SEQUENCE LISTING

<110> Micromet AG

<120> Pharmaceutical compositions with resistance to soluble CEA

<130> L1652 PCT S3

<150> EP 05 02 8064.3
<151> 2005-12-21

<150> US 60/751,963
<151> 2005-12-21

<150> US 60/780,861
<151> 2006-10-03

<160> 147

<170> PatentIn version 3.3

<210> 1
<211> 1476
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VLVH ; Bispecific single chain antibody

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cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

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aacctggctt ctggagtccc tgctcgcttc agtggcagtg ggtctgggac ctcttactct 960

ctcacaatca gcagagtgga ggctgaagat gctgccactt attactgcca acattggagt 1020

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gattactaca tgaactgggt ccgccagcct ccaggaaagg cacttgagtg gttgggtttt 1260

attggaaaca aagctaatgg ttacacaaca gagtacagtg catctgtgaa gggtcggttc 1320

accatctcca gagataaatc ccaaagcatc ctctatcttc aaatgaacac cctgagagct 1380

gaggacagtg ccacttatta ctgtaccaga gatagggggc tacggttcta ctttgactac 1440

tggggccaag ggaccacggt caccgtctcc tcctag 1476

<210> 2
<211> 491
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VLVH ; Bispecific single chain antibody

<400> 2

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

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Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
                245                 250                 255

Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
            260                 265                 270

Arg Ala Ser Ser Ser Val Thr Tyr Ile His Trp Tyr Gln Gln Lys Pro
        275                 280                 285

Gly Ser Ser Pro Lys Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
    290                 295                 300

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
305                 310                 315                 320

Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
                325                 330                 335

Gln His Trp Ser Ser Lys Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
            340                 345                 350
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Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro
    370                 375                 380

Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr
385                 390                 395                 400

Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
                405                 410                 415

Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr
            420                 425                 430

Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln
        435                 440                 445

Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala
    450                 455                 460

Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
                485                 490
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<210> 3
<211> 1476
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VHVL ; Bispecific single chain antibody

<400> 3

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cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac    180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac    240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat    300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc    360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta    420
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ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatcccag gtccaactgc aggagtcagg aggaggcttg 780

gtacagcctg ggggttctct gagactctcc tgtgcaactt ctgggttcac cttcactgat 840

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ggaaacaaag ctaatggtta cacaacagag tacagtgcat ctgtgaaggg tcggttcacc 960

atctccagag ataaatccca aagcatcctc tatcttcaaa tgaacaccct gagagctgag 1020

gacagtgcca cttattactg taccagagat agggggctac ggttctactt tgactactgg 1080

ggccaaggga ccacggtcac cgtctcctcc ggtggtggtg gttctggcgg cggcggctcc 1140

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cagcagaagc caggatcctc ccccaaatcc tggatttatg ccacatccaa cctggcttct 1320

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agagtggagg ctgaagatgc tgccacttat tactgccaac attggagtag taaaccaccg 1440

acgttcggtg gagggaccaa gctcgagatc aaatag 1476

<210> 4
<211> 491
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VHVL ; Bispecific single chain antibody

<400> 4

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr
305                 310                 315                 320

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro
385                 390                 395                 400

Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr
                405                 410                 415

Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Ser Trp Ile
            420                 425                 430

Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
        435                 440                 445

Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala
    450                 455                 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro
465                 470                 475                 480

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                485                 490
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<210> 5
<211> 1473
<212> DNA
<213> artificial sequence

<220>

<223> CEA I VLVH x SEQ ID NO: 77 VHVL ; Bispecific single-chain antibody

<400> 5

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tcctccccca aatcctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 240

gatgctgcca cttattactg ccaacattgg agtagtaaac caccgacgtt cggtggaggg 300

accaagctcg agatcaaagg tggtggtggt tctggcggcg gcggctccgg tggtggtggt 360

tctcaggtcc aactgcagga gtcaggagga ggcttggtac agcctggggg ttctctgaga 420

ctctcctgtg caacttctgg gttcaccttc actgattact acatgaactg ggtccgccag 480

cctccaggaa aggcacttga gtggttgggt tttattggaa acaaagctaa tggttacaca 540

acagagtaca gtgcatctgt gaagggtcgg ttcaccatct ccagagataa atcccaaagc 600

atcctctatc ttcaaatgaa caccctgaga gctgaggaca gtgccactta ttactgtacc 660

agagataggg ggctacggtt ctactttgac tactggggcc aagggaccac ggtcaccgtc 720

tcctccggag gtggtggatc cgacgtccaa ctggtgcagt caggggctga agtgaaaaaa 780

cctggggcct cagtgaaggt gtcctgcaag gcttctggct acacctttac taggtacacg 840

atgcactggg taaggcaggc acctggacag ggtctggaat ggattggata cattaatcct 900

agccgtggtt atactaatta cgcagacagc gtcaagggcc gcttcacaat cactacagac 960

aaatccacca gcacagccta catggaactg agcagcctgc gttctgagga cactgcaacc 1020

tattactgtg caagatatta tgatgatcat tactgccttg actactgggg ccaaggcacc 1080

acggtcaccg tctcctcagg cgaaggtact agtactggtt ctggtggaag tggaggttca 1140

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gagcgtgcca ccctgagctg cagagccagt caaagtgtaa gttacatgaa ctggtaccag 1260

cagaagccgg gcaaggcacc caaaagatgg atttatgaca catccaaagt ggcttctgga 1320

gtccctgctc gcttcagtgg cagtgggtct gggaccgact actctctcac aatcaacagc 1380

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ttcggtggcg ggaccaaggt ggagatcaaa tag 1473

<210> 6
<211> 490
<212> PRT
<213> artificial sequence

<220>
<223> CEA I VLVH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 6

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr Ile
20 25 30

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

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro Thr
85 90 95

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

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

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
130 135 140

Thr Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln
145 150 155 160

Pro Pro Gly Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala
165 170 175

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

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

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

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

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

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

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
        275                 280                 285

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
    290                 295                 300

Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr 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 Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys
            340                 345                 350

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

Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp
    370                 375                 380

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
385                 390                 395                 400

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
                405                 410                 415

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
            420                 425                 430

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
        435                 440                 445

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
    450                 455                 460
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Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
465 470 475 480

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 7
<211> 1476
<212> DNA
<213> artificial sequence

<220>
<223> CEA I VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

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ccaggaaagg cacttgagtg gttgggtttt attggaaaca aagctaatgg ttacacaaca 180

gagtacagtg catctgtgaa gggtcggttc accatctcca gagataaatc ccaaagcatc 240

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtaccaga 300

gatagggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tccggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga cattgagctc 420

acccagtctc cagcaatcct gtctgcatct ccaggggaga aggtcacaat gacttgcagg 480

gccagctcaa gtgtaactta cattcactgg taccagcaga agccaggatc ctcccccaaa 540

tcctggattt atgccacatc caacctggct tctggagtcc ctgctcgctt cagtggcagt 600

gggtctggga cctcttactc tctcacaatc agcagagtgg aggctgaaga tgctgccact 660

tattactgcc aacattggag tagtaaacca ccgacgttcg gtggagggac caagctcgag 720

atcaaatccg gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa 780

aaacctgggg cctcagtgaa ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840

acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900

cctagccgtg gttatactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca 960

gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020

acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080

accacggtca ccgtctcctc aggcgaaggt actagtactg gttctggtgg aagtggaggt 1140

tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200

ggggagcgtg ccaccctgag ctgcagagcc agtcaaagtg taagttacat gaactggtac 1260

cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320

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agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taacccgctc 1440

acgttcggtg gcgggaccaa gctggagatc aaatag 1476

<210> 8
<211> 491
<212> PRT
<213> artificial sequence

<220>
<223> CEA I VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 8

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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

Ala Ile Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg

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145                 150                 155                 160

Ala Ser Ser Ser Val Thr Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

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

Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

His Trp Ser Ser Lys Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
225                 230                 235                 240

Ile Lys Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
                245                 250                 255

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

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

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
    290                 295                 300

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

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

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
            340                 345                 350

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

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
    370                 375                 380

Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
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385 390 395 400

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 9
<211> 1491
<212> DNA
<213> artificial sequence

<220>
<223> CEA II VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

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tcctgcacag cttctggctt caacattaaa gacacctata tgcactgggt gaagcagagg 120

cctgaacagg gcctggaatg gattggaagg attgatcctg cgaatggtaa tagtaaatat 180

gtcccgaagt tccagggcaa ggccactata acagcagaca catcctccaa cacagcctac 240

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tactacgtgt ctgactatgc tatggcctac tggggtcaag gaacctcagt caccgtctcc 360

tccggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga cattgtgctg 420

acccaatctc cagcttcttt ggctgtgtct cttgggcaga gggccaccat gtcctgcaga 480

gccggtgaaa gtgttgatat ttttggcgtt gggtttttgc actggtacca gcagaaacca 540

ggacagccac ccaaactcct catctatcgt gcatccaacc tagaatctgg gatccctgtc 600

aggttcagtg gcactgggtc taggacagac ttcaccctca tcattgatcc tgtggaggct 660

gatgatgttg ccacctatta ctgtcagcaa actaatgagg atccgtacac gttcggaggg 720

gggaccaagc tcgagataaa atccggaggt ggtggatccg acgtccaact ggtgcagtca 780

ggggctgaag tgaaaaaacc tggggcctca gtgaaggtgt cctgcaaggc ttctggctac 840

acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900

attggataca ttaatcctag ccgtggttat actaattacg cagacagcgt caagggccgc 960

ttcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020

tctgaggaca ctgcaaccta ttactgtgca agatattatg atgatcatta ctgccttgac 1080

tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtactag tactggttct 1140

ggtggaagtg gaggttcagg tggagcagac gacattgtac tgacccagtc tccagcaact 1200

ctgtctctgt ctccagggga gcgtgccacc ctgagctgca gagccagtca aagtgtaagt 1260

tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320

tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380

tctctcacaa tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440

agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaata g 1491

<210> 10
<211> 496
<212> PRT
<213> artificial sequence

<220>
<223> CEA II VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 10

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

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

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

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

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

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

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                85                  90                  95

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

Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Met Ser Cys Arg
145                 150                 155                 160

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

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

Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser Gly Thr Gly Ser Arg
        195                 200                 205

Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu Ala Asp Asp Val Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val Gln
                245                 250                 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
            260                 265                 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
        275                 280                 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
    290                 295                 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
305                 310                 315                 320

Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
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                325                 330                 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr
            340                 345                 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
        355                 360                 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
    370                 375                 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
385                 390                 395                 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
                405                 410                 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
            420                 425                 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
        435                 440                 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
    450                 455                 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465                 470                 475                 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                485                 490                 495
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<210> 11
<211> 1470
<212> DNA
<213> artificial sequence

<220>
<223> CEA III VLVH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 11
gagaacgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atcacctgca gtgccagctc aagcgtcagc tacatgcact ggttccagca gaagccaggc 120

acctccccca aactctggat ttattctaca tccaacctgg cttctggagt ccctgctcgc 180

ttctctggca gtgggtctgg gacctcttac tctctcacaa tcagcagaat ggaggctgaa 240

gatgctgcca cttattactg ccagcagaga agtagttacc cactcacgtt cggtgctggg 300

accaagctcg agctgaaagg tggtggtggt tctggcggcg gcggctccgg tggtggtggt 360

tctcaggtta agctgcagca gtctggggca gagcttgtga gatcagggac atcagtcaag 420

ttgtcctgca cagcttctgg cttcaacatt aaagactcct atatgcactg gctgaggcag 480

gggcctgaac agggcctgga gtggattgga tggattgatc ctgagaatgg tgatactgaa 540

tatgccccga agttccaggg caaggccact ttcactactg acacatcctc caacacagcc 600

tacctgcagc tcagcagcct gacatctgag gacactgccg tctattactg taacgagggc 660

acacctacag ggccttacta ctttgactac tggggccaag gcaccactgt cacagtctcc 720

tccggaggtg gtggatccga cgtccaactg gtgcagtcag gggctgaagt gaaaaaacct 780

ggggcctcag tgaaggtgtc ctgcaaggct tctggctaca cctttactag gtacacgatg 840

cactgggtaa ggcaggcacc tggacagggt ctggaatgga ttggatacat taatcctagc 900

cgtggttata ctaattacgc agacagcgtc aagggccgct tcacaatcac tacagacaaa 960

tccaccagca cagcctacat ggaactgagc agcctgcgtt ctgaggacac tgcaacctat 1020

tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 1080

gtcaccgtct cctcaggcga aggtactagt actggttctg gtggaagtgg aggttcaggt 1140

ggagcagacg acattgtact gacccagtct ccagcaactc tgtctctgtc tccaggggag 1200

cgtgccaccc tgagctgcag agccagtcaa agtgtaagtt acatgaactg gtaccagcag 1260

aagccgggca aggcacccaa aagatggatt tatgacacat ccaaagtggc ttctggagtc 1320

cctgctcgct tcagtggcag tgggtctggg accgactact ctctcacaat caacagcttg 1380

gaggctgaag atgctgccac ttattactgc caacagtgga gtagtaaccc gctcacgttc 1440

ggtggcggga ccaaggtgga gatcaaatag 1470

<210> 12
<211> 489
<212> PRT
<213> artificial sequence

<220>
<223> CEA III VLVH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 12

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

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met

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            20                  25                  30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
                85                  90                  95

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

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

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

Ala Ser Gly Phe Asn Ile Lys Asp Ser Tyr Met His Trp Leu Arg Gln
145                 150                 155                 160

Gly Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn
                165                 170                 175

Gly Asp Thr Glu Tyr Ala Pro Lys Phe Gln Gly Lys Ala Thr Phe Thr
            180                 185                 190

Thr Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr
        195                 200                 205

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Asn Glu Gly Thr Pro Thr Gly
    210                 215                 220

Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
225                 230                 235                 240

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

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

Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly
        275                 280                 285

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
    290                 295                 300

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

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
                325                 330                 335

Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu
            340                 345                 350

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly
        355                 360                 365

Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp
    370                 375                 380

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
385                 390                 395                 400

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
                405                 410                 415

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
            420                 425                 430

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
        435                 440                 445

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
    450                 455                 460

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
465                 470                 475                 480

Gly Gly Gly Thr Lys Val Glu Ile Lys
                485
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<210> 13

<211> 1473
<212> DNA
<213> artificial sequence

<220>
<223> CEA III VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 13
caggttaagc tgcagcagtc tggggcagag cttgtgagat cagggacatc agtcaagttg 60

tcctgcacag cttctggctt caacattaaa gactcctata tgcactggct gaggcagggg 120

cctgaacagg gcctggagtg gattcgatgg attgatcctg agaatggtga tactgaatat 180

gccccgaagt tccagggcaa ggccactttc actactgaca catcctccaa cacagcctac 240

ctgcagctca gcagcctgac atctgaggac actgccgtct attactgtaa cgagggcaca 300

cctacagggc cttactactt tgactactgg ggccaaggca ccactgtcac agtctcctcc 360

ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagaa cgttctcacc 420

cagtctccag caatcatgtc tgcatctcca ggggagaagg tcaccatcac ctgcagtgcc 480

agctcaagcg tcagctacat gcactggttc cagcagaagc caggcacctc ccccaaactc 540

tggatttatt ctacatccaa cctggcttct ggagtccctg ctcgcttctc tggcagtggg 600

tctgggacct cttactctct cacaatcagc agaatggagg ctgaagatgc tgccacttat 660

tactgccagc agagaagtag ttacccactc acgttcggtg ctgggaccaa gctcgagctg 720

aaatccggag gtggtggatc cgacgtccaa ctggtgcagt caggggctga agtgaaaaaa 780

cctggggcct cagtgaaggt gtcctgcaag gcttctggct acacctttac taggtacacg 840

atgcactggg taaggcaggc acctggacag ggtctggaat ggattggata cattaatcct 900

agccgtggtt atactaatta cgcagacagc gtcaagggcc gcttcacaat cactacagac 960

aaatccacca gcacagccta catggaactg agcagcctgc gttctgagga cactgcaacc 1020

tattactgtg caagatatta tgatgatcat tactgccttg actactgggg ccaaggcacc 1080

acggtcaccg tctcctcagg cgaaggtact agtactggtt ctggtggaag tggaggttca 1140

ggtggagcag acgacattgt actgacccag tctccagcaa ctctgtctct gtctccaggg 1200

gagcgtgcca ccctgagctg cagagccagt caaagtgtaa gttacatgaa ctggtaccag 1260

cagaagccgg gcaaggcacc caaaagatgg atttatgaca catccaaagt ggcttctgga 1320

gtccctgctc gcttcagtgg cagtgggtct gggaccgact actctctcac aatcaacagc 1380

ttggaggctg aagatgctgc cacttattac tgccaacagt ggagtagtaa cccgctcacg 1440

ttcggtggcg ggaccaaggt ggagatcaaa tag 1473

<210> 14
<211> 490
<212> PRT
<213> artificial sequence

<220>
<223> CEA III VHVL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 14

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

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

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

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

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

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

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr

```
        195                 200                 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225                 230                 235                 240

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

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

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
        275                 280                 285

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
    290                 295                 300

Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr 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 Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys
            340                 345                 350

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

Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp
    370                 375                 380

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
385                 390                 395                 400

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
                405                 410                 415

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
            420                 425                 430

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
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435 440 445

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
450 455 460

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
465 470 475 480

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 15
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> CEA I VH-A240VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 15
gaggtgcagc tggtcgagtc aggaggaggc ttggtacagc ctgggggttc tctgagactc 60

tcctgtgcaa cttctgggtt caccttcact gattactaca tgaactgggt ccgccagcct 120

ccaggaaagg cacttgagtg gttgggtttt attggaaaca aagctaatgg ttacacaaca 180

gagtacagtg catctgtgaa gggtcggttc accatctcca gagataaatc ccaaagcatc 240

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtaccaga 300

gatagggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tcaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctca ggccgtgctg 420

actcagccgg cttccctctc tgcatctcct ggagcatcag ccagtctcac ctgcaccttg 480

cgcaggggca tcaatgttgg tgcctacagt atatactggt accagcagaa gccagggagt 540

cctccccagt atctcctgag gtacaaatca gactcagata agcagcaggg ctctggagtc 600

tccagccgct tctctgcatc caaagatgct tcggccaatg cagggatttt actcatctct 660

gggctccagt ctgaggatga ggctgactat tactgtatga tttggcacag cggcgcttct 720

gcggtgttcg gcggagggac caagttgacc gtcctaggcg gaggtggtgg atccgacgtc 780

caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 840

aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 900

cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac 960

agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1020

ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1080

cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc aggcgaaggt 1140

actagtactg gttctggtgg aagtggaggt tcaggtggag cagacgacat tgtactgacc 1200

cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 1260

agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 1320

tggatttatg acacatccaa agtggcttct ggagtccctg ctcgcttcag tggcagtggg 1380

tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1440

tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1500

aaatag 1506

<210> 16
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> CEA I VH-A240VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 16

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 Thr Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

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        115                 120                 125

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

Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220

Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

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

Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
            260                 265                 270

Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
        275                 280                 285

Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
    290                 295                 300

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp
305                 310                 315                 320

Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr
                325                 330                 335

Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr
            340                 345                 350

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
```

```
        355                 360                 365

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly
    370                 375                 380

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr
385                 390                 395                 400

Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
                405                 410                 415

Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
            420                 425                 430

Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
        435                 440                 445

Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    450                 455                 460

Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr
465                 470                 475                 480

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr
                485                 490                 495

Lys Val Glu Ile Lys
            500
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<210> 17
<211> 1503
<212> DNA
<213> artificial sequence

<220>
<223> A240VL - CEA I VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 17

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caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc     60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag    120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag    180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt    240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac    300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt    360
```

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtcaggagga 420

ggcttggtac agcctggggg ttctctgaga ctctcctgtg caacttctgg gttcaccttc 480

actgattact acatgaactg ggtccgccag cctccaggaa aggcacttga gtggttgggt 540

tttattggaa acaaagctaa tggttacaca acagagtaca gtgcatctgt gaagggtcgg 600

ttcaccatct ccagagataa atcccaaagc atcctctatc ttcaaatgaa caccctgaga 660

gctgaggaca gtgccactta ttactgtacc agagataggg ggctacggtt ctactttgac 720

tactggggcc aagggaccac ggtcaccgtc tcctccggag gtggtggatc cgacgtccaa 780

ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 840

gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 900

ggtctggaat ggattggata cattaatcct agccgtggtt atactaatta cgcagacagc 960

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tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 1260

caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1320

atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 1380

gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1440

tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1500

tag 1503

<210> 18
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> A240VL - CEA I VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 18

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

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

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

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

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

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

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

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

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
145                 150                 155                 160

Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu
                165                 170                 175

Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu
            180                 185                 190

Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser
        195                 200                 205

Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser
    210                 215                 220

Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp
225                 230                 235                 240

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
                245                 250                 255

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
            260                 265                 270
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Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
        275                 280                 285

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
    290                 295                 300

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
305                 310                 315                 320

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
                325                 330                 335

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
            340                 345                 350

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
        355                 360                 365

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
    370                 375                 380

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
385                 390                 395                 400

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
                405                 410                 415

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
            420                 425                 430

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
        435                 440                 445

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
    450                 455                 460

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
465                 470                 475                 480

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
                485                 490                 495

Val Glu Ile Lys
            500
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<210> 19
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VH - A240 VL ; Bispecific single chain antibody

<400> 19
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtcagg aggaggcttg 780

gtacagcctg ggggttctct gagactctcc tgtgcaactt ctgggttcac cttcactgat 840

tactacatga actgggtccg ccagcctcca ggaaaggcac ttgagtggtt gggttttatt 900

ggaaacaaag ctaatggtta cacaacagag tacagtgcat ctgtgaaggg tcggttcacc 960

atctccagag ataaatccca aagcatcctc tatcttcaaa tgaacaccct gagagctgag 1020

gacagtgcca cttattactg taccagagat agggggctac ggttctactt tgactactgg 1080

ggccaaggga ccacggtcac cgtctcctca ggtggtggtg gttctggcgg cggcggctcc 1140

ggtggtggtg gttctgagct cgtgctgact cagccggctt ccctctctgc atctcctgga 1200

gcatcagcca gtctcacctg caccttgcgc aggggcatca atgttggtgc ctacagtata 1260

tactggtacc agcagaagcc agggagtcct ccccagtatc tcctgaggta caaatcagac 1320

tcagataagc agcagggctc tggagtctcc agccgcttct ctgcatccaa agatgcttcg 1380

gccaatgcag ggattttact catctctggg ctccagtctg aggatgaggc tgactattac 1440

tgtatgattt ggcacagcgg cgcttctgcg gtgttcggcg gagggaccaa gttgaccgtc 1500

ctatag 1506

<210> 20
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x CEA I VH - A240 VL ; Bispecific single chain antibody

<400> 20

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

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

```
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr
305                 310                 315                 320

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

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

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
                405                 410                 415
```

```
Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
            420                 425                 430

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
        435                 440                 445

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
    450                 455                 460

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
465                 470                 475                 480

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
                485                 490                 495

Lys Leu Thr Val Leu

            500
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<210> 21
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - CEA I VH ; Bispecific single chain antibody

<400> 21

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gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg     60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca    120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac    180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac    240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat    300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc    360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta    420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc    480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc    540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc    600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc    660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg    720

gagatcaaat ccggaggtgg tggatcccag gccgtgctga ctcagccggc ttccctctct    780
```

gcatctcctg gagcatcagc cagtctcacc tgcaccttgc gcaggggcat caatgttggt 840

gcctacagta tatactggta ccagcagaag ccagggagtc ctccccagta tctcctgagg 900

tacaaatcag actcagataa gcagcagggc tctggagtct ccagccgctt ctctgcatcc 960

aaagatgctt cggccaatgc agggatttta ctcatctctg ggctccagtc tgaggatgag 1020

gctgactatt actgtatgat ttggcacagc ggcgcttctg cggtgttcgg cggagggacc 1080

aagttgaccg tcctaggtgg tggtggttct ggcggcggcg gctccggtgg tggtggttct 1140

gaggtgcagc tggtcgagtc aggaggaggc ttggtacagc ctgggggttc tctgagactc 1200

tcctgtgcaa cttctgggtt caccttcact gattactaca tgaactgggt ccgccagcct 1260

ccaggaaagg cacttgagtg gttgggtttt attggaaaca aagctaatgg ttacacaaca 1320

gagtacagtg catctgtgaa gggtcggttc accatctcca gagataaatc ccaaagcatc 1380

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtaccaga 1440

gatagggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 1500

tcctag 1506

<210> 22
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - CEA I VH ; Bispecific single chain antibody

<400> 22

Asp 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 Arg Tyr
20 25 30

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

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

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys

```
                85                  90                  95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro
                245                 250                 255

Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr
            260                 265                 270

Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln
        275                 280                 285

Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp
    290                 295                 300

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

Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln
```

325 330 335

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala
340 345 350

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
370 375 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
385 390 395 400

Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp
405 410 415

Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly
420 425 430

Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln
450 455 460

Met Asn Thr Leu Arg Ala Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg
465 470 475 480

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
485 490 495

Val Thr Val Ser Ser
500

<210> 23
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> A5 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 23
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctgagctcgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcaggga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tccggaggtg gtggatccga cgtccaactg 780

gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaaggtgtc ctgcaaggct 840

tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900

ctggaatgga ttggatacat taatcctagc cgtggttata ctaattacgc agacagcgtc 960

aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020

agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080

tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140

actggttctg gtggaagtgg aggttcaggt ggaggcagacg acattgtact gacccagtct 1200

ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380

accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaatag 1500

<210> 24
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> A5 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 24

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

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

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

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

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145                 150                 155                 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
            180                 185                 190

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
        195                 200                 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225                 230                 235                 240
```

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

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
            260                 265                 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
        275                 280                 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
    290                 295                 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
305                 310                 315                 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
                325                 330                 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
            340                 345                 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
        355                 360                 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
    370                 375                 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
    450                 455                 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465                 470                 475                 480
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Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 25
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> A240 VL - A5 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 25
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctgggggа 420

ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcctctgg attcaccctc 480

agtacctatg ccatgcactg ggtccgccag gctccaggca aggggctgga gtgggtggca 540

cttatatcaa atgatggaag caataaatac tatgcagact ccgtgaaggg ccgattcacc 600

atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 660

gacacggccg tgtattactg tgcgagagat agggggctac ggttctactt tgactactgg 720

ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacgt ccaactggtg 780

cagtcagggg ctgaagtgaa aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840

ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900

gaatggattg gatacattaa tcctagccgt ggttatacta attacgcaga cagcgtcaag 960

ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020

ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080

cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140

ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200

gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260

gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320

gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380

gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440

cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaatag 1497

<210> 26
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> A240 VL - A5 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 26

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

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

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

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

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

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

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

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

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu
145 150 155 160

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Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys Tyr Tyr Ala
            180                 185                 190

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        195                 200                 205

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    210                 215                 220

Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
            260                 265                 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
        275                 280                 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    290                 295                 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
                325                 330                 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
            340                 345                 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
    370                 375                 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385                 390                 395                 400
```

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 27
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - A5 VH ; Bispecific single chain antibody

<400> 27
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tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatcccag gccgtgctga ctcagccggc ttccctctct 780

gcatctcctg gagcatcagc cagtctcacc tgcaccttgc gcaggggcat caatgttggt 840

gcctacagta tactggtacc agcagaaag ccagggagtc ctccccagta tctcctgagg 900

tacaaatcag actcagataa gcagcagggc tctggagtct ccagccgctt ctctgcatcc 960

aaagatgctt cggccaatgc agggatttta ctcatctctg ggctccagtc tgaggatgag 1020

gctgactatt actgtatgat ttggcacagc ggcgcttctg cggtgttcgg cggagggacc 1080

aagttgaccg tcctaggtgg tggtggttct ggcggcggcg gctccggtgg tggtggttct 1140

gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 1200

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 1260

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 1320

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 1380

ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagatagg 1440

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcctag 1500

<210> 28
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - A5 VH ; Bispecific single chain antibody

<400> 28

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro

                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

                245                 250                 255

Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr
            260                 265                 270

Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln
        275                 280                 285

Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp
    290                 295                 300

Ser Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser
305                 310                 315                 320
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Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln
                325                 330                 335

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala
            340                 345                 350

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
385                 390                 395                 400

Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Thr Tyr Ala Met His Trp
                405                 410                 415

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Ser
            420                 425                 430

Asn Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
        435                 440                 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
    450                 455                 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg
465                 470                 475                 480

Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
                485                 490                 495

Val Ser Ser
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<210> 29
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A5 VH - A240 VL ; Bispecific single chain antibody

<400> 29

gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcgtg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcct ctggattcac cctcagtacc 840

tatgccatgc actgggtccg ccaggctcca ggcaaggggc tggagtgggt ggcacttata 900

tcaaatgatg gaagcaataa atactatgca gactccgtga agggccgatt caccatctcc 960

agagacaatt ccaagaacac gctgtatctg caaatgaaca gcctgagagc tgaggacacg 1020

gccgtgtatt actgtgcgag agataggggg ctacggttct actttgacta ctggggccaa 1080

gggaccacgg tcaccgtctc ctcaggtggt ggtggttctg gcggcggcgg ctccggtggt 1140

ggtggttctg agctcgtgct gactcagccg gcttccctct ctgcatctcc tggagcatca 1200

gccagtctca cctgcacctt gcgcaggggc atcaatgttg gtgcctacag tatatactgg 1260

taccagcaga agccagggag tcctccccag tatctcctga ggtacaaatc agactcagat 1320

aagcagcagg gctctggagt ctccagccgc ttctctgcat ccaaagatgc ttcggccaat 1380

gcagggattt tactcatctc tgggctccag tctgaggatg aggctgacta ttactgtatg 1440

atttggcaca gcggcgcttc tgcggtgttc ggcggaggga ccaagttgac cgtcctatag 1500

<210> 30
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A5 VH - A240 VL ; Bispecific single chain antibody

<400> 30

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Asp 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 Arg Tyr
            20                  25                  30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
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```
Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
                245                 250                 255

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    370                 375                 380

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

Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr
                405                 410                 415

Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu
            420                 425                 430

Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val Ser
        435                 440                 445

Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu
    450                 455                 460

Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met
465                 470                 475                 480
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Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys Leu
485 490 495

Thr Val Leu

<210> 31
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> B9 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 31
gaggtgcagc tggtcgagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccgtcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caagaacacg 240

ctgtatcttc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcaaga 300

gatagggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tcaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga gctcgtgctg 420

actcagccgg cttccctctc tgcatctcct ggagcatcag ccagtctcac ctgcaccttg 480

cgcaggggca tcaatgttgg tgcctacagt atatactggt accagcagaa gccagggagt 540

cctccccagt atctcctgag gtacaaatca gactcagata agcagcaggg ctctggagtc 600

tccagccgct tctctgcatc caaagatgct tcggccaatg cagggatttt actcatctct 660

gggctccagt ctgaggatga ggctgactat tactgtatga tttggcacag cggcgcttct 720

gcggtgttcg gcggagggac caagttgacc gtcctatccg gaggtggtgg atccgacgtc 780

caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 840

aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 900

cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac 960

agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1020

ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1080

cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc aggcgaaggt 1140

actagtactg gttctggtgg aagtggaggt tcaggtggag cagacgacat tgtactgacc 1200

cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 1260

agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 1320

tggatttatg acacatccaa agtggcttct ggagtccctg ctcgcttcag tggcagtggg 1380

tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1440

tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1500

aaatag 1506

<210> 32
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> B9 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 32

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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

```
Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220

Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

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

Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
            260                 265                 270

Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
        275                 280                 285

Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
    290                 295                 300

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp
305                 310                 315                 320

Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr
                325                 330                 335

Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr
            340                 345                 350

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
        355                 360                 365

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly
    370                 375                 380
```

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr
385 390 395 400

Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
405 410 415

Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
420 425 430

Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
435 440 445

Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
450 455 460

Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr
465 470 475 480

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr
485 490 495

Lys Val Glu Ile Lys
500

<210> 33
<211> 1503
<212> DNA
<213> artificial sequence

<220>
<223> A240 VL - B9 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 33
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctggggga 420

ggcttggtcc agcctgggag gtccctgaga ctctcctgtg cagcgtctgg attcaccgtc 480

agtagctact ggatgcactg ggtccgccaa gctccaggga aggggctgga atgggtaggt 540

ttcattagaa acaaagctaa tggtgggaca acagaatacg ccgcgtctgt gaaaggcaga 600

ttcaccatct caagagatga ttccaagaac acgctgtatc ttcaaatgaa cagcctgaga 660

gccgaggaca cggccgtgta ttactgtgca agagatagcg ggctacggtt ctactttgac 720

tactggggcc aagggaccac ggtcaccgtc tcctccggag gtggtggatc cgacgtccaa 780

ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 840

gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 900

ggtctggaat ggattggata cattaatcct agccgtggtt atactaatta cgcagacagc 960

gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1020

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tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 1260

caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1320

atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 1380

gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1440

tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1500

tag 1503

<210> 34
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> A240 VL - B9 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 34

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

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

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

Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val

```
    50                  55                  60

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

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

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

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

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

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

Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu
            180                 185                 190

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
        195                 200                 205

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
    210                 215                 220

Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp
225                 230                 235                 240

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
                245                 250                 255

Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
            260                 265                 270

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
        275                 280                 285

Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
```

290 295 300

Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser
305 310 315 320

Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala
325 330 335

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr
340 345 350

Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln
355 360 365

Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln
385 390 395 400

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
405 410 415

Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
420 425 430

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala
435 440 445

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
450 455 460

Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
465 470 475 480

Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
485 490 495

Val Glu Ile Lys
500

<210> 35
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x B9 VH-A240 VL ; Bispecific single chain antibody

<400> 35
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tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcttg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcgt ctggattcac cgtcagtagc 840

tactggatgc actgggtccg ccaagctcca gggaaggggc tggaatgggt aggtttcatt 900

agaaacaaag ctaatggtgg gacaacagaa tacgccgcgt ctgtgaaagg cagattcacc 960

atctcaagag atgattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 1020

gacacggccg tgtattactg tgcaagagat aggggggctac ggttctactt tgactactgg 1080

ggccaaggga ccacggtcac cgtctcctca ggtggtggtg gttctggcgg cggcggctcc 1140

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gcatcagcca gtctcacctg caccttgcgc aggggcatca atgttggtgc ctacagtata 1260

tactggtacc agcagaagcc agggagtcct ccccagtatc tcctgaggta caaatcagac 1320

tcagataagc agcagggctc tggagtctcc agccgcttct ctgcatccaa agatgcttcg 1380

gccaatgcag ggattttact catctctggg ctccagtctg aggatgaggc tgactattac 1440

tgtatgattt ggcacagcgg cgcttctgcg gtgttcggcg gagggaccaa gttgaccgtc 1500

ctatag 1506

<210> 36
<211> 501

<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x B9 VH - A240 VL ; Bispecific single chain antibody

<400> 36

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Asp 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 Arg Tyr
            20                  25                  30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205
```

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Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr
305                 310                 315                 320

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

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

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
                405                 410                 415

Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
            420                 425                 430

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
        435                 440                 445
```

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
450 455 460

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
465 470 475 480

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 37
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - B9 VH ; Bispecific single chain antibody

<400> 37
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tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga ttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatcccag gccgtgctga ctcagccggc ttccctctct 780

gcatctcctg gagcatcagc cagtctcacc tgcaccttgc gcaggggcat caatgttggt 840

gcctacagta tatactggta ccagcagaag ccagggagtc ctccccagta tctcctgagg 900

tacaaatcag actcagataa gcagcagggc tctggagtct ccagccgctt ctctgcatcc 960

aaagatgctt cggccaatgc agggatttta ctcatctctg ggctccagtc tgaggatgag 1020

gctgactatt actgtatgat ttggcacagc ggcgcttctg cggtgttcgg cggagggacc 1080

aagttgaccg tcctaggtgg tggtggttct ggcggcggcg gctccggtgg tggtggttct 1140

gaggtgcagc tggtcgagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc 1200

tcctgtgcag cgtctggatt caccgtcagt agctactgga tgcactgggt ccgccaagct 1260

ccagggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca 1320

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caagaacacg 1380

ctgtatcttc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcaaga 1440

gataggggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 1500

tcctag 1506

<210> 38
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - B9 VH ; Bispecific single chain antibody

<400> 38

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

```
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro
                245                 250                 255

Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr
            260                 265                 270

Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln
        275                 280                 285

Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp
    290                 295                 300

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

Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln
                325                 330                 335

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala
            340                 345                 350
```

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
370 375 380

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu
385 390 395 400

Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Tyr Trp Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Phe Ile Arg
420 425 430

Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
465 470 475 480

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
485 490 495

Val Thr Val Ser Ser
500

<210> 39
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> D8 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 39
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtac tagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctgagctcgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcagcga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tccggaggtg gtggatccga cgtccaactg 780

gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaaggtgtc ctgcaaggct 840

tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900

ctggaatgga ttggatacat taatcctagc cgtggttata ctaattacgc agacagcgtc 960

aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020

agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080

tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140

actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gacccagtct 1200

ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380

accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaatag 1500

<210> 40
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> D8 VH - A240 VL x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 40

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

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

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

Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys 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

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

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145                 150                 155                 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
            180                 185                 190

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
        195                 200                 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225                 230                 235                 240

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

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
            260                 265                 270
```

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
        275                 280                 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
    290                 295                 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
305                 310                 315                 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
                325                 330                 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
            340                 345                 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
        355                 360                 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
    370                 375                 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
    450                 455                 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys
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<210> 41
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> A240 VL - D8 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 41
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acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctgggggа 420

ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcctctgg attcaccctc 480

agtacctatg ccatgcactg ggtccgccag gctccaggca aggggctgga gtgggtggca 540

cttatatcaa atgatggaag caataaatac tatgcagact ccgtgaaggg ccgattcacc 600

atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 660

gacacggctg tgtattactg tactagagat agggggctac ggttctactt tgactactgg 720

ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacgt ccaactggtg 780

cagtcagggg ctgaagtgaa aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840

ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900

gaatggattg gatacattaa tcctagccgt ggttatacta attacgcaga cagcgtcaag 960

ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020

ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080

cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140

ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200

gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260

gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320

gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380

gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440

cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaatag 1497

<210> 42
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> A240 VL -D8 VH x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 42

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

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

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

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

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

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

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

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

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu
145 150 155 160

Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

Glu Trp Val Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys Tyr Tyr Ala
180 185 190

```
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        195                 200                 205

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    210                 215                 220

Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
            260                 265                 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
        275                 280                 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    290                 295                 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
305                 310                 315                 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
                325                 330                 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
            340                 345                 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
    370                 375                 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385                 390                 395                 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
                405                 410                 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
            420                 425                 430
```

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 43
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x D8 VH - A240 VL ; Bispecific single chain antibody

<400> 43
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact agctacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcgtg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcct ctggattcac cctcagtacc 840

tatgccatgc actgggtccg ccaggctcca ggcaaggggc tggagtgggt ggcacttata 900

tcaaatgatg gaagcaataa atactatgca gactccgtga agggccgatt caccatctcc 960

agagacaatt ccaagaacac gctgtatctg caaatgaaca gcctgagagc tgaggacacg 1020

gctgtgtatt actgtactag agatagggggg ctacggttct actttgacta ctggggccaa 1080

gggaccacgg tcaccgtctc ctcaggtggt ggtggttctg gcggcggcgg ctccggtggt 1140

ggtggttctg agctcgtgct gactcagccg gcttccctct ctgcatctcc tggagcatca 1200

gccagtctca cctgcacctt gcgcaggggc atcaatgttg gtgcctacag tatatactgg 1260

taccagcaga agccagggag tcctccccag tatctcctga ggtacaaatc agactcagat 1320

aagcagcagg gctctggagt ctccagccgc ttctctgcat ccaaagatgc ttcggccaat 1380

gcagggattt tactcatctc tgggctccag tctgaggatg aggctgacta ttactgtatg 1440

atttggcaca gcggcgcttc tgcggtgttc ggcggaggga ccaagttgac cgtcctatag 1500

<210> 44
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x D8 VH - A240 VL ; Bispecific single chain antibody

<400> 44

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

```
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    370                 375                 380

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

Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr
                405                 410                 415

Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu
            420                 425                 430

Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val Ser
        435                 440                 445

Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu
    450                 455                 460

Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met
465                 470                 475                 480

Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Thr Val Leu
```

<210> 45
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - D8 VH ; Bispecific single chain antibody

<400> 45

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gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg     60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca    120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac    180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac    240
```

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatcccag gccgtgctga ctcagccggc ttccctctct 780

gcatctcctg gagcatcagc cagtctcacc tgcaccttgc gcaggggcat caatgttggt 840

gcctacagta tatactggta ccagcagaag ccagggagtc ctccccagta tctcctgagg 900

tacaaatcag actcagataa gcagcagggc tctggagtct ccagccgctt ctctgcatcc 960

aaagatgctt cggccaatgc agggatttta ctcatctctg ggctccagtc tgaggatgag 1020

gctgactatt actgtatgat ttggcacagc ggcgcttctg cggtgttcgg cggagggacc 1080

aagttgaccg tcctaggtgg tggtggttct ggcggcggcg gctccggtgg tggtggttct 1140

gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 1200

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 1260

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 1320

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 1380

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtac tagagatagg 1440

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcctag 1500

<210> 46
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A240 VL - D8 VH ; Bispecific single chain antibody

<400> 46

Asp 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 Arg Tyr

```
            20                  25                  30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro
                245                 250                 255
```

```
Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr
            260                 265                 270

Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln
        275                 280                 285

Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp
    290                 295                 300

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

Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln
                325                 330                 335

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala
            340                 345                 350

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
    370                 375                 380

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
385                 390                 395                 400

Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Thr Tyr Ala Met His Trp
                405                 410                 415

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Ser
            420                 425                 430

Asn Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
        435                 440                 445

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
    450                 455                 460

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asp Arg
465                 470                 475                 480

Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
                485                 490                 495
```

Val Ser Ser

<210> 47
<211> 756
<212> DNA
<213> artificial sequence

<220>
<223> A5B7 VH - A240 VL ; Single chain Fv

<400> 47
gaggtgcagc tggtcgagtc aggaggaggc ttggtacagc ctgggggttc tctgagactc 60

tcctgtgcaa cttctgggtt caccttcact gattactaca tgaactgggt ccgccagcct 120

ccaggaaagg cacttgagtg gttgggtttt attggaaaca aagctaatgg ttacacaaca 180

gagtacagtg catctgtgaa gggtcggttc accatctcca gagataaatc ccaaagcatc 240

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtaccaga 300

gataggggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tcaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctca ggccgtgctg 420

actcagccgg cttccctctc tgcatctcct ggagcatcag ccagtctcac ctgcaccttg 480

cgcaggggca tcaatgttgg tgcctacagt atatactggt accagcagaa gccagggagt 540

cctccccagt atctcctgag gtacaaatca gactcagata agcagcaggg ctctggagtc 600

tccagccgct tctctgcatc caaagatgct tcggccaatg cagggatttt actcatctct 660

gggctccagt ctgaggatga ggctgactat tactgtatga tttggcacag cggcgcttct 720

gcggtgttcg gcggagggac caagttgacc gtccta 756

<210> 48
<211> 252
<212> PRT
<213> artificial sequence

<220>
<223> A5B7 VH - A240 VL ; Single chain Fv

<400> 48

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 Thr Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220

Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
```

<210> 49
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A5 VH - A240 VL ; Single chain Fv

<400> 49
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctcaggccgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcaggga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tag 753

<210> 50
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A5 VH - A240 VL ; Single chain Fv

<400> 50

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

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

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

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

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145                 150                 155                 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
            180                 185                 190

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
        195                 200                 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
```

<210> 51
<211> 759
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> B9 VH - A240 VL ; Single chain Fv

<400> 51

gaggtgcagc tggtcgagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccgtcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caagaacacg 240

ctgtatcttc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcaaga 300

gataggggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tcaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctca ggccgtgctg 420

actcagccgg cttccctctc tgcatctcct ggagcatcag ccagtctcac ctgcaccttg 480

cgcaggggca tcaatgttgg tgcctacagt atatactggt accagcagaa gccagggagt 540

cctccccagt atctcctgag gtacaaatca gactcagata agcagcaggg ctctggagtc 600

tccagccgct tctctgcatc caaagatgct tcggccaatg cagggatttt actcatctct 660

gggctccagt ctgaggatga ggctgactat tactgtatga tttggcacag cggcgcttct 720

gcggtgttcg gcggagggac caagttgacc gtcctatag 759

<210> 52
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> B9 VH - A240VL ; Single chain Fv

<400> 52

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

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

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

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

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

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

```
                85                  90                  95

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220

Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
```

<210> 53
<211> 753
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<223> D8 VH - A240VL ; Single chain Fv

<400> 53
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtac tagagatagg 300

gggctacggt tcgactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctcaggccgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcaggga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tag 753

<210> 54
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> D8 VH - A240VL ; Single chain Fv

<400> 54

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

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

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

Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys 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

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

```
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145                 150                 155                 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
            180                 185                 190

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
        195                 200                 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
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<210> 55
<211> 363
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> A5B7 VH ; VH region

<400> 55

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gaggtgcagc tggtcgagtc aggaggaggc ttggtacagc ctgggggttc tctgagactc     60

tcctgtgcaa cttctgggtt caccttcact gattactaca tgaactgggt ccgccagcct    120

ccaggaaagg cacttgagtg gttgggtttt attggaaaca aagctaatgg ttacacaaca    180

gagtacagtg catctgtgaa gggtcggttc accatctcca gagataaatc ccaaagcatc    240

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtaccaga    300

gataggggac tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc    360
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tca 363

<210> 56
<211> 121
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> A5B7 VH ; VH region

<400> 56

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 Thr Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 57
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A5 VH ; VH region

<400> 57
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctca 357

<210> 58
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A5 VH ; VH region

<400> 58

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

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

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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 59
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> B9 VH ; VH region

<400> 59
gaggtgcagc tggtcgagtc tgggggaggc ttggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccgtcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caagaacacg 240

ctgtatcttc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcaaga 300

gataggggggc tacggttcta ctttgactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 60
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> B9 VH ; VH region

<400> 60

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 61
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> D8 VH ; VH region

<400> 61
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtac tagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctca 357

<210> 62
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> D8 VH ; VH region

<400> 62

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

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

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

Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys 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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 63
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A240 VL ; VL region

<400> 63
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtccta 348

<210> 64
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A240VL ; VL region

<400> 64

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

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

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

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

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

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

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

Leu Thr Val Leu
115

<210> 65
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> CDR-H3* A5B7 Shorter CDR-3 of VH of A5B7 with D corresponding to Kabat position 95; Kabat positions 100, 100a, 100b, 101, 102 correspond to FYFDY, respectively

<220>
<221> MISC_FEATURE
<223> with "X1", "X2", "X3" and "X4" corresponding to Kabat positions 96 ("X1"), 97 ("X2"), 98 ("X3") and 99 ("X4"), respectively, of CDR-H3 of murine monoclonal antibody A5B7 and wherein "X" represents any amino acid residue. "X1" is preferably "R"

<220>
<221> misc_feature
<222> (2)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 65

Asp Xaa1 Xaa2 Xaa3 Xaa4 Phe Tyr Phe Asp Tyr
1 5 10

<210> 66
<211> 10
<212> PRT
<213> Mus musculus

<220>

<221> MISC_FEATURE
<223> CDR-H3 A5B7 CDR-3 of VH of A5B7 corresponding to Kabat positions 95, 96, 97, 98, 99, 100, 100a, 100b, 101, 102

<400> 66

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
1 5 10

<210> 67
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-H2 B9 ; CDR-2 of VH B9

<400> 67

Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser
1 5 10 15

Val Lys Gly

<210> 68
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-H1 B9 ; CDR1 of VH B9

<400> 68

Ser Tyr Trp Met His
1 5

<210> 69
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-H2 A5/D8 ; CDR-2 of VH A5/D8

<400> 69

Leu Ile Ser Asn Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 70
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-H1 A5/D8 ; CDR-1 of VH A5/D8

<400> 70

Thr Tyr Ala Met His
1 5

<210> 71
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-L3 A240 ; CDR-3 of VL A240

<400> 71

Met Ile Trp His Ser Gly Ala Ser Ala Val
1 5 10

<210> 72
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-L2 A240 ; CDR-2 of VL A240

<400> 72

Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser
1 5 10

<210> 73
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-L1 A240 ; CDR-1 of VL A240

<400> 73

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

<210> 74
<211> 32
<212> DNA
<213> artificial sequence

<220>
<223> 5' CEACAM5 EcoRI ; oligonucleotide

<400> 74
gaattcgcca ccatggagtc tccctcggcc cc 32

<210> 75
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> 3' CEACAM5 SalI ; oligonucleotide

<400> 75
gtcgacctat atcagagcaa cccc 24

<210> 76
<211> 702
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CEACAM5 (NM_004363) ; protein

<400> 76

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

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

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

```
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                  75                  80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            100                 105                 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
        115                 120                 125

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

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
        195                 200                 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210                 215                 220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
    290                 295                 300
```

```
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340                 345                 350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
        355                 360                 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                 390                 395                 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420                 425                 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435                 440                 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                 490                 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
            500                 505                 510

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                 520                 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530                 535                 540
```

```
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                 570                 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
            580                 585                 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        595                 600                 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
            660                 665                 670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
        675                 680                 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
    690                 695                 700
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<210> 77
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> De-immunized anti-CD3 VHVL single chain Fv as described in WO2005/040220

<400> 77

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Asp 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 Arg Tyr
            20                  25                  30
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```
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
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<210> 78
<211> 38
<212> DNA

<213> artificial sequence

<220>
<223> 5'-huVK1-SacI-2001 ; oligonucleotide

<400> 78
gagccgcacg agcccgagct ccagatgacc cagtctcc 38

<210> 79
<211> 38
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVK2/4-SacI-2001 ; oligonucleotide

<400> 79
gagccgcacg agcccgagct cgtgatgacy cagtctcc 38

<210> 80
<211> 38
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVK3-SacI-2001 ; oligonucleotide

<400> 80
gagccgcacg agcccgagct cgtgwtgacr cagtctcc 38

<210> 81
<211> 38
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVK5-SacI-2001 ; oligonucleotide

<400> 81
gagccgcacg agcccgagct cacactcacg cagtctcc 38

<210> 82
<211> 38
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> 5'-huVK6-SacI-2001 ; oligonucleotide

<400> 82
gagccgcacg agcccgagct cgtgctgact cagtctcc 38

<210> 83
<211> 47
<212> DNA

<213> artificial sequence

<220>
<223> 3'-hu-Vk-J1-SpeI-BsiWI ; oligonucleotide

<400> 83
gacgacacta gttgcagcca ccgtacgttt gatttccacc ttggtcc 47

<210> 84
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-Vk-J2/4-SpeI-Bsi/WI ; oligonucleotide

<400> 84
gacgacacta gttgcagcca ccgtacgttt gatctccasc ttggtcc 47

<210> 85
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-Vk-J3-SpeI-BsiWI ; oligonucleotide

<400> 85
gacgacacta gttgcagcca ccgtacgttt gatatccact ttggtcc 47

<210> 86
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-Vk-J5-SpeI-BsiWI ; oligonucleotide

<400> 86
gacgacacta gttgcagcca ccgtacgttt aatctccagt cgtgtcc 47

<210> 87
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL1a-SacI-2001 ; oligonucleotide

<400> 87
gagccgcacg agcccgagct cgtgttgacg cagccgccct c 41

<210> 88
<211> 41

<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL1b-SacI-2001 ; oligonucleotide

<400> 88
gagccgcacg agcccgagct cgtgctgact cagccaccct c 41

<210> 89
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL2-SacI-2001 ; oligonucleotide

<400> 89
gagccgcagg agcccgagct cgccctgact cagcctsccc ccgt 44

<210> 90
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL4-SacI-2001 ; oligonucleotide

<400> 90
acctgcgagc tcgtgctgac tcarycmycc tctgc 35

<210> 91
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL5-SacI-2001 ; oligonucleotide

<400> 91
acctgcgagc tcgtgctgac tcagccrsct tcc 33

<210> 92
<211> 32
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL6-SacI-2001 ; oligonucleotide

<400> 92
acctgcgagc tcatgctgac tcagccccac tc 32

<210> 93
<211> 41

<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL3/9-SacI-2001 ; oligonucleotide

<400> 93
gagccgcacg agcccgagct cgwgctgact cagccaccyt c 41

<210> 94
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVL7/8-SacI-2001 ; oligonucleotide

<400> 94
gagccgcacg agcccgagct cgtggtgacy caggagccmt c 41

<210> 95
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-VIam-BInI-SpeI-2001 ; oligonucleotide

<400> 95
cgtgggacta gtcttgggct gacctaggac ggt 33

<210> 96
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-V1am2-BInI-SpeI-2002 ; oligonucleotide

<400> 96
cgtgggacta gtcttgggct gaccgaggac ggt 33

<210> 97
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> 5'-primer 5'-AVH-XhoI ; oligonucleotide

<400> 97
gtcacactcg agtcaggagg aggcttggta c 31

<210> 98
<211> 31

<212> DNA
<213> artificial sequence

<220>
<223> 3'-primer 3'-AVH-BstEII ; oligonucleotide

<400> 98
gtcacaggtg accgtggtcc cttggcccca g 31

<210> 99
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> Flag tag

<400> 99

Thr Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 100
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVH1,3,5-XhoI-2001 ; oligonucleotide

<400> 100
aggtgcagct gctcgagtct gg 22

<210> 101
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVH4-XhoI-2001 ; oligonucleotide

<400> 101
caggtgcagc tgctcgagtc ggg 23

<210> 102
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> 5'-huVH4B-XhoI-2001 ; oligonucleotide

<400> 102
caggtgcagc tactcgagtg ggg 23

<210> 103
<211> 17
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-VH-BstEII-2001 ; oligonucleotide

<400> 103
ctgaggagac ggtgacc 17

<210> 104
<211> 17
<212> DNA
<213> artificial sequence

<220>
<223> 3'-hu-VH-J3-BstEII-2001 ; oligonucleotide

<400> 104
ctgaagagac ggtgacc 17

<210> 105
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 3'-A134-VH1A ; oligonucleotide

<400> 105
gtagtcaaag tagaaccgta gccccctatc tctygcacag taatacacgg c 51

<210> 106
<211> 51
<212> DNA
<213> artificial sequence

<220>

<223> 3'-A134-VH1B ; oligonucleotide

<400> 106
gtagtcaaag tagaaccgta gccccctatc tctygcacag taatacayrg c 51

<210> 107
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 3'-A134-VH3A ; oligonucleotide

<220>
<221> variation

<222> (34)..(34)
<223> /replace= "a"

/replace = "c"

/replace = "g"

<400> 107
gtagtcaaag tagaaccgta gccccctatc tcttgyacag taatacacrg c 51

<210> 108
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 3' -A134-VH3B ; oligonucleotide

<220>
<221> variation
<222> (34)..(34)
<223> /replace= "a"

/replace = "c"

/replace = "g"

<400> 108
gtagtcaaag tagaaccgta gccccctatc tcttgcacag taatacaarg c 51

<210> 109
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 3'-A134-VH4 ; oligonucleotide

<400> 109
gtagtcaaag tagaaccgta gccccctatc tctsgcacag taatacacrg c 51

<210> 110
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 3' A134-JH6-BstEII ; oligonucleotide

<400> 110
cgagacggtg accgtggtcc cttggcccca gtagtcaaag tagaaccgta gcc 53

<210> 111
<211> 207
<212> PRT

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD3 epsilon (NM_000733) ; protein

<400> 111

```
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

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> 112
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> CDR-H3 A5B7 Shorter CDR-3 of VH of A5B7 corresponding to Kabat positions 100, 100a, 100b, 101, 102

<400> 112

Phe Tyr Phe Asp Tyr
1 5

<210> 113
<211> 6
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> CDR-H3 A5B7 Shorter CDR-3 of VH of A5B7 corresponding to Kabat positions 99, 100, 100a, 100b, 101, 102

<400> 113

Arg Phe Tyr Phe Asp Tyr
1 5

<210> 114
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> CDR-H3 A5B7 Shorter CDR-3 of VH of A5B7 corresponding to Kabat positions 98, 99, 100, 100a, 100b, 101, 102

<400> 114

Leu Arg Phe Tyr Phe Asp Tyr
1 5

<210> 115
<211> 8
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE

<223> CDR-H3 A5B7 Shorter CDR-3 of VH of A5B7 corresponding to Kabat positions 97, 98, 99, 100, 100a, 100b, 101, 102

<400> 115

Gly Leu Arg Phe Tyr Phe Asp Tyr
1 5

<210> 116
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> DR-H3 A5B7 Shorter CDR-3 of VH of A5B7 corresponding to Kabat positions 96, 97, 98, 99, 100, 100a, 100b, 101, 102

<400> 116

Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
1 5

<210> 117
<211> 759
<212> DNA
<213> artificial sequence

<220>
<223> A240 VL -A5B7 VH ; single chain Fv

<400> 117
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtcaggagga 420

ggcttggtac agcctggggg ttctctgaga ctctcctgtg caacttctgg gttcaccttc 480

actgattact acatgaactg ggtccgccag cctccaggaa aggcacttga gtggttgggt 540

tttattggaa acaaagctaa tggttacaca acagagtaca gtgcatctgt gaagggtcgg 600

ttcaccatct ccagagataa atcccaaagc atcctctatc ttcaaatgaa caccctgaga 660

gctgaggaca gtgccactta ttactgtacc agagataggg ggctacggtt ctactttgac 720

tactggggcc aagggaccac ggtcaccgtc tcctcctga 759

<210> 118
<211> 252
<212> PRT
<213> artificial sequence

<220>
<223> A240 VL -A5B7 VH ; single chain Fv

<400> 118

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

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

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

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

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

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

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

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

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
145                 150                 155                 160

Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu
                165                 170                 175

Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu
            180                 185                 190
```

Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser
195 200 205

Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser
210 215 220

Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp
225 230 235 240

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
245 250

<210> 119
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A240VL -A5 VH ; single chain Fv

<400> 119
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctgggggg 420

ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcctctgg attcaccctc 480

agtacctatg ccatgcactg ggtccgccag gctccaggca aggggctgga gtgggtggca 540

cttatatcaa atgatggaag caataaatac tatgcagact ccgtgaaggg ccgattcacc 600

atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 660

gacacggccg tgtattactg tgcgagagat aggggggctac ggttctactt tgactactgg 720

ggccaaggga ccacggtcac cgtctcctcc tga 753

<210> 120
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A240VL -A5 VH ; single chain Fv

<400> 120

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

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

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

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

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

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

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

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

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu
145                 150                 155                 160

Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys Tyr Tyr Ala
            180                 185                 190

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        195                 200                 205

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    210                 215                 220
```

```
Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
                245                 250
```

<210> 121
<211> 759
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A240VL- B9 VH ; single chain Fv

<400> 121

```
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc     60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag    120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag    180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt    240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac    300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt    360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctgggggg    420

ggcttggtcc agcctgggag gtccctgaga ctctcctgtg cagcgtctgg attcaccgtc    480

agtagctact ggatgcactg ggtccgccaa gctccaggga aggggctgga atgggtaggt    540

ttcattagaa acaaagctaa tggtgggaca acagaatacg ccgcgtctgt gaaaggcaga    600

ttcaccatct caagagatga ttccaagaac acgctgtatc ttcaaatgaa cagcctgaga    660

gccgaggaca cggccgtgta ttactgtgca agagataggg ggctacggtt ctactttgac    720

tactggggcc aagggaccac ggtcaccgtc tcctcctga                           759
```

<210> 122
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A240VL- B9 VH ; single chain Fv

<400> 122

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

Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala

            20                  25                  30

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

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

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

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

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

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

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

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

Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu
            180                 185                 190

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
        195                 200                 205

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
    210                 215                 220

Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp
225                 230                 235                 240
```

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
245 250

<210> 123
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A240VL -D8 VH ; single chain Fv

<400> 123
caggccgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60

acctgcacct tgcgcagggg catcaatgtt ggtgcctaca gtatatactg gtaccagcag 120

aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga taagcagcag 180

ggctctggag tctccagccg cttctctgca tccaaagatg cttcggccaa tgcagggatt 240

ttactcatct ctgggctcca gtctgaggat gaggctgact attactgtat gatttggcac 300

agcggcgctt ctgcggtgtt cggcggaggg accaagttga ccgtcctagg tggtggtggt 360

tctggcggcg gcggctccgg tggtggtggt tctgaggtgc agctggtcga gtctgggggа 420

ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcctctgg attcaccctc 480

agtacctatg ccatgcactg ggtccgccag gctccaggca aggggctgga gtgggtggca 540

cttatatcaa atgatggaag caataaatac tatgcagact ccgtgaaggg ccgattcacc 600

atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 660

gacacggctg tgtattactg tactagagat agggggctac ggttctactt tgactactgg 720

ggccaaggga ccacggtcac cgtctcctcc tga 753

<210> 124
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> A240VL -D8 VH ; single chain Fv

<400> 124

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

Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala

```
            20                  25                  30

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

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

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

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

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

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

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu
145                 150                 155                 160

Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Val Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys Tyr Tyr Ala
            180                 185                 190

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
        195                 200                 205

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    210                 215                 220

Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
                245                 250
```

<210> 125
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> A5 VH - A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 125
gaggtgcagc tggtcgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctcaggccgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcaggga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tccggaggtg gtggatccga cgtccaactg 780

gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaaggtgtc ctgcaaggct 840

tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900

ctggaatgga ttggatacat taatcctagc cgtggttata ctaattacgc agacagcgtc 960

aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020

agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080

tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140

actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gacccagtct 1200

ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380

accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaatag 1500

<210> 126
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> A5 VH - A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 126

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

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

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

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

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145 150 155 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
180 185 190

```
Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
        195                 200                 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225                 230                 235                 240

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

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
            260                 265                 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
        275                 280                 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
    290                 295                 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
305                 310                 315                 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
                325                 330                 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
            340                 345                 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
        355                 360                 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
    370                 375                 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430
```

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 127
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A5 VH - A240 VL# ; Bispecific single chain antibody

<400> 127
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aagccaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcgtg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcct ctggattcac cctcagtacc 840

tatgccatgc actgggtccg ccaggctcca ggcaaggggc tggagtgggt ggcacttata 900

tcaaatgatg gaagcaataa atactatgca gactccgtga agggccgatt caccatctcc 960

agagacaatt ccaagaacac gctgtatctg caaatgaaca gcctgagagc tgaggacacg 1020

gccgtgtatt actgtgcgag agataggggg ctacggttct actttgacta ctggggccaa 1080

gggaccacgg tcaccgtctc ctcaggtggt ggtggttctg gcggcggcgg ctccggtggt 1140

ggtggttctc aggccgtgct gactcagccg gcttccctct ctgcatctcc tggagcatca 1200

gccagtctca cctgcacctt gcgcaggggc atcaatgttg gtgcctacag tatatactgg 1260

taccagcaga agccagggag tcctccccag tatctcctga ggtacaaatc agactcagat 1320

aagcagcagg gctctggagt ctccagccgc ttctctgcat ccaaagatgc ttcggccaat 1380

gcagggattt tactcatctc tgggctccag tctgaggatg aggctgacta ttactgtatg 1440

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<210> 128
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x A5 VH - A240 VL# ; Bispecific single chain antibody

<400> 128

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

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Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    370                 375                 380

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

Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr
                405                 410                 415

Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu
            420                 425                 430

Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val Ser
        435                 440                 445

Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu
    450                 455                 460

Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met
465                 470                 475                 480

Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Thr Val Leu
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<210> 129
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> B9 VH -A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 129

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tcctgtgcag cgtctggatt caccgtcagt agctactgga tgcactgggt ccgccaagct    120

ccagggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca    180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caagaacacg    240
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ctgtatcttc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcaaga 300

gataggggge tacggttcta ctttgactac tggggccaag gaccacggt caccgtctcc 360

tcaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctca ggccgtgctg 420

actcagccgg cttccctctc tgcatctcct ggagcatcag ccagtctcac ctgcaccttg 480

cgcaggggca tcaatgttgg tgcctacagt atatactcgt accagcagaa gccagggagt 540

cctccccagt atctcctgag gtacaaatca gactcagata agcagcaggg ctctggagtc 600

tccagccgct tctctgcatc caaagatgct tcggccaatg cagggatttt actcatctct 660

gggctccagt ctgaggatga ggctgactat tactgtatga tttggcacag cggcgcttct 720

gcggtgttcg gcggagggac caagttgacc gtcctatccg gaggtggtgg atccgacgtc 780

caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 840

aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 900

cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac 960

agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1020

ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1080

cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc aggcgaaggt 1140

actagtactg gttctggtgg aagtggaggt tcaggtggag cagacgacat tgtactgacc 1200

cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 1260

agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 1320

tggatttatg acacatccaa agtggcttct ggagtccctg ctcgcttcag tggcagtggg 1380

tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1440

tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1500

aaatag 1506

<210> 130
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> B9 VH -A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 130

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220

Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Gly
                245                 250                 255
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Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
            260                 265                 270

Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
        275                 280                 285

Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
    290                 295                 300

Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp
305                 310                 315                 320

Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr
                325                 330                 335

Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr
            340                 345                 350

Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly
        355                 360                 365

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly
    370                 375                 380

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr
385                 390                 395                 400

Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
                405                 410                 415

Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
            420                 425                 430

Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val
        435                 440                 445

Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    450                 455                 460

Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr
465                 470                 475                 480

Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr
                485                 490                 495
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Lys Val Glu Ile Lys
500

<210> 131
<211> 1506
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x B9 VH - A240 VL# ; Bispecific single chain antibody

<400> 131
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcttg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcgt ctggattcac cgtcagtagc 840

tactggatgc actgggtccg ccaagctcca gggaaggggc tggaatgggt aggtttcatt 900

agaaacaaag ctaatggtgg gacaacagaa tacgccgcgt ctgtgaaagg cagattcacc 960

atctcaagag atgattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 1020

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tcagataagc agcagggctc tggagtctcc agccgcttct ctgcatccaa agatgcttcg 1380

gccaatgcag ggattttact catctctggg ctccagtctg aggatgaggc tgactattac 1440

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ctatag 1506

<210> 132
<211> 501
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x B9 VH - A240 VL# ; Bispecific single chain antibody

<400> 132

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro

```
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr
305                 310                 315                 320

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380

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

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
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405 410 415

Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
420 425 430

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
435 440 445

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
450 455 460

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
465 470 475 480

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 133
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> D8 VH - A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 133
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tcctgtgcag cctctggatt caccctcagt acctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcactt atatcaaatg atggaagcaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtac tagagatagg 300

gggctacggt tctactttga ctactggggc caagggacca cggtcaccgt ctcctcaggt 360

ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctcaggccgt gctgactcag 420

ccggcttccc tctctgcatc tcctggagca tcagccagtc tcacctgcac cttgcgcagg 480

ggcatcaatg ttggtgccta cagtatatac tggtaccagc agaagccagg gagtcctccc 540

cagtatctcc tgaggtacaa atcagactca gataagcagc agggctctgg agtctccagc 600

cgcttctctg catccaaaga tgcttcggcc aatgcaggga ttttactcat ctctgggctc 660

cagtctgagg atgaggctga ctattactgt atgatttggc acagcggcgc ttctgcggtg 720

ttcggcggag ggaccaagtt gaccgtccta tccggaggtg gtggatccga cgtccaactg 780

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ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380

accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaatag 1500

<210> 134
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> D8 VH - A240 VL# x SEQ ID NO: 77 VHVL ; Bispecific single chain antibody

<400> 134

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

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

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

Ala Leu Ile Ser Asn Asp Gly Ser Asn Lys 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

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

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
145 150 155 160

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
180 185 190

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
195 200 205

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
210 215 220

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
225 230 235 240

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

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
305 310 315 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr

```
                325                 330                 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
            340                 345                 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
        355                 360                 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
    370                 375                 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
    450                 455                 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys
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<210> 135
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x D8 VH - A240 VL# ; Bispecific single chain antibody

<400> 135
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cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcgtg 780

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tcaaatgatg gaagcaataa atactatgca gactccgtga agggccgatt caccatctcc 960

agagacaatt ccaagaacac gctgtatctg caaatgaaca gcctgagagc tgaggacacg 1020

gctgtgtatt actgtactag agataggggg ctacggttct actttgacta ctggggccaa 1080

gggaccacgg tcaccgtctc ctcaggtggt ggtggttctg gcggcggcgg ctccggtggt 1140

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aagcagcagg gctctggagt ctccagccgc ttctctgcat ccaaagatgc ttcggccaat 1380

gcagggattt tactcatctc tgggctccag tctgaggatg aggctgacta ttactgtatg 1440

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<210> 136
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> SEQ ID NO: 77 VHVL x D8 VH - A240 VL# ; Bispecific single chain antibody

<400> 136

Asp 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 Arg Tyr
            20                  25                  30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
        115                 120                 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
```

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                245                 250                 255

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    370                 375                 380

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

Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr
                405                 410                 415

Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu
            420                 425                 430

Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val Ser
        435                 440                 445

Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu
    450                 455                 460

Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met
465                 470                 475                 480
```

Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys Leu
485 490 495

Thr Val Leu

<210> 137
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> 5'CEAI LH ; oligonucleotide

<400> 137
aggtgtacac tccgacattg agctcaccca g 31

<210> 138
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 3'CEAI VL Linker ; oligonucleotide

<400> 138
ggagccgccg ccgccagaac caccaccacc tttgatctcg agcttgg 47

<210> 139
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> 5'CEAI VH Linker ; oligonucleotide

<400> 139
ggcggcggcg gctccggtgg tggtggttct caggtccaac tgcaggag 48

<210> 140
<211> 22
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> 3'CEAI LH ; oligonucleotide

<400> 140
aatccggagg agacggtgac cg 22

<210> 141
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> De-immunized polypeptide linker

<400> 141

Gly Glu Gly Thr Ser Thr Gly Ser Gly Ser Gly Gly Ala Asp
1 5 10

<210> 142
<211> 1524
<212> DNA
<213> artificial sequence

<220>
<223> SEQ ID NO:77 VHVL x E12 VH - A240 VL ; Bispecific single chain antibody

<400> 142
gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtacta gtactggttc tggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720

gagatcaaat ccggaggtgg tggatccgag gtgcagctgg tcgagtctgg gggaggcttg 780

gtccagcctg ggaggtccct gagactctcc tgtgcagcgt ctggattcac cgtcagtagc 840

tactggatgt actgggtccg ccaagctcca gggaaggggc tggaatgggt aggtttcatt 900

ctcaacaaag ctaatggtgg aacaacagaa tacgccgcgt ctgtgaaagg cagattcacc 960

atctcaagag atgattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 1020

gacacggccg tgtattactg tgcaagagat aggggggctac ggttctactt tgactactgg 1080

ggccaaggga ccacggtcac cgtctcctca ggtggtggtg gttctggcgg cggcggctcc 1140

ggtggtggtg gttctgagct cgtgctgact cagccggctt ccctctctgc atctcctgga 1200

gcatcagcca gtctcacctg caccttgcgc aggggcatca atgttggtgc ctacagtata 1260

tactggtacc agcagaagcc agggagtcct ccccagtatc tcctgaggta caaatcagac 1320

tcagataagc agcagggctc tggagtctcc agccgcttct ctgcatccaa agatgcttcg 1380

gccaatgcag ggattttact catctctggg ctccagtctg aggatgaggc tgactattac 1440

tgtatgattt ggcacagcgg cgcttctgcg gtgttcggcg gagggaccaa gttgaccgtc 1500

ctacatcatc accatcatca ttag 1524

<210> 143
<211> 507
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> SEQ ID NO: 77 VHVL x E12 VH - A240 VL ; Bispecific single chain antibody

<400> 143

Asp 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 Arg Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

```
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
        195                 200                 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

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

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

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

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

Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr
305                 310                 315                 320

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

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

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

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    370                 375                 380
```

```
Ser Glu Leu Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly
385                 390                 395                 400

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
                405                 410                 415

Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
            420                 425                 430

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
        435                 440                 445

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
    450                 455                 460

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
465                 470                 475                 480

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
                485                 490                 495

Lys Leu Thr Val Leu His His His His His His
            500                 505
```

<210> 144
<211> 5
<212> PRT
<213> HOMO SAPIENS

<220>
<221> MISC_FEATURE
<223> CDR-H1 E12 ; CDR1 of VH E12

<400> 144

```
Ser Tyr Trp Met His
1               5
```

<210> 145
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CDR-H2 E12 ; CDR-2 of VH E12

<400> 145

```
Phe Ile Leu Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser
1               5                   10                  15

Val Lys Gly
```

<210> 146
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> E12 VH ; VH region

<400> 146

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 147
<211> 252
<212> PRT
<213> HOMO SAPIENS

<220>

<221> MISC_FEATURE
<223> E12 VH - A240 VL ; Single chain Fv

<400> 147

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

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

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

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

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

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

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


Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu
145                 150                 155                 160

Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser
            180                 185                 190

Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys
        195                 200                 205

Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser
    210                 215                 220
```

```
Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser
225                 230                 235                 240

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
```