SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha
<120> ANTI-GLYPICAN-3 ANTIBODY HAVING IMPROVED KINETICS IN PLASMA
<130> PCG-9023WO
<150> JP 2007-256063
<151> 2007-09-28
<160> 35
<170> PatentIn version 3.1
<210> 1
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 1
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 2
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 2
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Ile Arg Gln Pro Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 3
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 3
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Met
35 40 45
Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Ser Phe
50 55 60
Gln Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 4
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 4
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Ala Leu Asn Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Arg Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 5
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 5
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Ser Phe
50 55 60
Gln Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 6
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody H chain
<400> 6
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Asn Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Arg Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 7
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 7
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 8
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 8
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 9
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 9
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Glu Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80
Ser Ser Leu Gln Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 10
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 10
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ala Ser Arg Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Arg Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 11

<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 11
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Glu Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80
Ser Ser Leu Gln Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110
<210> 12
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Humanized antibody L chain
<400> 12
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ala Ser Arg Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Arg Gly Thr Lys Leu Glu Ile Lys
100 105 110
<210> 13
<211> 545
<212> PRT
<213> homo sapiens
<400> 13
Gln Pro Pro Pro Pro Pro Pro Asp Ala Thr Cys His Gln Val Arg Ser
1 5 10 15
Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp Val Pro Glu Thr Pro
20 25 30
Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro Lys Gly Pro Thr Cys
35 40 45
Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu Thr Ala Arg Leu Asn
50 55 60
Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu Leu Lys Phe Leu Ile
65 70 75 80
Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe Glu Ile Val Val Arg
85 90 95
His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys Asn Asn Tyr Pro Ser
100 105 110
Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu Phe Phe Thr Asp Val
115 120 125
Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val Asp Asp Met Val Asn
130 135 140
Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr Thr Gln Leu Met Asn
145 150 155 160
Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn Glu Cys Leu Arg Gly
165 170 175
Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe Pro Lys Leu Ile Met
180 185 190
Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg Ile Phe Leu Gln Ala
195 200 205
Leu Asn Leu Gly Ile Glu Val Ile Asn Thr Thr Asp His Leu Lys Phe
210 215 220
Ser Lys Asp Cys Gly Arg Met Leu Thr Arg Met Trp Tyr Cys Ser Tyr
225 230 235 240
Cys Gln Gly Leu Met Met Val Lys Pro Cys Gly Gly Tyr Cys Asn Val

```
                245                 250                 255
Val Met Gln Gly Cys Met Ala Gly Val Val Glu Ile Asp Lys Tyr Trp
            260                 265                 270
Arg Glu Tyr Ile Leu Ser Leu Glu Glu Leu Val Asn Gly Met Tyr Arg
        275                 280                 285
Ile Tyr Asp Met Glu Asn Val Leu Leu Gly Leu Phe Ser Thr Ile His
    290                 295                 300
Asp Ser Ile Gln Tyr Val Gln Lys Asn Ala Gly Lys Leu Thr Thr Thr
305                 310                 315                 320
Ile Gly Lys Leu Cys Ala His Ser Gln Gln Arg Gln Tyr Arg Ser Ala
                325                 330                 335
Tyr Tyr Pro Glu Asp Leu Phe Ile Asp Lys Lys Val Leu Lys Val Ala
            340                 345                 350
His Val Glu His Glu Glu Thr Leu Ser Ser Arg Arg Arg Glu Leu Ile
        355                 360                 365
Gln Lys Leu Lys Ser Phe Ile Ser Phe Tyr Ser Ala Leu Pro Gly Tyr
    370                 375                 380
Ile Cys Ser His Ser Pro Val Ala Glu Asn Asp Thr Leu Cys Trp Asn
385                 390                 395                 400
Gly Gln Glu Leu Val Glu Arg Tyr Ser Gln Lys Ala Ala Arg Asn Gly
                405                 410                 415
Met Lys Asn Gln Phe Asn Leu His Glu Leu Lys Met Lys Gly Pro Glu
            420                 425                 430
Pro Val Val Ser Gln Ile Ile Asp Lys Leu Lys His Ile Asn Gln Leu
        435                 440                 445
Leu Arg Thr Met Ser Met Pro Lys Gly Arg Val Leu Asp Lys Asn Leu
    450                 455                 460
Asp Glu Glu Gly Phe Glu Ala Gly Asp Cys Gly Asp Asp Glu Asp Glu
465                 470                 475                 480
Cys Ile Gly Gly Ala Gly Asp Gly Met Ile Lys Val Lys Asn Gln Leu
                485                 490                 495
Arg Phe Leu Ala Glu Leu Ala Tyr Asp Leu Asp Val Asp Asp Ala Pro
            500                 505                 510
Gly Asn Ser Gln Gln Ala Thr Pro Lys Asp Asn Glu Ile Ser Thr Phe
        515                 520                 525
His Asn Leu Gly Asn Val His Ser Pro Leu Lys His His His His His
    530                 535                 540
His
545
```

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 14
ggatcctgcg catgaaaaag cctgaactca cc 32

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 15
gcggccgcct attcctttgc cctcggacg 29

<210> 16
<211> 10939
<212> DNA
<213> Cricetulus griseus
<400> 16

```
gagctcaatt aaccctcact aaagggagtc gactcgatcc tttacagaaa acttgcaaac     60
cctcttggag tagaaaagta gtagtatctg acacaagtat cagcaaaatg caaacttctc    120
cccatcccca gaaaaccatt ataaaaaccc ccatatctta tgcccaactg tagtgatata    180
ttatttatga tttattaaaa cttgcttaag gattcagaaa gcaaagtcag ccttaagcta    240
tagagaccag gcagtcagtg gtggtacaca cctttaatcc caggactcag gattaagaag    300
tagacggacc tctgttagtt caagtctacc attacctaca caagagtgaa gagtaaccga    360
tctcatgcct ttgatcccag cagctgggat catgtgcatt caatcccagc attcgggagt    420
tatataagac aggagcaagg tctcagagct ggcattcatt ctccagccac attgaggata    480
ggaaaacatt gaagtgtcag gatgctgagg agaggcagca gtttgaggtt tggtagaacc    540
aggatcacct tttggtctga ggtagagtaa gaactgtggc tggctgcttt gcttttctga    600
tcttcagctt gaagcttgaa ctccaatatt tgtctctggg tctattatta tcatgttaca    660
cctaacttta aagctgattt acgcaagaca gttgtaggtg gacctttctt tcctgcccac    720
cagttcccaa ataactgaca cggagactca atattaatta taaatgattg gttaatagct    780
cagtcttgtt actggctaac tcttacattt taaattaact catttccatc cctttacttg    840
ctgccatgtg gttcatggct tgttcaagtc ctgcttcttc tgtctctggc tggtgatgcc    900
tctggttctg ccctttatcc cagaattctc ctagtctggc tctcctgccc agctataggc    960
cagtcagctg tttattaacc aatgagaata atacatattt atagtgtaca aagattgctc   1020
```

ctcaacaccc aatttttttat gtgcaacctg agaatctgga ctcattgccc tcatgcttgc 1080
agaggcggca cccttaccca ctaagccacc tttctagccc tgttgctttt gtttttgag 1140
acaggttcca ctatgtagcc caggctggcc tcaaactgac cattctcctg cctaaacctc 1200
ccgaacactg gaattatagt caaggcctac ctgccctggc attttcacac ttttatttcc 1260
tggctgagtc cattgacttt acactcatca aggttgaacc agttggagtt taattacagt 1320
gccaatcgca ctgaatccca cataatcaaa caacttcaag gaagcaaaaa accagttttt 1380
cctgaagatc aatgtcagct tgcctgattc agaatagacc cccgaaaaaa ggcaaatgct 1440
tgataaccaa tttcttctta ttgttcaatc ccctgctgct gtgtgtaagc tcctgagaaa 1500
ggacagtaag gggacattca tgatcagaga aagagcccca actccccccc cagccccacc 1560
cccaccctgt ccacagtctg ttggtttggt ttccccctgg ctgacaccca gaaatcacaa 1620
cataatcacc taggtcactg taacaagttc ctttctggaa aatgctacaa atgatattgg 1680
taacatgagt aatgaataat gcctggagtc caactccctt gtgacccagc aatgttttcc 1740
gtgggtgctc ccttccccag ctgcaggcct gacatgtacc ttaaaaagcc tcccctggag 1800
gacagaattt tgtgggtact atagtgttct cacaaatact tcccctaata cccttactta 1860
gttaccataa ataacatgca gcccctggtg aggcacacag ggctccaatg tacagcttct 1920
cagacactgc aggaaccttc ctctcctaat gcagcactgg tctcttcagg ctggacagca 1980
ggaacccata ccactccaat cctagtgtgg agtagagctg tctacgaaaa ccagcagatc 2040
tatagctaaa tgtgtttcaa ttttatgctt tgacaaattg tactgacccc acccccaccc 2100
cttccccctt gctgtgctgg gaattgaacc caggaccttg tgcatgccag gcaagtactc 2160
taacactgag ctatagcccc aatctttcat ccaagtctct atgtgtgccc acactcgctt 2220
tttattttga gacaaaaggt tcttattttg agataaggtc tcactatgtt gccttgactt 2280
ttttttttt ttttttttga acttttgacc ttcctacctc agctgagact acaagtcttt 2340
taccatcagg cccggctgat ggtaaaataa cagtatttga aatagtttaa acacatcatc 2400
ttaatggtca accacacaat ttccgaaatg ttgctggctc agtctggggc aaacctgtcc 2460
gccccaacat tggtgctagg aagaaagcac agacaagtag ccctcccagc tcaggagtaa 2520
aagacctgga gggggtggcc cacttcggtc aagttcacgg gatggggagg ggtaccctcc 2580
tccagtagtg gtggtatttg gcagttcctc caccgacgcc ctctggaagc acctgcttgg 2640
acccgcaaag ccaggaatgc agcttcctca agggactcgc cagcgagggt aacaggacag 2700
aggcgtccca agagggctgg ggcggaaggg ggaagacagg gtcggcctta gatagggcaa 2760
agggccttct ggctgtgttc ccggggtaac cgccccacca cgcctggagc ccgacgtggc 2820
gagcgatggg gacagcgagc aggaagtcgt actggggagg gccgcgtagc agatgcagcc 2880
gagggcggcg ctgccaggta cacccgaggg caccgcgggg gtgagcgcca ggtccctgaa 2940
ccagccaggc ctccagagcc gagtccggcg gaccgacggt acgttctgga atgggaaggg 3000
atccgggaca ccgaattgct gcattgaggg gctcagaggt tctgatgtgg gagtccagaa 3060
agggttttat ctaccggagg tgatgtgact tccggcctct ggaagtgctg ttggagtctc 3120
tgggaccttg ggtcctctcg actaggtttg gaaggggtga aataggggta gggagaaagg 3180
agaggactgc agcaatgtct tcccgaacga cctgggttcg ggaggggtcg aaggacaagg 3240
ggctgttgtg gggggtcttc agacgcggag gggtggtatt ctattttctg ggaagatggt 3300
gtcgatgcac ttgaccaagt ctagtcgatc tgaagaggct aggggaacag acagtgagag 3360
aggatggtgg agggagtggc agaacccttc cagaaactgg gagaggctct agcacctgca 3420
acccttccc tggcctccgg ggagtcccag aagagggcag gaccatggac acaggtgcat 3480
tcgtgccggc gcgctccggc ctggcgaagg tgcgcgctct tggaggccgc gggagggcca 3540
gacgcgcgcc cggagagctg gccctttaag gctacccgga ggcgtgtcag gaaatgcgcc 3600
ctgagcccgc ccctcccgga acgcggcccg agacctggca agctgagacg gaactcggaa 3660
ctagcactcg gctcgcggcc tcggtgaggc cttgcgcccg ccatgcctct gtcattgccc 3720
ctcgggccgc ctccctgaac ctccgtgacc gccctgcagt cctccctccc ccccttcgac 3780
tcggcgggcg cttccgggcg ctcccgcagc ccgccctcca cgtagcccac acctccctct 3840
cggcgctccg cttcccacgc ggtccccgac ctgttctttc ctcctccacc ctgcccttct 3900
gtcccctctcc cttcctttct cccctcgact cgtccctatt aggcaacagc ccctgtggtc 3960
cagccggcca tggctgtcaa ggctcacacc cttagctagg ccccttctcc cttccctggg 4020
tcttgtctca tgacccccctg ccccgcccgg gagcgagcgc gatgtggagc agtgcctctg 4080
gcaagcagaa cttcacccaa gccatgtgac aattgaaggc tgtaccccca gaccctaaca 4140
tcttggagcc ctgtagacca gggagtgctt ctggccgtgg ggtgacctag ctcttctacc 4200
accatgaaca gggcccctct gaagcggtcc aggatcctgc gcatggcgct gactggaggc 4260
tccactgcct ctgaggaggc agatgaagac agcaggaaca agccgtttct gctgcgggcg 4320
ctgcagatcg cgctggtcgt ctctctctac tgggtcacct ccatctccat ggtattcctc 4380
aacaagtacc tgctggacag cccctccctg cagctggata cccctatctt cgtcactttc 4440
taccaatgcc tggtgacctc tctgctgtgc aagggcctca gcactctggc cacctgctgc 4500
cctggcaccg ttgacttccc caccctgaac ctggacctta aggtggcccg cagcgtgctg 4560
ccactgtcgg tagtcttcat tggcatgata agtttcaata acctctgcct caagtacgta 4620
ggggtggcct tctacaacgt ggggcgctcg ctcaccaccg tgttcaatgt gcttctgtcc 4680
tacctgctgc tcaaacagac cacttccttc tatgccctgc tcacatgtgg catcatcatt 4740
ggtgagtggg gcccgggggc tgtgggagca ggatgggcat cgaactgaag ccctaaaggt 4800
caacactgta ggtaccttta cttactgtcc caggtccctt gcatcagcag ttacaggaag 4860
agccctgtag aaaacaaata acttccttat ggtcattcaa caagttaggg acccagccag 4920
ggtgaaaata atgttagcag caactacagc aaagatggct ctcgccactt gcatgattaa 4980
aatgtgccag gtactcagat ctaagcattg gatccacatt aactcaacta atccctatta 5040
caaggtaaaa tatatccgaa ttttacagag ggaaaaccaa ggcacagaga ggctaagtag 5100
cttgaccagg atcacacagc taataatcac tgacatagct gggatttaaa cataagcagt 5160
tacctccata gatcacacta tgaccaccat gccactgttc cttctcaaga gttccaggat 5220
cctgtctgtc cagttctctt taaagaggac aacacatctg acattgctac cttgaggtaa 5280
catttgaaat agtgggtaga catatgtttt aagttttatt cttacttttt atgtgtgtgt 5340
gtttgggggg ccaccacagt gtatgggtgg agataagggg acaacttaag aattggtcct 5400
ttctcccacc acatgggtgc tgaggtctga actcaggtca tcaggattgg cacaaatccc 5460
tttacccact gagccatttc actggtccaa tatatgtgtg cttttaagag gctttaacta 5520
ttttcccaga tgtgaatgtc ctgctgatca ttatcccctt ttacccggaa gccctctggg 5580
aggtgccatc cctgtggtcg tctgcatacа aatggggaaa ctgcaactca gagaaacaag 5640

gctacttgcc agggccccac aagtaagata ggctgggatg ccatcccaga ctggccacac 5700
tccctggcct gtgcttcaag ccagtttact ttgttcctgc ccattggaag ttagcatgtt 5760
gcagtcaaac acaataacta caggccaaaa gtgcttttaa attaaagtca gatgaacttt 5820
taaacatcca gagctcctca actgcaggag ttacaacctg attctgcaac catctttgca 5880
gtgcccggta gtcatatgta gctagaggct cttggctagg acagcatgtg ttaggaaaca 5940
tctggccctg agatcattga attgagtgac tgctgggtga caaagaccaa ggcatccgtt 6000
ccctgagagt cctgggcaag cagcaatgtg accttcattt gtacctactc aggttcttta 6060
tctgtcctgt ttgacctact tagtctcctc tggtgtctca gaggcccagg ctgggtactc 6120
tggatgtcag gatcaggcca atgcgcacat ctgccctaga aatgtccccc tggttgagca 6180
gctcctgaat ccatcggtaa agggtctgga ccagggagga gtcagataaa aagctgacag 6240
cactgggggа ctccatgggg aactcccacc tgcccccaca catccatcct aagagaactg 6300
gtattccttg tttcctcttt gtcctacaag gcaccctggg atcccacttc agtctcccag 6360
ccttgccagg gttagagggc atgagcctcc ttgtggggaa tttagatgca agaaggtaca 6420
gtcactagag aacctgagct cagatcccca aagtaaccag tacctgatag tgaggcagct 6480
gagaaccgca gcagcctgcc tgagtggctg aactctgcgg cctccggaac tggccccaac 6540
tgttgggtct cctcttcctt cctcctgtga gggagggccc atctctgata agtgctgtgg 6600
ggactctaga gtagggagga ggaggagcaa tctaagcagg ccttactgag aagtccttgc 6660
tggcatgtgg ctgcctgagg agtacagact gggaacaccc atttgaatga gtaaggtttt 6720
tcctgaaggc catggggagc cacggaggaa aatcatttta gttacaagac aaagagtaga 6780
ttggttaaca tgggagcaag gacatggccc caattttcat agatgaagga aattggaact 6840
cagagaggtt aagtaacttc tcccaaatag ctcagcttca aaatcacaga acagtcagag 6900
tctagatctc tctgatgcct gtgatggtcc tgccattcca tgttgctgat ccctgtggca 6960
tcagtaagcc tctaccttgt gggaatgcag gatctaaatg aagagaggaa gtgctggccc 7020
catgctgtgg tctggaaagc tatgcaggct ctttgagcag agagtgaccc acaagtgaat 7080
agagtcctat gagactcaaa gcaacatcca cccttaagca gctctaacca aatgctcaca 7140
ctgagggagc caaagccaag ttagagtcct gtgcttgccc aaggtcactt tgcctggccc 7200
tcctcctata gcacccgtgt tatcttatag ccctcattac agtgattaca attataatta 7260
gagaggtaac agggccacac tgtccttaca cattcccctg ctagattgta gctgggagag 7320
ggggagatgt aggtggctgg gggagtggga gggaagatgc agattttcat tctgggctct 7380
actccctcag ccatttttтg gtgtgggagt tagactttgg atatgttgat gatgaggtaa 7440
gggccacaga acagtctgaa ctgtggtatc agaatcctgt ccctctccct ctctcctcat 7500
ccctcttcac cttgtcactc ctctgtctgc tacaggtggt ttctggctgg gtatagacca 7560
agagggagct gagggcaccc tgtccctcat aggcaccatc ttcggggtgc tggccagcct 7620
ctgcgtctcc ctcaatgcca tctataccaa gaaggtgctc ccagcagtgg acaacagcat 7680
ctggcgccta accttctata acaatgtcaa tgcctgtgtg ctcttcttgc ccctgatggt 7740
tctgctgggt gagctccgtg ccctccttga ctttgctcat ctgtacagtg cccacttctg 7800
gctcatgatg acgctgggtg gcctcttcgg ctttgccatt ggctatgtga caggactgca 7860
gatcaaattc accagtcccc tgacccacaa tgtatcaggc acagccaagg cctgtgcgca 7920
gacagtgctg gccgtgctct actatgaaga gactaagagc ttcctgtggt ggacaagcaa 7980
cctgatggtg ctgggtggct cctcagccta tacctgggtc aggggctggg agatgcagaa 8040
gacccaagag gaccccagct ccaaagaggg tgagaagagt gctattgggg tgtgagcttc 8100
ttcagggacc tgggactgaa cccaagtggg gcctacacag cactgaaggc ttcccatgga 8160
gctagccagt gtggccctga gcaatactgt ttacatcctc cttggaatat gatctaagag 8220
gagccagggt ctttcctggt aatgtcagaa agctgccaaa tctcctgtct gccccatctt 8280
gttttgggaa aaccctacca ggaatggcac ccctacctgc ctcctcctag agcctgtcta 8340
cctccatatc atctctgggg ttgggaccag ctgcagcctt aaggggctgg attgatgaag 8400
tgatgtcttc tacacaaggg agatgggttg tgatcccact aattgaaggg atttgggtga 8460
ccccacacct ctgggatcca gggcaggtag agtagtagct taggtgctat taacatcagg 8520
aacacctcag cctgcctttg aagggaagtg ggagcttggc caagggagga aatggccatt 8580
ctgccctctt cagtgtggat gagtatggca gacctgttca tggcagctgc accctggggt 8640
ggctgataag aaaacattca cctctgcatt tcatatttgc agctctagaa cgggggagag 8700
ccacacatct tttacgggtt aagtagggtg atgagctcct ccgcagtccc taaccccagc 8760
tttacctgcc tggcttccct tggcccagct acctagctgt actccctttc tgtactcttc 8820
tcttctccgt catggcctcc cccaacacct ccatctgcag gcaggaagtg gagtccactt 8880
gtaacctctg ttcccatgac agagcccttt gaatacctga acccctcatg acagtaagag 8940
acatttatgt tctctggggc tggggctgaa ggagcccact ggttctcact tagcctatct 9000
ggctcctgtc acaaaaaaaa aaaaagaaaa aaaaaaagca taaaccaagt tactaagaac 9060
agaagttggt ttataacgtt ctggggcagc aaagcccaga tgaagggacc catcgaccct 9120
ctctgtccat atcctcatgc tgcagaagta caggcaagct cctttaagcc tcatatagga 9180
acactagcct cactcatgag ggttttactc catgacctgt caacctcaaa gccttcaaca 9240
tgaggactcc aacgtaaatt tggggacaga agcactcaga ccatacccca gcaccacacc 9300
ctcctaacct cagggtagct gtcattctcc tagtctcctc tcttgggcct ttagaacccc 9360
catttccttg gggtaatgtc tgatgttttt gtccctgtca taaaaagatg gagagactgt 9420
gtccagcctt tgattcctac ttcctacaat cccaggttct aatgaagttt gtgggggcctg 9480
atgccctgag ttgtatgtga tttaataata aaaaagcaag atacagcatg tgtgtggact 9540
gagtgagggc cacagggatc taaaagccaa gtgtgagggg acccagctac agcaggcagc 9600
atcctgagcc tggaatctct tcaggacaag aattctccat atacctacct actctgggga 9660
gtaggtggcc agagttcaag cttcccttag taccaactac cactggctgt gctcttactg 9720
aaggcagaca tggcactgag tgctgtccat ctgtcactca tctccacagc cattcctaat 9780
gtgtggggtg ggagccatca ccaaacccca ttttcagata aggacacagg ctcagagagg 9840
cttgtgtgga gaaaagtagc agcagaattc agagagctgg gtctcctgca gcaccttgga 9900
ctgccagcag ccacagtgct tgtcacacag cacatactca aaagaatgcc agcccctca 9960
gcctagagtg cctggccttt ctttcagatg aggaagaggg tcaaagctgt tagcttgccc 10020
accatatgac cacatacatg accaacagct tgagggaggg aggattactg tggctcccag 10080
cctgagaggt gggacaccca aatgtattag gtccttgaat cagggctgac cttgtgattc 10140
agtcactcct accagaatgc tggggaatgg ggatgccaaa ggcaaaggag gctttctaag 10200
gtgtggtgta agataggcat ttctgcttcc atgtacacct gtgagcagag taggaaggcc 10260

ctgtggagaa tatatcccac aaaccagtag cccttcctgg cagtgggtga atactgccac 10320
cctataccc tatgcaaggc cagtagaacc acccaaccca caacatctag agaaattaca 10380
ggtcatctta agcctctaaa ttgtggagaa actcgacatg cgcacgattc ctaacctgct 10440
agcctagggt gcggggtgga taatttaagg aaactggggt ttcttataga atcggaggct 10500
ccatgaagtc accctgacaa gaggtcagca atagccagca gcagtggcta ctcctaagcc 10560
tccagacaga gcaccctgtg aatgtacctt attctcacat ctgggtgtct ataggtgtga 10620
ctgggtcaga tgtcacccag gccattgcaa tgggccctta gccccatggg gtgttgggat 10680
agcagccaag cagctcccat gctgagatac tgcctgcagt agactgatgg ataagaaaac 10740
aaggcccaaa atgttttctt tccagacttg atctttcttt gttcaaaaat gctgttttcc 10800
cttaaacttg cccaaaccca ttgttttgca gttgaggaaa ataaggcata gaaagattaa 10860
aggaagtttc tgaggttaca gagcaaagta ctggcttcac ctgaaataga caggtgtgcc 10920
ctgatcctga tttgagctc 10939

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 17
atgcatgcca ccatgaaaaa gcctgaactc acc 33

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 18
ggatcccagg ctttacactt tatgcttc 28

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 19
gctgtctgga gtactgtgca tctgc 25

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 20
ggaatgcagc ttcctcaagg gactcgc 27

<210> 21
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 21
tgcatcaggt cggagacgct gtcgaac 27

<210> 22
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 22
gcactcgtcc gagggcaaag gaatagc 27

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 23
tgtgctggga attgaaccca ggac 24

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 24
ctacttgtct gtgctttctt cc 22

<210> 25

<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 25
ctcgactcgt ccctattagg caacagc 27
<210> 26
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 26
tcagaggcag tggagcctcc agtcagc 27
<210> 27
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 27
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Glu Ser Phe
50 55 60
Gln Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115
<210> 28
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 28
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Gln Ala Ser Glu Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
85 90 95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110
<210> 29
<211> 112
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 29
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Gln Ala Ser Glu Ser Leu Val His Ser
20 25 30
Asn Arg Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn

```
                85                  90                  95
Thr His Val Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu
            100                 105                 110
<210>  30
<211>  327
<212>  PRT
<213>  homo sapiens
<400>  30
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
Leu Ser Leu Ser Leu Gly Lys
                325
<210>  31
<211>  330
<212>  PRT
<213>  homo sapiens
<400>  31
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175
```

```
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 32
<211> 328
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 32

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
Gln Lys Ser Leu Ser Leu Ser Pro
                325
```

<210> 33
<211> 328
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 33

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

```
1               5                   10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140
Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
145                 150                 155                 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
225                 230                 235                 240
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
    290                 295                 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
Gln Lys Ser Leu Ser Leu Ser Pro
                325
```

<210> 34
<211> 443
<212> PRT
<213> Artificial Sequence
<220>
<223> Modified antibody
<400> 34

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30
Glu Met His Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
        35                  40                  45
Gly Ala Ile Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Glu Ser Phe
    50                  55                  60
Gln Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
```

225 230 235 240
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440

〈210〉 35
〈211〉 443
〈212〉 PRT
〈213〉 Artificial Sequence
〈220〉
〈223〉 Modified antibody
〈400〉 35

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

```
                340                 345                 350
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440
```