Sequence Listing

<110> SHANGHAI YIJIE BIOTECHNOLOGY CO. LTD

<120> TUMOR-SPECIFIC ANTI-EGFR ANTIBODY AND APPLICATION THEREOF

<130> P2016-1103

<150> CN201510431481.6
<151> 2015-07-21

<160> 77

<170> PatentIn version 3.3

<210> 1
<211> 16
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<213> Homo Sapiens

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ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcgttcag tacgcccagt tcccatatac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

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accagctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

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<223> amino acid sequence of single chain antibody 7B3

<400> 3

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Val Gln Tyr Ala Gln Phe Pro Tyr
                85                  90                  95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
        115                 120                 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
    130                 135                 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
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Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
                165                 170                 175

Tyr Arg Gly Arg Thr Ser Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
            180                 185                 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
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Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
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<223> Primer

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<223> Primer

<400> 11
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acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

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

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Ile Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

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<210> 15
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<400> 15
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<210> 16
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<223> eGFP-F2A-Y022 scFv-¦ÄZ nucleotide sequence

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aggtgaactt caagatccgc cacaacatcg aggacggcag cgtgcagctc gccgaccact 660

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<221> misc_feature
<223> eGFP-F2A-Y022 scFv-Z nucleotide sequence

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taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc tacggcaagc 240

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ccaccctgac ctacggcgtg cagtgcttca gccgctaccc cgaccacatg aagcagcacg 360

acttcttcaa gtccgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg 420

acgacggcaa ctacaagacc cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc 480

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aggtcgacct c 2231

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gcaagggcga ggagctgttc accggggtgg tgcccatcct ggtcgagctg gacggcgacg 180

taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc tacggcaagc 240

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ccaccctgac ctacggcgtg cagtgcttca gccgctaccc cgaccacatg aagcagcacg 360

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acgacggcaa ctacaagacc cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc 480

gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg cacaagctgg 540

agtacaacta caacagccac aacgtctata tcatggccga caagcagaag aacggcatca 600

aggtgaactt caagatccgc cacaacatcg aggacggcag cgtgcagctc gccgaccact 660

accagcagaa cacccccatc ggcgacggcc ccgtgctgct gcccgacaac cactacctga 720

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tcctgtcact ggttatcacc aaacggggca gaaagaaact cctgtatata ttcaaacaac 1920

catttatgag accagtacaa actactcaag aggaagatgg ctgtagctgc cgatttccag 1980

aagaagaaga aggaggatgt gaactgagag tgaagttcag caggagcgca gacgcccccg 2040

cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga agagaggagt 2100

acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag ccgcagagaa 2160

ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg gcggaggcct 2220

acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc 2280

agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag gccctgcccc 2340

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<220>
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<223> eGFP-F2A-Y022 scFv-28Z nucleotide sequence

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taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc tacggcaagc 240

tgaccctgaa gttcatctgc accaccggca agctgcccgt gccctggccc accctcgtga 300

ccaccctgac ctacggcgtg cagtgcttca gccgctaccc cgaccacatg aagcagcacg 360

acttcttcaa gtccgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg 420

acgacggcaa ctacaagacc cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc 480

gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg cacaagctgg 540

agtacaacta caacagccac aacgtctata tcatggccga caagcagaag aacggcatca 600

aggtgaactt caagatccgc cacaacatcg aggacggcag cgtgcagctc gccgaccact 660

accagcagaa cacccccatc ggcgacggcc ccgtgctgct gcccgacaac cactacctga 720

gcacccagtc cgccctgagc aaagacccca acgagaagcg cgatcacatg gtcctgctgg 780

agttcgtgac cgccgccggg atcactctcg gcatggacga gctgtacaag tccggagtga 840

aacagacttt gaattttgac cttctgaagt tggcaggaga cgttgagtcc aaccctgggc 900

ccatggcctt accagtgacc gccttgctcc tgccgctggc cttgctgctc cacgccgcca 960

ggccggatat tcagatgacc cagagcccga gcagcctgag cgcgagcgtg ggcgaccgtg 1020

tgaccattac ctgccatgcg agccaggata ttaacgtgaa cattggctgg ctgcagcaga 1080

aaccgggcaa agcgtttaaa ggcctgattt atcatggcaa aaacctggaa gatggcgtgc 1140

cgagccgttt tagcggcagc ggcagcggca ccgattttac cctgaccatt agcagcctgc 1200

agccggaaga ttttgcgacc tattattgca atcagtatga aaatatccca ctgacatttg 1260

gccagggcac caaagtggaa attaaacgtg gtggaggcgg ttcaggcgga ggtggctctg 1320

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gccgcaccca gtataacccg agcctgaaaa gccgtattag cattacccgt gataacagca 1560

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tggacttcgc ctgtgatttt tgggtgctgg tggtggttgg tggagtcctg gcttgctata 1860

gcttgctagt aacagtggcc tttattattt tctgggtgag gagtaagagg agcaggctcc 1920

tgcacagtga ctacatgaac atgactcccc gccgccccgg gccaacccgc aagcattacc 1980

agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag ttcagcagga 2040

gcgcagacgc ccccgcgtac cagcagggcc agaaccagct ctataacgag ctcaatctag 2100

gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct gagatggggg 2160

gaaagccgca gagaaggaag aaccctcagg aaggcctgta caatgaactg cagaaagata 2220

agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg ggcaaggggc 2280

acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac gcccttcaca 2340

tgcaggccct gccccctcgc taggtcgacc tc 2372

<210> 35
<211> 2498
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> eGFP-F2A-Y022 scFv-28BBZ nucleotide sequence

<400> 35

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gtgacgcgga tccaggccta agcttacgcg tcctagcgct accggtcgcc accatggtga 120

gcaagggcga ggagctgttc accggggtgg tgcccatcct ggtcgagctg gacggcgacg 180

taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc tacggcaagc 240

tgaccctgaa gttcatctgc accaccggca agctgcccgt gccctggccc accctcgtga 300

ccaccctgac ctacggcgtg cagtgcttca gccgctaccc cgaccacatg aagcagcacg 360

acttcttcaa gtccgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg 420

acgacggcaa ctacaagacc cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc 480

gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg cacaagctgg 540

agtacaacta caacagccac aacgtctata tcatggccga caagcagaag aacggcatca 600

aggtgaactt caagatccgc cacaacatcg aggacggcag cgtgcagctc gccgaccact 660

accagcagaa cacccccatc ggcgacggcc ccgtgctgct gcccgacaac cactacctga 720

gcacccagtc cgccctgagc aaagacccca acgagaagcg cgatcacatg gtcctgctgg 780

agttcgtgac cgccgccggg atcactctcg gcatggacga gctgtacaag tccggagtga 840

aacagacttt gaattttgac cttctgaagt tggcaggaga cgttgagtcc aaccctgggc 900

ccatggcctt accagtgacc gccttgctcc tgccgctggc cttgctgctc cacgccgcca 960

ggccggatat tcagatgacc cagagcccga gcagcctgag cgcgagcgtg ggcgaccgtg 1020

tgaccattac ctgccatgcg agccaggata ttaacgtgaa cattggctgg ctgcagcaga 1080

aaccgggcaa agcgtttaaa ggcctgattt atcatggcaa aaacctggaa gatggcgtgc 1140

cgagccgttt tagcggcagc ggcagcggca ccgattttac cctgaccatt agcagcctgc 1200

agccggaaga ttttgcgacc tattattgca atcagtatga aaatatccca ctgacatttg 1260

gccagggcac caaagtggaa attaaacgtg gtggaggcgg ttcaggcgga ggtggctctg 1320

gcggtggcgg atcggatgtg cagctggtgg aaagcggcgg cggcctggtg cagccgggcg 1380

gcagcctgcg tctgagctgc gcggtgagcg gctatagcat taccagcgat tatgcgtgga 1440

actggattcg tcaggcgccg ggcaaaggcc tggaatggct gggctatatt agctatcgtg 1500

gccgcaccca gtataacccg agcctgaaaa gccgtattag cattacccgt gataacagca 1560

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gcgcgcgcat gggtaagaat tgggattact ggggccaggg caccctggtg accgtgagca 1680

gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc 1740

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tggacttcgc ctgtgatttt tgggtgctgg tggtggttgg tggagtcctg gcttgctata 1860

gcttgctagt aacagtggcc tttattattt tctgggtgag gagtaagagg agcaggctcc 1920

tgcacagtga ctacatgaac atgactcccc gccgccccgg gccaacccgc aagcattacc 1980

agccctatgc cccaccacgc gacttcgcag cctatcgctc caaacggggc agaaagaaac 2040

tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa gaggaagatg 2100

gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga gtgaagttca 2160

gcaggagcgc agacgccccc gcgtaccagc agggccagaa ccagctctat aacgagctca 2220

atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg gaccctgaga 2280

tgggggggaaa gccgcagaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga 2340

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 2400

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ttcacatgca ggccctgccc cctcgctagg tcgacctc 2498

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<211> 601
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> eGFP-F2A-Y022 scFv-¦ÄZ amino acid sequence

<400> 36

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225                 230                 235                 240

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
                245                 250                 255

Val Glu Ser Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
            260                 265                 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met
        275                 280                 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
    290                 295                 300

Ile Thr Cys His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly Trp Leu
305                 310                 315                 320

Gln Gln Lys Pro Gly Lys Ala Phe Lys Gly Leu Ile Tyr His Gly Lys
                325                 330                 335

Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            340                 345                 350
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```
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
        355                 360                 365

Thr Tyr Tyr Cys Asn Gln Tyr Glu Asn Ile Pro Leu Thr Phe Gly Gln
    370                 375                 380

Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400

Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Glu Ser Gly Gly
                405                 410                 415

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser
            420                 425                 430

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Ala
        435                 440                 445

Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser Tyr Arg Gly Arg
    450                 455                 460

Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp
465                 470                 475                 480

Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser Leu Arg Ala Glu
                485                 490                 495

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Lys Asn Trp Asp Tyr
            500                 505                 510

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
        515                 520                 525

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    530                 535                 540

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
545                 550                 555                 560

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                565                 570                 575

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Arg Val Lys
            580                 585                 590

Phe Ser Arg Ser Ala Asp Ala Pro Ala
        595                 600
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<210> 37
<211> 702
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> eGFP-F2A-Y022 scFv-Z amino acid sequence

<400> 37

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

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

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

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

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

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

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

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

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

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

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

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

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu

195 200 205

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

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
245 250 255

Val Glu Ser Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
260 265 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met
275 280 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
290 295 300

Ile Thr Cys His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly Trp Leu
305 310 315 320

Gln Gln Lys Pro Gly Lys Ala Phe Lys Gly Leu Ile Tyr His Gly Lys
325 330 335

Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
340 345 350

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
355 360 365

Thr Tyr Tyr Cys Asn Gln Tyr Glu Asn Ile Pro Leu Thr Phe Gly Gln
370 375 380

Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Glu Ser Gly Gly
405 410 415

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser
420 425 430

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Ala
435 440 445

```
Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser Tyr Arg Gly Arg
    450                 455                 460

Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp
465                 470                 475                 480

Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser Leu Arg Ala Glu
                485                 490                 495

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Lys Asn Trp Asp Tyr
            500                 505                 510

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
        515                 520                 525

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    530                 535                 540

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
545                 550                 555                 560

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                565                 570                 575

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Arg Val Lys
            580                 585                 590

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        595                 600                 605

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    610                 615                 620

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
625                 630                 635                 640

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

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            660                 665                 670

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
        675                 680                 685

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    690                 695                 700
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<210> 38
<211> 744
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> eGFP-F2A-Y022 scFv-BBZ amino acid sequence

<400> 38

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

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

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

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

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

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

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

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

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

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

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

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

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225                 230                 235                 240

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
                245                 250                 255

Val Glu Ser Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
            260                 265                 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met
        275                 280                 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
    290                 295                 300

Ile Thr Cys His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly Trp Leu
305                 310                 315                 320

Gln Gln Lys Pro Gly Lys Ala Phe Lys Gly Leu Ile Tyr His Gly Lys
                325                 330                 335

Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            340                 345                 350

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
        355                 360                 365

Thr Tyr Tyr Cys Asn Gln Tyr Glu Asn Ile Pro Leu Thr Phe Gly Gln
    370                 375                 380

Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400

Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Glu Ser Gly Gly
                405                 410                 415

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser
            420                 425                 430

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Ala
        435                 440                 445

Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser Tyr Arg Gly Arg
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    450                 455                 460

Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp
465                 470                 475                 480

Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser Leu Arg Ala Glu
                485                 490                 495

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Lys Asn Trp Asp Tyr
            500                 505                 510

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
        515                 520                 525

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    530                 535                 540

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
545                 550                 555                 560

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                565                 570                 575

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Lys Arg Gly
            580                 585                 590

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        595                 600                 605

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    610                 615                 620

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
625                 630                 635                 640

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                645                 650                 655

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            660                 665                 670

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
        675                 680                 685

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
    690                 695                 700
```

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
705 710 715 720

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
725 730 735

His Met Gln Ala Leu Pro Pro Arg
740

<210> 39
<211> 749
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> eGFP-F2A-Y022 scFv-28Z amino acid sequence

<400> 39

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225                 230                 235                 240

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
                245                 250                 255

Val Glu Ser Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
            260                 265                 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met
        275                 280                 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
    290                 295                 300

Ile Thr Cys His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly Trp Leu
305                 310                 315                 320

Gln Gln Lys Pro Gly Lys Ala Phe Lys Gly Leu Ile Tyr His Gly Lys
                325                 330                 335

Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            340                 345                 350

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
        355                 360                 365

Thr Tyr Tyr Cys Asn Gln Tyr Glu Asn Ile Pro Leu Thr Phe Gly Gln
    370                 375                 380

Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400

Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Glu Ser Gly Gly
                405                 410                 415
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Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser
            420                 425                 430

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Ala
        435                 440                 445

Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser Tyr Arg Gly Arg
    450                 455                 460

Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp
465                 470                 475                 480

Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser Leu Arg Ala Glu
                485                 490                 495

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Lys Asn Trp Asp Tyr
            500                 505                 510

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
        515                 520                 525

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    530                 535                 540

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
545                 550                 555                 560

Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly
                565                 570                 575

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
            580                 585                 590

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
        595                 600                 605

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
    610                 615                 620

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
625                 630                 635                 640

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
                645                 650                 655

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
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660 665 670

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg
675 680 685

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
690 695 700

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
705 710 715 720

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
725 730 735

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
740 745

<210> 40
<211> 791
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> eGFP-F2A-Y022 scFv-28BBZ amino acid sequence

<400> 40

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225                 230                 235                 240

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
                245                 250                 255

Val Glu Ser Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
            260                 265                 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met
        275                 280                 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
    290                 295                 300

Ile Thr Cys His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly Trp Leu
305                 310                 315                 320

Gln Gln Lys Pro Gly Lys Ala Phe Lys Gly Leu Ile Tyr His Gly Lys
                325                 330                 335

Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            340                 345                 350

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
        355                 360                 365
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Thr Tyr Tyr Cys Asn Gln Tyr Glu Asn Ile Pro Leu Thr Phe Gly Gln
    370                 375                 380

Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
385                 390                 395                 400

Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Glu Ser Gly Gly
                405                 410                 415

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser
            420                 425                 430

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Ala
        435                 440                 445

Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser Tyr Arg Gly Arg
    450                 455                 460

Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp
465                 470                 475                 480

Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser Leu Arg Ala Glu
                485                 490                 495

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Lys Asn Trp Asp Tyr
            500                 505                 510

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
        515                 520                 525

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    530                 535                 540

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
545                 550                 555                 560

Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly
                565                 570                 575

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
            580                 585                 590

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
        595                 600                 605

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
    610                 615                 620
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg
625 630 635 640

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
645 650 655

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
660 665 670

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
675 680 685

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
690 695 700

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
705 710 715 720

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
725 730 735

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
740 745 750

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
755 760 765

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
770 775 780

Met Gln Ala Leu Pro Pro Arg
785 790

<210> 41
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> Y022 light chain CDR1

<400> 41

His Ala Ser Gln Asp Ile Asn Val Asn Ile Gly
1 5 10

<210> 42

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

<220>
<221> MISC_FEATURE
<223> Y022 light chainCDR2

<400> 42

His Gly Lys Asn Leu Glu Asp
1 5

<210> 43
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> Y022 light chain CDR3

<400> 43

Asn Gln Tyr Glu Asn Ile Pro Leu Thr
1 5

<210> 44
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> Y022 heavy chain CDR1

<400> 44

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn
1 5 10

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

<220>
<221> MISC_FEATURE
<223> Y022 heavy chain CDR2

<400> 45

Tyr Ile Ser Tyr Arg Gly Arg Thr Gln Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 46
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> Y022 heavy chain CDR3

<400> 46

Met Gly Lys Asn Trp Asp Tyr
1 5

<210> 47
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M14 light chain CDR1

<220>
<221> MISC_FEATURE
<223> M14 light chain CDR1 amino acid sequence

<400> 47

His Ala Ser Gln Asp Ile Asn Ser Asn Ile Gly
1 5 10

<210> 48
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M14 light chain CDR3 amino acid sequence

<400> 48

Asn Gln Tyr Glu Asn Asn Pro Ile Thr
1 5

<210> 49
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M14 heavy chain CDR2

<400> 49

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

<210> 50
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M14 heavy chain CDR3

<400> 50

Leu Gly Arg Gly Phe Arg Tyr
1 5

<210> 51
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M15 heavy chain CDR2

<400> 51

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

<210> 52
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> M25 heavy chain CDR2

<400> 52

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

<210> 53
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> S7 light chain CDR2

<400> 53

His Gly Thr Asn Leu Glu Asp
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> S7 light chain CDR3

<400> 54

Asn Gln Tyr Glu Asn Asn Pro Ile Thr
1 5

<210> 55
<211> 11
<212> PRT
<213> S17 light chain CDR1

<400> 55

His Ala Ser Gln Asp Ile Asn Thr Asn Ile Gly
1 5 10

<210> 56
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> S17 light chain CDR3

<400> 56

Asn Gln Tyr Glu Asn Asn Pro Leu Thr
1 5

<210> 57
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> S23 light chain CDR3

<400> 57

Asn Gln Tyr Glu Asn Phe Pro Leu Thr
1 5

<210> 58
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody M14

<400> 58
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac agcaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccaattac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

accaactata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 59
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody M14

<400> 59

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 His Ala Ser Gln Asp Ile Asn Ser Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Ile
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 60
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody M15

<400> 60
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccaattac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

accagctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 61
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody M15

<400> 61

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Ile
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Ser Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 62
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody M25

<400> 62
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata tcccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccgctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 63
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody M25

<400> 63

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Ile Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Arg Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser

195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 64
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody M26

<400> 64
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata tcccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccagtata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 65
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody M26

<400> 65

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Ile Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 66
<211> 717
<212> DNA
<213> Artificial sequence

<220>

<221> misc_feature
<223> nucleotide sequence of single chain antibody S7

<400> 66
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaccaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccaattac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

accagctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 67
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S7

<400> 67

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Thr Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Ile
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Ser Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 68
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody S8

<400> 68
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaaagct ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccaattac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

accagctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 69
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S8

<400> 69

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Ile
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Ser Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 70
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody S17

<400> 70
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac accaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccagtata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 71
<211> 239
<212> PRT
<213> Artificial sequence

<220>

<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S17

<400> 71

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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 His Ala Ser Gln Asp Ile Asn Thr Asn
            20                  25                  30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Leu
                85                  90                  95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
        115                 120                 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
    130                 135                 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145                 150                 155                 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
                165                 170                 175

Tyr Arg Gly Arg Thr Gln Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
            180                 185                 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
    210                 215                 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235
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<210> 72
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody S22

<400> 72
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaccaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccgctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 73
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S22

<400> 73

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Thr Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Arg Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 74
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody S23

<400> 74
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaaagct ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaata acccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccgctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 75
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S23

<400> 75

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Asn Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Arg Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235

<210> 76
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<223> nucleotide sequence of single chain antibody S29

<400> 76
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga ccgtgtgacc 60

attacctgcc atgcgagcca ggatattaac gtgaacattg gctggctgca gcagaaaccg 120

ggcaaagcgt ttaaaggcct gatttatcat ggcaaaaacc tggaagatgg cgtgccgagc 180

cgttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gaagattttg cgacctatta ttgcaatcag tatgaaaatt tcccactgac atttggccag 300

ggcaccaaag tggaaattaa acgtggtgga ggcggttcag gcggaggtgg ctctggcggt 360

ggcggatcgg atgtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc 420

ctgcgtctga gctgcgcggt gagcggctat agcattacca gcgattatgc gtggaactgg 480

attcgtcagg cgccgggcaa aggcctggaa tggctgggct atattagcta tcgtggccgc 540

acccgctata acccgagcct gaaaagccgt attagcatta cccgtgataa cagcaaaaac 600

acctttttcc tgcagctgaa cagcctgcgt gcggaagata ccgcggtgta ttattgcgcg 660

cgcctgggac gcggcttccg ctactggggc cagggcaccc tggtgaccgt gagcagc 717

<210> 77
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<221> MISC_FEATURE
<223> amino acid sequence of single chain antibody S29

<400> 77

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 His Ala Ser Gln Asp Ile Asn Val Asn
20 25 30

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

Tyr His Gly Lys Asn Leu Glu Asp 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 Asn Gln Tyr Glu Asn Phe Pro Leu
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
130 135 140

Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn Trp
145 150 155 160

Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr Ile Ser
165 170 175

Tyr Arg Gly Arg Thr Arg Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser
180 185 190

Ile Thr Arg Asp Asn Ser Lys Asn Thr Phe Phe Leu Gln Leu Asn Ser

195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Leu Gly Arg
210 215 220

Gly Phe Arg Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235