccga gcccgtgaca gtgtcttgga acagcggagc cctgacaagc 480

ggcgtgcaca ccttccctgc cgtgctgcag agcagcggcc tgtactccct gagcagcgtg 540

gtcaccgtgc ctagcagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag 600

cccagcaaca ccaaagtgga caagaaggtg gagcccaaga gctgtgatgg cggaggaggg 660

tccggaggcg gaggatccga agtgcagctg gtggaaagcg gcggaggcct ggtgcagcct 720

aagggctctc tgaagctgag ctgtgccgcc agcggcttca ccttcaacac ctacgccatg 780

aactgggtgc gccaggcccc tggcaaaggc ctggaatggg tggcccggat cagaagcaag 840

tacaacaatt acgccaccta ctacgccgac agcgtgaagg accggttcac catcagccgg 900

gacgacagcc agagcatcct gtacctgcag atgaacaacc tgaaaaccga ggacaccgcc 960

atgtactact gcgtgcggca cggcaacttc ggcaacagct atgtgtcttg gtttgcctac 1020

tggggccagg gcaccctcgt gacagtgtct gctgctagcg tggccgctcc ctccgtgttt 1080

atctttcccc catccgatga acagctgaaa agcggcaccg cctccgtcgt gtgtctgctg 1140

aacaattttt accctaggga agctaaagtg cagtggaaag tggataacgc actgcagtcc 1200

ggcaactccc aggaatctgt gacagaacag gactccaagg acagcaccta ctccctgtcc 1260

tccaccctga cactgtctaa ggctgattat gagaaacaca aagtctacgc ctgcgaagtc 1320

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgtgacaag 1380

acccacacct gtccccttg tcctgcccct gaagctgctg gcggcccttc tgtgttcctg 1440

ttccccccaa agcccaagga caccctgatg atcagccgga cccccgaagt gacctgcgtg 1500

gtggtggatg tgtcccacga ggaccctgaa gtgaagttca attggtacgt ggacggcgtg 1560

gaagtgcaca acgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1620

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1680

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1740

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1800

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1860

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1920

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1980

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 2040

ctgtctccgg gtaaa 2055

<210> 221
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33(VL-CL)

<400> 221

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 Glu Ser Val Asp Asn Tyr
20 25 30

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

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
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 Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Lys
85 90 95

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 222
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD33(VL-CL)

<400> 222

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gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc       60

atcacctgtc gggccagcga gagcgtggac aactacggca tcagcttcat gaactggttc      120

cagcagaagc ccggcaaggc ccccaagctg ctgatctacg ccgccagcaa tcagggcagc      180

ggcgtgccca gcagattcag cggctctggc agcggcaccg acttcaccct gaccatcagc      240

agcctgcagc ccgacgactt cgccacctac tactgccagc agagcaaaga ggtgccctgg      300

accttcggcc agggcaccaa ggtggaaatc aagcgtacgg tggctgcacc atctgtcttc      360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg      420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg      480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc      540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc      600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt             654
```

<210> 223
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-anti-CD33(VH-CH1)-Fc(knob) P329G LALA

<400> 223

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr
```

20 25 30

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

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

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

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

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

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

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

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
195 200 205

Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
210 215 220

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val
225 230 235 240

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met
245 250 255

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
260 265 270

Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser
275 280 285

Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu

290 295 300

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
305 310 315 320

Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
325 330 335

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
340 345 350

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
355 360 365

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
370 375 380

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
385 390 395 400

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
405 410 415

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
420 425 430

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg

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565 570 575

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 224
<211> 2004
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-anti-CD33(VH-CH1)-Fc(knob) P329G LALA

<400> 224
gatatccaga tgacccagag ccccagctct ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagac tggaaagcgg cgtgccctcc 180

agattttccg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggatttcg ccacatatta ctgccagcag ggcaataccc tgccctggac cttcggacag 300

ggcacaaaag tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg 360

gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat 420

tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat 480

actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg 540

cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac 600

accaaggtgg acaagaaggt ggaacccaag tcttgtggcg gaggcggatc cggcggaggc 660

ggatctcagg tgcagctggt gcagtctggc gccgaagtga agaaacccgg cagcagcgtg 720

aaggtgtcct gcaaggccag cggctacacc ttcaccgact acaacatgca ctgggtccgc 780

caggccccag gccagggact ggaatggatc ggctacatct acccctacaa cggcggcacc 840

ggctacaacc agaagttcaa gagcaaggcc accatcaccg ccgacgagag caccaacacc 900

gcctacatgg aactgagcag cctgcggagc gaggacaccg ccgtgtacta ctgcgccaga 960

ggcagacccg ccatggacta ctggggccag ggcaccctgg tgacagtgtc cagcgccagc 1020

acaaagggcc ccagcgtgtt ccccctggca cccagcagca agagcacatc tggcggaaca 1080

gccgctctgg gctgtctggt gaaagactac ttccccgagc ccgtgaccgt gtcttggaac 1140

tctggcgccc tgaccagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg 1200

tactccctgt cctccgtggt caccgtgccc tctagctccc tgggaacaca gacatatatc 1260

tgtaatgtca atcacaagcc ttccaacacc aaagtcgata agaaagtcga gcccaagagc 1320

tgcgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 1380

gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1440

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1500

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1560

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1620

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1680

aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc 1740

aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg 1800

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1860

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1920

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1980

agcctctccc tgtctccggg taaa 2004

<210> 225
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33(VH-CH1)-Fc(hole) P329G LALA

<400> 225

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 Thr Phe Thr Asp Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val

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355 360 365

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

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

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

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

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

<210> 226
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD33(VH-CH1)-Fc(hole) P329G LALA

<400> 226
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gactacaaca tgcactgggt ccgccaggcc 120

ccaggccagg gactggaatg gatcggctac atctacccct acaacggcgg caccggctac 180

aaccagaagt tcaagagcaa ggccaccatc accgccgacg agagcaccaa caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcgc cagaggcaga 300

cccgccatgg actactgggg ccagggcacc ctggtgacag tgtccagcgc tagcaccaag 360

ggcccctccg tgttcccct ggccccagc agcaagagca ccagcggcgg cacagccgct 420

ctgggctgcc tggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga 480

gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttctgg cctgtatagc 540

ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagaccta catctgcaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgcgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 227
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD20(VL-CL)

<400> 227

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> 228
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD20(VL-CL)

<400> 228
gatatcgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gcccgccagc 60

attagctgca ggtctagcaa gagcctcttg cacagcaatg gcatcactta tttgtattgg 120

tacctgcaaa agccagggca gtctccacag ctcctgattt atcaaatgtc caaccttgtc 180

tctggcgtcc ctgaccggtt ctccggatcc gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgcg ctcagaatct agaacttcct 300

tacaccttcg gcggagggac caaggtggag atcaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 229
<211> 671
<212> PRT
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-anti-CD20(VH-CH1)-Fc(knob) P329G LALA

<400> 229

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

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

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

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

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

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

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

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
130 135 140

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
145 150 155 160

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

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
195 200 205

Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
210 215 220

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val
225 230 235 240

Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Tyr Ser Trp Ile
245 250 255

Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg
260 265 270

Ile Phe Pro Gly Asp Gly Asp Thr Asp Tyr Asn Gly Lys Phe Lys Gly
275 280 285

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
290 295 300

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
305 310 315 320

Asn Val Phe Asp Gly Tyr Trp Leu Val Tyr Trp Gly Gln Gly Thr Leu
325 330 335

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

```
            340                 345                 350

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
        355                 360                 365

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
    370                 375                 380

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
385                 390                 395                 400

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
                405                 410                 415

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
            420                 425                 430

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
        435                 440                 445

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
    450                 455                 460

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
465                 470                 475                 480

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
                485                 490                 495

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
            500                 505                 510

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
        515                 520                 525

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
    530                 535                 540

Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
545                 550                 555                 560

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

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
            580                 585                 590

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
        595                 600                 605

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
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610 615 620

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
625 630 635 640

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
645 650 655

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665 670

<210> 230
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> V9(VL-CH1)-anti-CD20(VH-CH1)-Fc(knob) P329G LALA

<400> 230
gatatccaga tgacccagag ccccagctct ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca ggacatcaga aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagac tggaaagcgg cgtgccctcc 180

agattttccg gcagcggctc cggcaccgac tacaccctga ccatcagcag cctgcagccc 240

gaggatttcg ccacatatta ctgccagcag ggcaataccc tgccctggac cttcggacag 300

ggcacaaaag tggaaatcaa gagcagcgct tccaccaaag gcccttccgt gtttcctctg 360

gctcctagct ccaagtccac ctctggaggc accgctgctc tcggatgcct cgtgaaggat 420

tattttcctg agcctgtgac agtgtcctgg aatagcggag cactgacctc tggagtgcat 480

actttccccg ctgtgctgca gtcctctgga ctgtacagcc tgagcagcgt ggtgacagtg 540

cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac 600

accaaggtgg acaagaaggt ggaacccaag tcttgtggcg gaggcggatc cggcggaggg 660

ggatctcagg tgcaattggt gcagtctggc gctgaagtta agaagcctgg gagttcagtg 720

aaggtctcct gcaaggcttc cggatacgcc ttcagctatt cttggatcaa ttgggtgcgg 780

caggcgcctg gacaagggct cgagtggatg ggacggatct ttcccggcga tggggatact 840

gactacaatg ggaaattcaa gggcagagtc acaattaccg ccgacaaatc cactagcaca 900

gcctatatgg agctgagcag cctgagatct gaggacacgg ccgtgtatta ctgtgcaaga 960

aatgtctttg atggttactg gcttgtttac tggggccagg gaaccctggt caccgtctcc 1020

tcagctagca ccaagggccc cagcgtgttc cccctggcac ccagcagcaa gagcacatct 1080

ggcggaacag ccgctctggg ctgtctggtg aaagactact tccccgagcc cgtgaccgtg 1140

tcttggaact ctggcgccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc 1200

agcggcctgt actccctgtc ctccgtggtc accgtgccct ctagctccct gggaacacag 1260

acatatatct gtaatgtcaa tcacaagcct tccaacacca aagtcgataa gaaagtcgag 1320

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 1380

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 1440

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 1500

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1560

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1620

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1680

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atgccgggat 1740

gagctgacca agaaccaggt cagcctgtgg tgcctggtca aaggcttcta tcccagcgac 1800

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1860

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1920

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1980

acgcagaaga gcctctccct gtctccgggt aaa 2013

<210> 231
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD20(VH-CH1)-Fc(hole) P329G LALA

<400> 231

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 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 Cys Thr
340 345 350

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

Cys Ala 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 Val Ser Lys Leu Thr Val Asp Lys

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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> 232
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD20(VH-CH1)-Fc(hole) P329G LALA

<400> 232
caggtgcaat tggtgcagtc tggcgctgaa gttaagaagc ctgggagttc agtgaaggtc 60

tcctgcaagg cttccggata cgccttcagc tattcttgga tcaattgggt gcggcaggcg 120

cctggacaag ggctcgagtg gatgggacgg atctttcccg gcgatgggga tactgactac 180

aatgggaaat tcaagggcag agtcacaatt accgccgaca aatccactag cacagcctat 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aagaaatgtc 300

tttgatggtt actggcttgt ttactggggc cagggaaccc tggtcaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 233
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR1

<400> 233

Gly Gly Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 234
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR1

<400> 234
ggcggcagca tcaccagcgg ctactactgg aac 33

<210> 235
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR2

<400> 235

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

<210> 236
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR2

<400> 236
tacatcacct acgacggcag caacaactac aaccccagcc tgaagtcc 48

<210> 237
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR3

<400> 237

Phe Asp Tyr
1

<210> 238
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 HCDR3

<400> 238
ttcgactac 9

<210> 239
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 VH

<400> 239

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

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

Tyr Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

<210> 240
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 VH

<400> 240
caggtgcagc tgcaggaaag cggccctggc ctggtcaagc ccagccagac cctgagcctg 60

acctgcaccg tgtccggcgg cagcatcacc agcggctact actggaactg gatccggcag 120

caccccggca agggcctgga atggatcggc tacatcacct acgacggcag caacaactac 180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc 240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac 300

tactggggcc agggcaccct ggtcaccgtg tccagc 336

<210> 241
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR1

<400> 241

Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 242
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR1

<400> 242
cgggccagcc agggcatccg gaactacctg aac 33

<210> 243
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR2

<400> 243

Tyr Thr Ser Ser Leu His Ser
1 5

<210> 244
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR2

<400> 244
tacaccagca gcctgcacag c 21

<210> 245
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR3

<400> 245

Gln Gln Tyr Ser Lys Leu Pro Trp Thr

1 5

<210> 246
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 LCDR3

<400> 246
cagcagtaca gcaagctgcc ctggacc 27

<210> 247
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> M4-3 ML2 VL

<400> 247

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 Tyr
20 25 30

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

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

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

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

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

<210> 248
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> M4-3 ML2 VL

<400> 248
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgcc gggccagcca gggcatccgg aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagcc tgcacagcgg cgtgcctagc 180

cggtttagcg gcagcggctc cggcaccgac ttcaccctga ccattagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacagcaagc tgccctggac cttcggccag 300

ggaacaaagg tggagatcaa g 321

<210> 249
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR1

<400> 249

Thr Tyr Ala Met Asn
1 5

<210> 250
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR1

<400> 250
acctacgcca tgaac 15

<210> 251
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR2

<400> 251

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 252
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR2

<400> 252
cggatcagaa gcaagtacaa caattacgcc acctactacg ccgacagcgt gaaggac 57

<210> 253
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR3

<400> 253

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 254
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 HCDR3

<400> 254
cacggcaact tcggcaacag ctatgtgtct tggtttgcct ac 42

<210> 255
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 VH

<400> 255

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

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120 125

<210> 256
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 VH

<400> 256
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctaagggctc tctgaagctg 60

agctgtgccg ccagcggctt caccttcaac acctacgcca tgaactgggt gcgccaggcc 120

cctggcaaag gcctggaatg ggtggcccgg atcagaagca agtacaacaa ttacgccacc 180

tactacgccg acagcgtgaa ggaccggttc accatcagcc gggacgacag ccagagcatc 240

ctgtacctgc agatgaacaa cctgaaaacc gaggacaccg ccatgtacta ctgcgtgcgg 300

cacggcaact tcggcaacag ctatgtgtct tggtttgcct actggggcca gggcaccctc 360

gtgacagtgt ctgct 375

<210> 257
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR1

<400> 257

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

<210> 258
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR1

<400> 258
agatctagca caggcgccgt gaccaccagc aactacgcca ac 42

<210> 259
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR2

<400> 259

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 260
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR2

<400> 260

ggcaccaaca aaagggctcc a 21

<210> 261
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR3

<400> 261

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 262
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 LCDR3

<400> 262
gccctgtggt acagcaacct gtgggtg 27

<210> 263
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 VL

<400> 263

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

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

<210> 264

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CD3 VL

<400> 264
caggccgtcg tgacccagga aagcgccctg acaacaagcc ctggcgagac agtgaccctg 60

acctgcagat ctagcacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccgacc acctgttcac cggcctgatc ggcggcacca acaaaagggc tccaggcgtg 180

ccagccagat tcagcggcag cctgattggc gataaggccg ccctgaccat cactggcgcc 240

cagacagagg acgaggccat ctacttttgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtgctg 327

<210> 265
<211> 207
<212> PRT
<213> Homo sapiens

<400> 265

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95

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

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115 120 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130 135 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145 150 155 160

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Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
165 170 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
180 185 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
195 200 205

<210> 266
<211> 198
<212> PRT
<213> Macaca fascicularis

<400> 266

Met Gln Ser Gly Thr Arg Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Ile Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr
20 25 30

Gln Thr Pro Tyr Gln Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
35 40 45

Cys Ser Gln His Leu Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys
50 55 60

Asn Lys Glu Asp Ser Gly Asp Arg Leu Phe Leu Pro Glu Phe Ser Glu
65 70 75 80

Met Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly Ser Asn Pro
85 90 95

Glu Asp Ala Ser His His Leu Tyr Leu Lys Ala Arg Val Cys Glu Asn
100 105 110

Cys Met Glu Met Asp Val Met Ala Val Ala Thr Ile Val Ile Val Asp
115 120 125

Ile Cys Ile Thr Leu Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys
130 135 140

Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly
145 150 155 160

Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn
165 170 175

Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Gln Asp Leu Tyr Ser Gly
180 185 190

Leu Asn Gln Arg Arg Ile

195