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Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
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Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
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Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
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Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
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Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
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His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
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Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
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Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
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Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
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Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
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Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
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Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
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Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
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Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
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Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
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Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
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Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
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Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
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Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
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Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
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Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
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Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
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Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
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Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
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Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
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Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
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Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
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Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
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Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
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Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
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Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
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Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
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Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
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Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
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Asp Leu Gly Pro Ala Ser Pro Leu  Asp Ser Thr Phe Tyr  Arg Ser Leu
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Glu Ala  Pro Arg Ser Pro Leu  Ala Pro Ser Glu Gly  Ala Gly Ser
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Asp Val  Phe Asp Gly Asp Leu  Gly Met Gly Ala Ala  Lys Gly Leu
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Gln Ser  Leu Pro Thr His Asp  Pro Ser Pro Leu Gln  Arg Tyr Ser
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Ser Pro  Gly Lys Asn Gly Val  Val Lys Asp Val Phe  Ala Phe Gly
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Gly Ala  Val Glu Asn Pro Glu  Tyr Leu Thr Pro Gln  Gly Gly Ala
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Ala Pro  Gln Pro His Pro Pro  Pro Ala Phe Ser Pro  Ala Phe Asp
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Gln Gly Tyr Val Leu Ile Ala His Ser Gln Val Arg Gln Ile Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Glu Gly Gly Ile Pro
        115                 120                 125

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

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Ser Pro Gln
145                 150                 155                 160

Leu Cys His Gln Asp Thr Ile Leu Trp Lys Asp Val Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Phe Ser Ala Cys
            180                 185                 190

Pro Pro Cys Ser Pro Ala Cys Lys Asp Ala His Cys Trp Gly Ala Ser
        195                 200                 205
```

```
Ser Gly Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

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

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ser Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu Asn Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Arg Val Phe
385                 390                 395                 400
```

```
Glu Ala Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asn Leu Ser Val Phe Gln Asn Leu Arg Val Ile Arg
            420                 425                 430

Gly Arg Val Leu His Asp Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His Arg Asn Ala Arg Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Ser
                485                 490                 495

Ala Asn Arg Pro Glu Glu Glu Cys Val Gly Glu Gly Leu Ala Cys Tyr
            500                 505                 510

Pro Cys Ala His Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val
        515                 520                 525

Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg
    530                 535                 540

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Lys Asp Arg Tyr Cys Leu
545                 550                 555                 560

Pro Cys His Ser Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe
                565                 570                 575

Gly Ser Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro
            580                 585                 590
```

```
Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser
        595                 600                 605

Phe Met Pro Ile Trp Lys Phe Ala Asp Glu Glu Gly Thr Cys Gln Pro
    610                 615                 620

Cys Pro Ile Asn Cys Thr His Ser Cys Ala Asp Leu Asp Glu Lys Gly
625                 630                 635                 640

Cys Pro Ala Glu Gln Arg Ala Ser Pro Val Thr Ser Ile Ile Ala Ala
                645                 650                 655

Val Val Gly Ile Leu Leu Ala Val Val Val Gly Leu Val Leu Gly Ile
            660                 665                 670

Leu Ile Lys Arg Arg Arg Gln Lys Ile Arg Lys Tyr Thr Met Arg Arg
        675                 680                 685

Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Ala
    690                 695                 700

Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu Arg
705                 710                 715                 720

Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly
                725                 730                 735

Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys
            740                 745                 750

Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp
        755                 760                 765

Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu
    770                 775                 780
```

```
Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu Met
785                 790                 795                 800


Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu His Arg Gly Arg Leu
                805                 810                 815


Gly Ser Gln Asp Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met
            820                 825                 830


Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala Arg
        835                 840                 845


Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly
    850                 855                 860


Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp Gly
865                 870                 875                 880


Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Pro Pro Arg
                885                 890                 895


Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp
            900                 905                 910


Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala Arg
        915                 920                 925


Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro
    930                 935                 940


Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met Ile
945                 950                 955                 960


Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ala Glu Phe Ser
                965                 970                 975
```

```
Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu Asp
            980                 985                 990

Leu Gly Pro Ala Ser Pro Leu Asp  Ser Thr Phe Tyr Arg  Ser Leu Leu
        995                 1000                1005

Glu Asp  Asp Asp Met Gly Asp  Leu Val Asp Ala Glu  Glu Tyr Leu
    1010                1015                1020

Val Pro  Gln Gln Gly Phe Phe  Cys Pro Glu Pro Thr  Pro Gly Ala
    1025                1030                1035

Gly Gly  Thr Ala His Arg Arg  His Arg Ser Ser Ser  Thr Arg Asn
    1040                1045                1050

Gly Gly  Gly Glu Leu Thr Leu  Gly Leu Glu Pro Ser  Glu Glu Glu
    1055                1060                1065

Pro Pro  Lys Ser Pro Leu Ala  Pro Ser Glu Gly Ala  Gly Ser Asp
    1070                1075                1080

Val Phe  Asp Gly Asp Leu Gly  Met Gly Ala Ala Lys  Gly Leu Gln
    1085                1090                1095

Ser Leu  Pro Ser Gln Asp Pro  Ser Pro Leu Gln Arg  Tyr Ser Glu
    1100                1105                1110

Asp Pro  Thr Val Pro Leu Pro  Pro Glu Thr Asp Gly  Lys Val Ala
    1115                1120                1125

Pro Leu  Thr Cys Ser Pro Gln  Pro Glu Tyr Val Asn  Gln Pro Glu
    1130                1135                1140

Val Trp  Pro Gln Pro Pro Leu  Ala Leu Glu Gly Pro  Leu Pro Pro
    1145                1150                1155
```

```
Ser Arg  Pro Ala Gly Ala Thr  Leu Glu Arg Pro Lys  Thr Leu Ser
    1160                1165                1170


Pro Lys  Thr Leu Ser Pro Gly  Lys Asn Gly Val Val  Lys Asp Val
    1175                1180                1185


Phe Ala  Phe Gly Ser Ala Val  Glu Asn Pro Glu Tyr  Leu Ala Pro
    1190                1195                1200


Arg Gly  Arg Ala Ala Pro Gln  Pro His Pro Pro Pro  Ala Phe Ser
    1205                1210                1215


Pro Ala  Phe Asp Asn Leu Tyr  Tyr Trp Asp Gln Asp  Pro Ser Glu
    1220                1225                1230


Arg Gly  Ser Pro Pro Ser Thr  Phe Glu Gly Thr Pro  Thr Ala Glu
    1235                1240                1245


Asn Pro  Glu Tyr Leu Gly Leu  Asp Val Pro Val
    1250                1255
```

<210> 5
<211> 1311
<212> DNA
<213> Homo sapiens

<300>
<308> NM_000073.2
<309> 2014-05-03
<313> (1)..(1311)

<400> 5

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agtctagctg ctgcacaggc tggctggctg gctggctgct aagggctgct ccacgctttt       60

gccggaggac agagactgac atggaacagg ggaagggcct ggctgtcctc atcctggcta      120

tcattcttct tcaaggtact ttggcccagt caatcaaagg aaaccacttg gttaaggtgt      180

atgactatca agaagatggt tcggtacttc tgacttgtga tgcagaagcc aaaaatatca      240

catggtttaa agatgggaag atgatcggct tcctaactga agataaaaaa aaatggaatc      300
```

tgggaagtaa tgccaaggac cctcgaggga tgtatcagtg taaaggatca cagaacaagt 360

caaaaccact ccaagtgtat tacagaatgt gtcagaactg cattgaacta aatgcagcca 420

ccatatctgg ctttctcttt gctgaaatcg tcagcatttt cgtccttgct gttggggtct 480

acttcattgc tggacaggat ggagttcgcc agtcgagagc ttcagacaag cagactctgt 540

tgcccaatga ccagctctac cagcccctca aggatcgaga agatgaccag tacagccacc 600

ttcaaggaaa ccagttgagg aggaattgaa ctcaggactc agagtagtcc aggtgttctc 660

ctcctattca gttcccagaa tcaaagcaat gcattttgga aagctcctag cagagagact 720

ttcagcccta aatctagact caaggttccc agagatgaca aatggagaag aaaggccatc 780

agagcaaatt tgggggtttc tcaaataaaa taaaaataaa aacaaatact gtgtttcaga 840

agcgccacct attggggaaa attgtaaaag aaaaatgaaa agatcaaata acccccctgga 900

tttgaatata atttttttgtg ttgtaatttt tatttcgttt ttgtataggt tataattcac 960

atggctcaaa tattcagtga aagctctccc tccaccgcca tcccctgcta cccagtgacc 1020

ctgttgccct cttcagagac aaattagttt ctctttttttt ttttttttttt ttttttttttg 1080

agacagtctg gctctgtcac ccaggctgaa atgcagtggc accatctcgg ctcactgcaa 1140

cctctgcctc ctgggttcaa gcgattctcc tgcctcagcc tcccgggcag ctgggattac 1200

aggcacacac taccacacct ggctaatttt tgtattttta gtagagacag ggttttgctc 1260

tgttggccaa gctggtctcg aactcctgac ctcaagtgat ccgcccgcct c 1311

<210> 6
<211> 182
<212> PRT
<213> Homo sapiens

<300>
<308> NP_000064.1
<309> 2014-05-03
<313> (1)..(182)

<400> 6

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Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
1               5                  10                  15

Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys
            20                  25                  30

Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
        35                  40                  45

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

Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
65                  70                  75                  80

Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
                85                  90                  95

Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
            100                 105                 110

Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
        115                 120                 125

Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
    130                 135                 140

Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
145                 150                 155                 160

Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
                165                 170                 175

Asn Gln Leu Arg Arg Asn
            180
```

<210> 7
<211> 771
<212> DNA
<213> Homo sapiens

<300>
<308> NM_000732.4
<309> 2014-05-03
<313> (1)..(771)

<400> 7
agagaagcag acatcttcta gttcctcccc cactctcctc tttccggtac ctgtgagtca 60

gctaggggag ggcagctctc acccaggctg atagttcggt gacctggctt tatctactgg 120

atgagttccg ctgggagatg gaacatagca cgtttctctc tggcctggta ctggctaccc 180

ttctctcgca agtgagcccc ttcaagatac ctatagagga acttgaggac agagtgtttg 240

tgaattgcaa taccagcatc acatgggtag agggaacggt gggaacactg ctctcagaca 300

ttacaagact ggacctggga aaacgcatcc tggacccacg aggaatatat aggtgtaatg 360

ggacagatat atacaaggac aaagaatcta ccgtgcaagt tcattatcga atgtgccaga 420

gctgtgtgga gctggatcca gccaccgtgg ctggcatcat tgtcactgat gtcattgcca 480

ctctgctcct tgctttggga gtcttctgct ttgctggaca tgagactgga aggctgtctg 540

gggctgccga cacacaagct ctgttgagga atgaccaggt ctatcagccc ctccgagatc 600

gagatgatgc tcagtacagc caccttggag gaaactgggc tcggaacaag tgaacctgag 660

actggtggct tctagaagca gccattacca actgtacctt cccttcttgc tcagccaata 720

aatatatcct ctttcactca gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 771

<210> 8
<211> 171
<212> PRT
<213> Homo sapiens

<300>
<308> NP_000723.1
<309> 2014-05-03
<313> (1)..(171)

<400> 8

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Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1               5                   10                  15

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
            20                  25                  30

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
        35                  40                  45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
    50                  55                  60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
65                  70                  75                  80

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

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
            100                 105                 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
        115                 120                 125

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
    130                 135                 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
145                 150                 155                 160

Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
                165                 170
```

<210> 9
<211> 1534

<212> DNA
<213> Homo sapiens

<300>
<308> NM_000733.3
<309> 2014-05-03
<313> (1)..(1534)

<400> 9
tattgtcaga gtcctcttgt ttggccttct aggaaggctg tgggacccag ctttcttcaa 60

ccagtccagg tggaggcctc tgccttgaac gtttccaagt gaggtaaaac ccgcaggccc 120

agaggcctct ctacttcctg tgtggggttc agaaaccctc ctcccctccc agcctcaggt 180

gcctgcttca gaaaatgaag tagtaagtct gctggcctcc gccatcttag taaagtaaca 240

gtcccatgaa acaaagatgc agtcgggcac tcactggaga gttctgggcc tctgcctctt 300

atcagttggc gtttgggggc aagatggtaa tgaagaaatg ggtggtatta cacagacacc 360

atataaagtc tccatctctg gaaccacagt aatattgaca tgccctcagt atcctggatc 420

tgaaatacta tggcaacaca atgataaaaa cataggcggt gatgaggatg ataaaaacat 480

aggcagtgat gaggatcacc tgtcactgaa ggaattttca gaattggagc aaagtggtta 540

ttatgtctgc taccccagag gaagcaaacc agaagatgcg aacttttatc tctacctgag 600

ggcaagagtg tgtgagaact gcatggagat ggatgtgatg tcggtggcca caattgtcat 660

agtggacatc tgcatcactg ggggcttgct gctgctggtt tactactgga gcaagaatag 720

aaaggccaag gccaagcctg tgacacgagg agcgggtgct ggcggcaggc aaaggggaca 780

aaacaaggag aggccaccac ctgttcccaa cccagactat gagcccatcc ggaaaggcca 840

gcgggacctg tattctggcc tgaatcagag acgcatctga ccctctggag aacactgcct 900

cccgctggcc caggtctcct ctccagtccc cctgcgactc cctgtttcct gggctagtct 960

tggaccccac gagagagaat cgttcctcag cctcatggtg aactcgcgcc ctccagcctg 1020

atcccccgct ccctcctccc tgccttctct gctggtaccc agtcctaaaa tattgctgct 1080

tcctcttcct ttgaagcatc atcagtagtc acaccctcac agctggcctg ccctcttgcc 1140

aggatattta tttgtgctat tcactccctt ccctttggat gtaacttctc cgttcagttc 1200

cctccttttc ttgcatgtaa gttgtccccc atcccaaagt attccatcta cttttctatc 1260

gccgtcccct tttgcagccc tctctgggga tggactgggt aaatgttgac agaggccctg 1320

ccccgttcac agatcctggc cctgagccag ccctgtgctc ctccctcccc caacactccc 1380

taccaacccc ctaatcccct actccctcca ccccccctcc actgtaggcc actggatggt 1440

catttgcatc tccgtaaatg tgctctgctc ctcagctgag agagaaaaaa ataaactgta 1500

tttggctgca agaaaaaaaa aaaaaaaaaa aaaa 1534

<210> 10
<211> 207
<212> PRT
<213> Homo sapiens

<300>
<308> NP_000724.1
<309> 2014-05-03
<313> (1)..(207)

<400> 10

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> 11
<211> 1436
<212> DNA
<213> Canine

<300>
<308> NM_001003379.1
<309> 2014-02-22
<313> (1)..(1436)

<400> 11

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aaagacagta taatacagca gctcacacag actttcggat tcagaaaaac agttgtgtcg      120

ggccttgggt aaattatgta aggcaagcct cagtttgctc agcggtaaaa cgaggaaagt      180

aataagccac ccgcctccgc cattttgggt agaataaggg tgcatccagt gagagaagga      240
```

tgcagtcgag gaacctctgg agaattctgg gactctgtct cttatcagtt ggtgcttggg 300

ggcaggacga ggatttcaaa gcttctgatg acttgacaag tatatctcca gagaaacggt 360

ttaaggtctc catctctgga accgaggtag tggtgacatg ccctgatgtt tttggatatg 420

ataatataaa atgggaaaaa aatgataacc ttgtggaagg tgctagtaac agagagctat 480

ctcagaagga gttttcagaa gtggacgaca gtggttatta tgcctgctat gcagattcca 540

taaaggagaa gagctatctc tacctgagag caagagtgtg tgcaaactgc atagaggtga 600

atctgatggc agtggtcaca atcattgtag ctgacatctg ccttactctg gggttgctgc 660

tgatggtgta ttactggagc aagactagaa aggccaatgc caagcctgtg atgagaggaa 720

caggtgccgg cagcaggccc aggggacaaa acaaggagaa gccaccacct gttcccaatc 780

cagactacga gcccatccgg aaaggccagc aggacctgta ttctggcctg aatcagagag 840

gcatctgacg gctcctgagg acacggcctc cccagggccc aggtcttggt gtctccaggt 900

cctgctactc ccagtaccct gggtaaatct tgaaccccag aagagaatta ttcctctgcc 960

ttctggagaa ctaactccca gcctgcagcc ttatccccag caccctccaa cccgccttct 1020

ctgctggcac ttggtcctgc aatatcacct cctcatcatg gccactcacc gccccccac 1080

cagccagact gccctctggt cggggtattt atttctgtta ccctgacgcc cccaccatca 1140

ccaattcctt cctacccttc agaggtatcc ttgctccctt ccgtacccct ctcccggaca 1200

gaacctgccc ccatccctta ctatcccacc tacctttccg tttttccagc tctctctttg 1260

gtgaccctct gtggggatgg actaggtaac tctggtagag gtcctgcccc atccatgacc 1320

ttggcccaga gccaccctct gccagcaggc ccctggatga tcatttgcat tcttacaaat 1380

gtgctaggct ccttgacagc tagagagaaa ataataaagt gtatttggtt gaaaaa 1436

<210> 12
<211> 202
<212> PRT
<213> Canine

<300>

<308> NP_001003379.1
<309> 2014-02-22
<313> (1)..(202)

<400> 12

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Met Gln Ser Arg Asn Leu Trp Arg Ile Leu Gly Leu Cys Leu Leu Ser
1               5                  10                  15


Val Gly Ala Trp Gly Gln Asp Glu Asp Phe Lys Ala Ser Asp Asp Leu
            20                  25                  30


Thr Ser Ile Ser Pro Glu Lys Arg Phe Lys Val Ser Ile Ser Gly Thr
        35                  40                  45


Glu Val Val Val Thr Cys Pro Asp Val Phe Gly Tyr Asp Asn Ile Lys
    50                  55                  60


Trp Glu Lys Asn Asp Asn Leu Val Glu Gly Ala Ser Asn Arg Glu Leu
65                  70                  75                  80


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


Tyr Ala Asp Ser Ile Lys Glu Lys Ser Tyr Leu Tyr Leu Arg Ala Arg
            100                 105                 110


Val Cys Ala Asn Cys Ile Glu Val Asn Leu Met Ala Val Val Thr Ile
        115                 120                 125


Ile Val Ala Asp Ile Cys Leu Thr Leu Gly Leu Leu Leu Met Val Tyr
    130                 135                 140


Tyr Trp Ser Lys Thr Arg Lys Ala Asn Ala Lys Pro Val Met Arg Gly
145                 150                 155                 160


Thr Gly Ala Gly Ser Arg Pro Arg Gly Gln Asn Lys Glu Lys Pro Pro
                165                 170                 175
```

Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Gln Asp
180 185 190

Leu Tyr Ser Gly Leu Asn Gln Arg Gly Ile
195 200

<210> 13
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Peptide linker (G4S)3

<400> 13
ggcggcggag gatctggcgg aggtggaagt gggggaggcg gatct 45

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker (G4S)3

<400> 14

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

<210> 15
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VH

<400> 15

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

```
Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

Thr Pro Val Thr Val Ser Ser
        115


<210>  16
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  OKT3 VL

<400>  16

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

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
```

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

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

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

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

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
            100                 105
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<210> 17
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VH C105S

<400> 17

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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

Thr Pro Val Thr Val Ser Ser
115

<210> 18
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> OKT3 scFv C105S

<400> 18
caggtgcagc tggtgcagag tggtggcgga gtggtgcagc ctggcagatc cctgagactg 60

tcttgcaagg ccagcggcta caccttcacc cggtacacca tgcactgggt gcgacaggcc 120

cctggcaagg gcctggaatg gatcggctac atcaacccct cccggggcta caccaactac 180

aaccagaagt tcaaggaccg gttcaccatc agccgggaca actccaagaa caccgccttt 240

ctgcagatgg actccctgcg gcctgaggat accggcgtgt actttgcgc ccggtactac 300

gacgaccact actctctgga ctactggggc cagggaaccc ctgtgacagt gtctagcgga 360

gggggaggtt caggtggcgg tggatcaggg ggcggaggct ctgatatcca gatgacccag 420

tccccctcca gcctgtctgc ctctgtggga gacagagtga caattacatg ctccgccagc 480

tccagcgtgt cctacatgaa ttggtatcag cagacccctg gcaaggctcc caagcggtgg 540

atctacgaca cctccaagct ggcctccggc gtgccctcca gattttctgg cagcggctcc 600

ggcacagact atacctttac aatcagctcc ctgcagcccg aagatatcgc cacctactac 660

tgccagcagt ggtcctccaa ccccttcacc tttggccagg ggacaaaact gcagatcacc 720

aga 723

<210> 19
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 scFv C105S

<400> 19

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


Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45


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


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


Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95


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


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


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140
```

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
145 150 155 160

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp
210 215 220

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

Arg

<210> 20
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplary heavy chain N297A

<400> 20
gaggtgcagc tggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcttgtgccg cctccggctt caacatcaag gacacctaca tccactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180

gccgactctg tgaagggccg gttcaccatc tccgccgaca cctccaagaa caccgcctac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300

ggcgacggct tctacgccat ggactattgg ggccagggca ccctcgtgac cgtgtcctct 360

gcttctacca agggcccctc tgtgtttcct ctggcccccc ccagcaagtc cacctctggt 420

ggaacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480

tggaactctg gcgctctgac ctctggcgtg cacaccttcc ctgctgtgct gcagtctagc 540

ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagccctcc aataccaagg tggacaagcg ggtggaaccc 660

aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaact gctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagtacgcc 900

tccacctacc gggtggtgtc cgtgctgaca gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaagtgtc caacaaggcc ctgcctgccc ccatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg ggaaccccag gtgtacacac tgcccccctag cagggacgag 1080

ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140

gccgtggaat gggagtccaa cggccagcct gagaacaact acaagaccac ccccccctgtg 1200

ctggactccg acggctcatt cttcctgtac agcaagctga ccgtggacaa gtcccggtgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag ccccggcaaa 1350

<210> 21
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplary heavy chain K322A

<400> 21
gaggtgcagc tggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcttgtgccg cctccggctt caacatcaag gacacctaca tccactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180

gccgactctg tgaagggccg gttcaccatc tccgccgaca cctccaagaa caccgcctac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300

ggcgacggct tctacgccat ggactattgg ggccagggca ccctcgtgac cgtgtcctct 360

gcttctacca agggcccctc tgtgtttcct ctggcccccc ccagcaagtc cacctctggt 420

ggaacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480

tggaactctg gcgctctgac ctctggcgtg cacaccttcc ctgctgtgct gcagtctagc 540

ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagccctcc aataccaagg tggacaagcg ggtggaaccc 660

aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaact gctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagtacaac 900

tccacctacc gggtggtgtc cgtgctgaca gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcgccgtgtc caacaaggcc ctgcctgccc ccatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg ggaaccccag gtgtacacac tgcccccctag cagggacgag 1080

ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140

gccgtggaat gggagtccaa cggccagcct gagaacaact acaagaccac ccccccctgtg 1200

ctggactccg acggctcatt cttcctgtac agcaagctga ccgtggacaa gtcccggtgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag ccccggcaaa 1350

<210> 22
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplary heavy chain

<400> 22
gaggtgcagc tggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcttgtgccg cctccggctt caacatcaag gacacctaca tccactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180

gccgactctg tgaagggccg gttcaccatc tccgccgaca cctccaagaa caccgcctac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300

ggcgacggct tctacgccat ggactattgg ggccagggca ccctcgtgac cgtgtcctct 360

gcttctacca agggcccctc tgtgtttcct ctggcccccc ccagcaagtc cacctctggt 420

ggaacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480

tggaactctg gcgctctgac ctctggcgtg cacaccttcc ctgctgtgct gcagtctagc 540

ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagccctcc aataccaagg tggacaagcg ggtggaaccc 660

aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaact gctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagtacaac 900

tccacctacc gggtggtgtc cgtgctgaca gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaagtgtc caacaaggcc ctgcctgccc ccatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg ggaaccccag gtgtacacac tgcccccctag cagggacgag 1080

ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140

gccgtggaat gggagtccaa cggccagcct gagaacaact acaagaccac ccccccctgtg 1200

ctggactccg acggctcatt cttcctgtac agcaagctga ccgtggacaa gtcccggtgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag ccccggcaaa 1350

<210> 23
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary heavy chain

<400> 23

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
```

<210> 24
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain

<400> 24
gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc gggcctccca ggacgtgaac accgccgtgg cttggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactcc gcctccttcc tgtactccgg cgtgccctcc 180

agattctccg gcagcagatc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag cactacacca ccccccccac ctttggccag 300

ggcaccaagg tggaaatcaa gcggaccgtg gccgctccct ccgtgttcat cttcccacct 360

tccgacgagc agctgaagtc cggcaccgct tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gc 642

<210> 25
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain

<400> 25

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys Thr Ser
210 215

<210> 26
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2-BsAb heavy chain

<400> 26
gaggtgcagc tggtggaatc tggcggagga ctggtgcagc ctggcggctc tctgagactg 60

tcttgtgccg cctccggctt caacatcaag gacacctaca tccactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180

gccgactctg tgaagggccg gttcaccatc tccgccgaca cctccaagaa caccgcctac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300

ggcgacggct tctacgccat ggactattgg ggccagggca ccctcgtgac cgtgtcctct 360

gcttctacca agggcccctc tgtgtttcct ctggcccccc ccagcaagtc cacctctggt 420

ggaacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480

tggaactctg gcgctctgac ctctggcgtg cacaccttcc ctgctgtgct gcagtctagc 540

ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagccctcc aataccaagg tggacaagcg ggtggaaccc 660

aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaact gctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagtacgcc 900

tccacctacc gggtggtgtc cgtgctgaca gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcgccgtgtc caacaaggcc ctgcctgccc ccatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg ggaaccccag gtgtacacac tgcccccctag cagggacgag 1080

ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140

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ctggactccg acggctcatt cttcctgtac agcaagctga ccgtggacaa gtcccggtgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag ccccggcaaa 1350

<210> 27
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb heavy chain

<400> 27

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


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


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


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


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


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


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


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


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
```

<210> 28
<211> 1416
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide

<400> 28
gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc gggcctccca ggacgtgaac accgccgtgg cttggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactcc gcctccttcc tgtactccgg cgtgccctcc 180

agattctccg gcagcagatc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag cactacacca ccccccccac ctttggccag 300

ggcaccaagg tggaaatcaa gcggaccgtg gccgctccct ccgtgttcat cttcccacct 360

tccgacgagc agctgaagtc cggcaccgct tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gcactagtgg cggcggagga 660

tctggcggag gtggaagtgg gggaggcgga tctcaggtgc agctggtgca gagtggtggc 720

ggagtggtgc agcctggcag atccctgaga ctgtcttgca aggccagcgg ctacaccttc 780

acccggtaca ccatgcactg ggtgcgacag gcccctggca agggcctgga atggatcggc 840

tacatcaacc cctcccgggg ctacaccaac tacaaccaga agttcaagga ccggttcacc 900

atcagccggg acaactccaa gaacaccgcc tttctgcaga tggactccct gcggcctgag 960

gataccggcg tgtacttttg cgcccggtac tacgacgacc actactctct ggactactgg 1020

ggccagggaa cccctgtgac agtgtctagc ggaggggggag gttcaggtgg cggtggatca 1080

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ggcgtgccct ccagatttc tggcagcggc tccggcacag actatacctt tacaatcagc 1320

tccctgcagc ccgaagatat cgccacctac tactgccagc agtggtcctc caacccttc 1380

acctttggcc aggggacaaa actgcagatc accaga 1416

<210> 29
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide

<400> 29

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
        355                 360                 365

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    370                 375                 380

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
385                 390                 395                 400
```

```
Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                405                 410                 415


Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            420                 425                 430


Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        435                 440                 445


Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln
    450                 455                 460


Gly Thr Lys Leu Gln Ile Thr Arg
465                 470
```

<210> 30
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (5aa scFv linker)

<400> 30

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


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


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


Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255
```

```
Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
        355                 360                 365

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
    370                 375                 380

Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg
385                 390                 395                 400

Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
                405                 410                 415

Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu
            420                 425                 430

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn
        435                 440                 445
```

Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
450 455 460

<210> 31
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (10aa scFv linker)

<400> 31

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

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

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

```
    130                 135                 140

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
```

325 330 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
340 345 350

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
355 360 365

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
370 375 380

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly
385 390 395 400

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
405 410 415

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe
420 425 430

Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
435 440 445

Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln
450 455 460

Ile Thr Arg
465

<210> 32
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (20aa scFv linker)

<400> 32

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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


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


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240


Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255


Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270


Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285


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


Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320


Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335


Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365


Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
    370                 375                 380
```

```
Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
385                 390                 395                 400


Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp
                405                 410                 415


Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
            420                 425                 430


Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln
        435                 440                 445


Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
    450                 455                 460


Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
465                 470                 475


<210>  33
<211>  482
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HER2-BsAb light chain fusion polypeptide (25aa scFv linker)

<400>  33

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


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


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


Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
```

```
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
```

245 250 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
260 265 270

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
275 280 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305 310 315 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
325 330 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
340 345 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
370 375 380

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

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

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
420 425 430

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr

435 440 445

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
450 455 460

Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile
465 470 475 480

Thr Arg

<210> 34
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (30aa scFv linker)

<400> 34

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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


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


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


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


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


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


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


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


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240


Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255


Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270


Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285
```

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    370                 375                 380

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

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
                405                 410                 415

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

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

Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
    450                 455                 460

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly
465                 470                 475                 480
```

Thr Lys Leu Gln Ile Thr Arg
485

<210> 35
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> T(G4S)3 Linker

<400> 35
tsggggsggg gsggggs 17

<210> 36
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<223> G4S Linker

<400> 36
ggggs 5

<210> 37
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> (G4S)2 Linker

<400> 37
ggggsggggs 10

<210> 38
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> (G4S)3 Linker

<400> 38
ggggsggggs ggggs 15

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> (G4S)4 Linker

<400> 39
ggggsggggs ggggsggggs 20

<210> 40
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> (G4S)5 Linker

<400> 40
ggggsggggs ggggsggggs ggggs 25

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> (G4S)6 Linker

<400> 41
ggggsggggs ggggsggggs ggggsggggs 30

<210> 42
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide

(5aa scFv linker) + disulfide mut

<400> 42

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


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


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


Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


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


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95


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


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


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


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


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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
        355                 360                 365
```

```
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val
    370                 375                 380

Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg
385                 390                 395                 400

Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
                405                 410                 415

Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu
            420                 425                 430

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn
        435                 440                 445

Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu Gln Ile Thr Arg
    450                 455                 460
```

<210> 43
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (10aa scFv linker) + disulfide mut

<400> 43

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
```

```
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
```

245 250 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
260 265 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
275 280 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305 310 315 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
325 330 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
340 345 350

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
355 360 365

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
370 375 380

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly
385 390 395 400

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
405 410 415

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe
420 425 430

Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln

435 440 445

Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu Gln
450 455 460

Ile Thr Arg
465

<210> 44
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (15aa scFv linker) + disulfide mut

<400> 44

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

```
Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
        355                 360                 365

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    370                 375                 380

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
385                 390                 395                 400

Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                405                 410                 415

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            420                 425                 430

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        435                 440                 445

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Cys
    450                 455                 460

Gly Thr Lys Leu Gln Ile Thr Arg
465                 470
```

<210> 45
<211> 477

<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (20aa scFv linker)
+ disulfide mut

<400> 45

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


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


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


Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


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


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95


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


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


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


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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365


Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
    370                 375                 380


Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
385                 390                 395                 400


Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp
                405                 410                 415


Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
            420                 425                 430


Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln
        435                 440                 445


Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
    450                 455                 460


Phe Thr Phe Gly Cys Gly Thr Lys Leu Gln Ile Thr Arg
465                 470                 475


<210>  46
<211>  483
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HER2-BsAb light chain fusion polypeptide (25aa scFv linker)
       + disulfide mut

<400>  46

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    370                 375                 380

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

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

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
420 425 430

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr
435 440 445

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
450 455 460

Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Cys Gly Thr Lys Leu Gln
465 470 475 480

Ile Thr Arg

<210> 47
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-BsAb light chain fusion polypeptide (30aa scFv linker)
+ disulfide mut

<400> 47

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

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

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

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

50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225 230 235 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser

```
                245                 250                 255

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        355                 360                 365

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
    370                 375                 380

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

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
                405                 410                 415

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

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
```

435 440 445

Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
450 455 460

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

Thr Lys Leu Gln Ile Thr Arg
485

<210> 48
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) (5 aa scFv linker)

<400> 48

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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


Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
        115                 120                 125


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


Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
145                 150                 155                 160


Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
                165                 170                 175


Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
            180                 185                 190


Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
        195                 200                 205


Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly
    210                 215                 220


Thr Lys Leu Gln Ile Thr Arg
225                 230
```

<210> 49
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) (10 aa scFv linker)

<400> 49

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
```

```
1               5                   10                  15

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

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

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
    130                 135                 140

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

Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile
                165                 170                 175

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

Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro
```

195 200 205

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

Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
225 230 235

<210> 50
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) (20 aa scFv linker)

<400> 50

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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

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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
                165                 170                 175


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


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


Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr
225                 230                 235                 240


Lys Leu Gln Ile Thr Arg
                245


<210>  51
<211>  251
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huOKT3scFv(C105S) (25 aa scFv linker)

<400>  51

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
```

```
1               5                   10                  15

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145                 150                 155                 160

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
                165                 170                 175

Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
            180                 185                 190

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
```

195 200 205

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
210 215 220

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
245 250

<210> 52
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) (30 aa scFv linker)

<400> 52

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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


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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140


Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
145                 150                 155                 160


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser
                165                 170                 175


Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro
            180                 185                 190


Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser
        195                 200                 205


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser
    210                 215                 220


Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
225                 230                 235                 240


Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
                245                 250                 255


<210>  53
<211>  231
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huOKT3scFv(C105S) + disulfide mut (5 aa scFv linker)
```

<400> 53

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

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
        115                 120                 125

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

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
145                 150                 155                 160

Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
                165                 170                 175

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
```

180 185 190

Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
195 200 205

Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Cys Gly
210 215 220

Thr Lys Leu Gln Ile Thr Arg
225 230

<210> 54
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) + disulfide mut (10 aa scFv linker)

<400> 54

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

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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


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


Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
    130                 135                 140


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


Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile
                165                 170                 175


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


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


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


Thr Phe Gly Cys Gly Thr Lys Leu Gln Ile Thr Arg
225                 230                 235


<210>  55
<211>  241
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huOKT3scFv(C105S) + disulfide mut (15 aa scFv linker)

<400>  55

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
```

```
1               5                   10                  15

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

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

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
145                 150                 155                 160

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
```

195 200 205

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp
210 215 220

Ser Ser Asn Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu Gln Ile Thr
225 230 235 240

Arg

<210> 56
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) + disulfide mut (20 aa scFv linker)

<400> 56

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

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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


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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
                165                 170                 175


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


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


Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Cys Gly Thr
225                 230                 235                 240


Lys Leu Gln Ile Thr Arg
                245


<210>  57
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huOKT3scFv(C105S) + disulfide mut (25 aa scFv linker)
```

<400> 57

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

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
        35                  40                  45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145                 150                 155                 160

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
                165                 170                 175

Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
```

180 185 190

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

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
210 215 220

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
225 230 235 240

Phe Gly Gln Cys Gly Thr Lys Leu Gln Ile Thr Arg
245 250

<210> 58
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3scFv(C105S) + disulfide mut (30 aa scFv linker)

<400> 58

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

Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
35 40 45

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

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

```
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95


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


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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140


Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
145                 150                 155                 160


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser
                165                 170                 175


Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro
            180                 185                 190


Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser
        195                 200                 205


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser
    210                 215                 220


Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
225                 230                 235                 240


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


<210>  59
<211>  241
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> huOKT3scFv + disulfide mut (15 aa scFv linker)

<400> 59

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


Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
        35                  40                  45


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


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


Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95


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


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


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
145                 150                 155                 160


Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala
```

165 170 175

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp
210 215 220

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

Arg

<210> 60
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Her2-BsAb light chain fusion polypeptide

<400> 60

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
225                 230                 235                 240

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
                245                 250                 255
```

```
Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
            260                 265                 270

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
        275                 280                 285

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

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
305                 310                 315                 320

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys
                325                 330                 335

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
        355                 360                 365

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    370                 375                 380

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
385                 390                 395                 400

Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                405                 410                 415

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            420                 425                 430

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        435                 440                 445
```

```
Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln
    450                 455                 460


Gly Thr Lys Leu Gln Ile Thr Arg
465                 470


<210>  61
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Her2-bsab light chain sequence

<400>  61

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


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


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


Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


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


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95


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


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
```

115 120 125

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 62
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> her2 bsab heavy chain sequence

<400> 62

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 63
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Trastuzumab heavy chain K322A

<400> 63

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

```
        115                 120                 125

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

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

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

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

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

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

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

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

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

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
```

305 310 315 320

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 64
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3 VH C105S + VH44

<400> 64

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


Ser Leu Arg Leu 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 Lys Cys Leu Glu Trp Ile
        35                  40                  45


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


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


Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95


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


Thr Pro Val Thr Val Ser Ser
        115


<210>  65
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huOKT3 VL + VL100

<400>  65

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


Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
```

20 25 30

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

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

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

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

Phe Gly Cys Gly Thr Lys Leu Gln Ile Thr Arg
100 105

<210> 66
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> huOKT3 scFv; 15 aa linker

<400> 66

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

Ser Leu Arg Leu 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 Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

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

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
145                 150                 155                 160

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp
    210                 215                 220

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

Arg
```

<210> 67
<211> 1416
<212> DNA
<213> Artifiial Sequence

<220>
<223> DNA encoding sequence of SEQ ID NO:60

<400> 67
gatattcaga tgactcagtc tccctcttcc ctgtccgctt cagtcggcga tcgggtcact 60

attacttgtc gggcttcaca ggatgtcaac acagccgtgg cttggtacca gcagaagccc 120

gggaaagcac ctaagctgct gatctactct gccagtttcc tgtattctgg cgtcccaagt 180

aggttttcag gctcccggag cggaactgac ttcaccctga caatttccag cctgcagccc 240

gaggattttg ctacctacta ttgccagcag cattatacta ccccccccaac attcggccag 300

ggcacaaaag tcgaaatcaa gcggaccgtg gccgcccccct ccgtgttcat cttccccccc 360

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gagtccgtga ccgagcagga ctccaaggac tccacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600

ctgtcctccc ccgtgaccaa gtccttcaac cggggcgagt gcactagtgg aggaggaggt 660

agcggaggag gaggttctgg cggaggggggt tcccaggtgc agctggtgca gagcggagga 720

ggagtggtgc agccaggaag gagcctgcga ctgtcttgca aggctagtgg ctacaccttc 780

acacgatata ctatgcactg ggtgaggcag gcacctggta aaggcctgga gtggatcggc 840

tacattaacc cctctagggg atacaccaac tataatcaga agttcaaaga caggttcacc 900

atctcacgcg ataactccaa gaataccgcc ttcctgcaga tggactccct gcggcccgaa 960

gatacaggcg tgtatttttg cgctagatac tatgacgatc attactgtct ggactattgg 1020

ggacagggga cccctgtgac agtgtccagc ggtggaggag ggtcaggtgg aggagggagc 1080

ggtggcggag ggtctgacat ccagatgacc cagtccccat ctagtctgag cgcctctgtg 1140

ggcgatagag tgactattac ctgcagtgct tcatccagcg tgagctacat gaactggtat 1200

cagcagacac ccggaaaggc acctaaacgc tggatctacg atactagcaa gctggcctct 1260

ggcgtgccca gtcgattcag tggttcaggc tccggaaccg actatacctt caccatctct 1320

agtctgcagc ctgaggatat tgccacatac tattgtcagc agtggtcatc caatccattc 1380

acttttgggc agggtaccaa actgcagatt acaagg 1416

<210> 68
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding sequence of SEQ ID NO:62

<400> 68
gaagtgcagc tggtcgagag cggaggaggt ctggtgcagc ccggaggttc cctgagactg 60

tcctgtgccg catctgggtt taatatcaag gacacataca tccactgggt gagacaggca 120

cccggcaaag gactggagtg ggtcgccagg atctacccta ccaacgggta cacaagatat 180

gctgactctg tgaagggccg gttcaccatc tccgccgata ctagcaaaaa caccgcttac 240

ctgcagatga attccctgag ggcagaagat accgctgtct actactgttc aagatggggg 300

ggggatggtt tttacgctat ggattattgg ggccagggca ccctggtgac cgtgtcctcc 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggccgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 69
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2-C825 Light Chain

<400> 69
gatattcaga tgactcagtc tccctcttcc ctgtccgctt cagtcggcga tcgggtcact 60

attacttgtc gggcttcaca ggatgtcaac acagccgtgg cttggtacca gcagaagccc 120

gggaaagcac ctaagctgct gatctactct gccagtttcc tgtattctgg cgtcccaagt 180

aggttttcag gctcccggag cggaactgac ttcaccctga caatttccag cctgcagccc 240

gaggattttg ctacctacta ttgccagcag cattatacta ccccccccaac attcggccag 300

ggcacaaaag tcgaaatcaa gcggaccgtg gccgcccccct ccgtgttcat cttccccccc 360

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa caacttctac 420

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gagtccgtga ccgagcagga ctccaaggac tccacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600

ctgtcctccc ccgtgaccaa gtccttcaac cggggcgagt gcggtggtgg tggtagcggc 660

ggcggtggaa gcgcatccca tgtgaaactg caggaaagcg gcccaggtct ggtccagcca 720

tcccagtctc tgagcctgac atgcactgtg agcggattct ctctgacaga ctatggggtg 780

cactgggtca gacagagtcc aggaaagggg ctggagtggc tgggcgtcat ctggtcaggc 840

ggagggactg cttataacac cgcactgatc agcagactga atatctaccg cgacaactct 900

aaaaatcagg tgttcctgga gatgaacagt ctgcaggccg aagataccgc tatgtactat 960

tgcgccaggc ggggcagcta cccttataat tactttgacg cttggggttg tggcaccaca 1020

gtgacagtct ccagcggtgg aggagggagt ggtggaggag ggtcaggtgg aggagggtcc 1080

caggcagtgg tcattcagga gtctgccctg actacccccc ctggagaaac cgtgacactg 1140

acttgcggat ctagtacagg ggcagtgact gcctccaact atgcaaattg ggtccaggaa 1200

aagcctgatc actgtttcac tggcctgatc ggtggccata acaatcgacc acccggagtg 1260

ccagctaggt tttcaggttc cctgatcggc gacaaagccg ctctgaccat tgctggcacc 1320

cagacagagg atgaagcaat ctacttttgt gccctgtggt attccgatca ctgggtcatt 1380

ggggggggga cacgtctgac tgtgctgggg 1410

<210> 70
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2-C825 Heavy Chain

<400> 70
gaagtgcagc tggtcgagag cggaggaggt ctggtgcagc ccggaggttc cctgagactg 60

tcctgtgccg catctgggtt taatatcaag gacacataca tccactgggt gagacaggca 120

cccggcaaag gactggagtg ggtcgccagg atctacccta ccaacgggta cacaagatat 180

gctgactctg tgaagggccg gttcaccatc tccgccgata ctagcaaaaa caccgcttac 240

ctgcagatga attccctgag ggcagaagat accgctgtct actactgttc aagatggggg 300

ggggatggtt tttacgctat ggattattgg ggccagggca ccctggtgac cgtgtcctcc 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggccgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

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cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 71
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-C825 Light Chain sequence

<400> 71

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

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

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

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr
                245                 250                 255

Asp Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu
            260                 265                 270

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

Leu Ile Ser Arg Leu Asn Ile Tyr Arg Asp Asn Ser Lys Asn Gln Val
    290                 295                 300

Phe Leu Glu Met Asn Ser Leu Gln Ala Glu Asp Thr Ala Met Tyr Tyr
305                 310                 315                 320

Cys Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Ala Trp Gly
                325                 330                 335

Cys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
            340                 345                 350

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Ile Gln Glu Ser
        355                 360                 365

Ala Leu Thr Thr Pro Pro Gly Glu Thr Val Thr Leu Thr Cys Gly Ser
    370                 375                 380

Ser Thr Gly Ala Val Thr Ala Ser Asn Tyr Ala Asn Trp Val Gln Glu
385                 390                 395                 400
```

```
Lys Pro Asp His Cys Phe Thr Gly Leu Ile Gly Gly His Asn Asn Arg
                405                 410                 415


Pro Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys
            420                 425                 430


Ala Ala Leu Thr Ile Ala Gly Thr Gln Thr Glu Asp Glu Ala Ile Tyr
        435                 440                 445


Phe Cys Ala Leu Trp Tyr Ser Asp His Trp Val Ile Gly Gly Gly Thr
    450                 455                 460


Arg Leu Thr Val Leu Gly
465                 470


<210>  72
<211>  450
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HER2-C825 Heavy Chain sequence

<400>  72

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


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


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


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


Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
```

```
65                  70                  75                  80

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

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

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

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

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

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

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

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

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

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

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
```

```
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
```

450