SEQUENCE LISTING

<110> Corat Therapeutics GmbH

<120> Therapeutic antibodies with neutralizing activity against SARS-CoV-2 Glycoprotein S

<130> WIPO (to be assigned)

<140> PCT Application Number (to be assigned)
<141> 2021-05-19

<150> EP20178386.7
<151> 2020-06-04

<150> EP20178327.1
<151> 2020-06-04

<150> EP20179323.9
<151> 2020-06-10

<150> EP20180942.3
<151> 2020-06-18

<150> EP20184057.6
<151> 2020-07-03

<150> EP20210462.6
<151> 2020-11-27

<150> EP20210803.1
<151> 2020-11-30

<160> 1844

<170> PatentIn version 3.5

<210> 1
<211> 3822
<212> DNA
<213> SARS-CoV-2

<400> 1
atgtttgttt ttcttgtttt attgccacta gtctctagtc agtgtgttaa tcttacaacc 60

agaactcaat tacccctgc atacactaat tctttcacac gtggtgttta ttaccctgac 120

aaagttttca gatcctcagt tttacattca actcaggact tgttcttacc tttcttttcc 180

aatgttactt ggttccatgc tatacatgtc tctgggacca atggtactaa gaggtttgat 240

aaccctgtcc taccatttaa tgatggtgtt tattttgctt ccactgagaa gtctaacata 300

ataagaggct ggatttttgg tactacttta gattcgaaga cccagtccct acttattgtt 360

aataacgcta ctaatgttgt tattaaagtc tgtgaatttc aattttgtaa tgatccattt 420

ttgggtgttt attaccacaa aaacaacaaa agttggatgg aaagtgagtt cagagtttat 480

tctagtgcga ataattgcac ttttgaatat gtctctcagc cttttcttat ggaccttgaa 540

ggaaaacagg gtaatttcaa aaatcttagg gaatttgtgt ttaagaatat tgatggttat 600

tttaaaatat attctaagca cacgcctatt aatttagtgc gtgatctccc tcagggtttt 660

tcggctttag aaccattggt agatttgcca ataggtatta acatcactag gtttcaaact 720

ttacttgctt tacatagaag ttatttgact cctggtgatt cttcttcagg ttggacagct 780

ggtgctgcag cttattatgt gggttatctt caacctagga cttttctatt aaaatataat 840

gaaaatggaa ccattacaga tgctgtagac tgtgcacttg accctctctc agaaacaaag 900

tgtacgttga aatccttcac tgtagaaaaa ggaatctatc aaacttctaa ctttagagtc 960

caaccaacag aatctattgt tagatttcct aatattacaa acttgtgccc ttttggtgaa 1020

gtttttaacg ccaccagatt tgcatctgtt tatgcttgga acaggaagag aatcagcaac 1080

tgtgttgctg attattctgt cctatataat tccgcatcat tttccacttt taagtgttat 1140

ggagtgtctc ctactaaatt aaatgatctc tgctttacta atgtctatgc agattcattt 1200

gtaattagag gtgatgaagt cagacaaatc gctccagggc aaactggaaa gattgctgat 1260

tataattata aattaccaga tgattttaca ggctgcgtta tagcttggaa ttctaacaat 1320

cttgattcta aggttggtgg taattataat tacctgtata gattgtttag gaagtctaat 1380

ctcaaacctt ttgagagaga tatttcaact gaaatctatc aggccggtag cacaccttgt 1440

aatggtgttg aaggttttaa ttgttacttt cctttacaat catatggttt ccaacccact 1500

aatggtgttg gttaccaacc atacagagta gtagtacttt cttttgaact tctacatgca 1560

ccagcaactg tttgtggacc taaaaagtct actaatttgg ttaaaaacaa atgtgtcaat 1620

ttcaacttca atggtttaac aggcacaggt gttcttactg agtctaacaa aaagtttctg 1680

cctttccaac aatttggcag agacattgct gacactactg atgctgtccg tgatccacag 1740

acacttgaga ttcttgacat tacaccatgt tcttttggtg gtgtcagtgt tataacacca 1800

ggaacaaata cttctaacca ggttgctgtt ctttatcagg atgttaactg cacagaagtc 1860

cctgttgcta ttcatgcaga tcaacttact cctacttggc gtgtttattc tacaggttct 1920

aatgtttttc aaacacgtgc aggctgttta ataggggctg aacatgtcaa caactcatat 1980

gagtgtgaca tacccattgg tgcaggtata tgcgctagtt atcagactca gactaattct 2040

cctcggcggg cacgtagtgt agctagtcaa tccatcattg cctacactat gtcacttggt 2100

gcagaaaatt cagttgctta ctctaataac tctattgcca tacccacaaa ttttactatt 2160

agtgttacca cagaaattct accagtgtct atgaccaaga catcagtaga ttgtacaatg 2220

tacatttgtg gtgattcaac tgaatgcagc aatcttttgt tgcaatatgg cagtttttgt 2280

acacaattaa accgtgcttt aactggaata gctgttgaac aagacaaaaa cacccaagaa 2340

gtttttgcac aagtcaaaca aatttacaaa acaccaccaa ttaaagattt tggtggtttt 2400

aatttttcac aaatattacc agatccatca aaaccaagca agaggtcatt tattgaagat 2460

ctacttttca acaaagtgac acttgcagat gctggcttca tcaaacaata tggtgattgc 2520

cttggtgata ttgctgctag agacctcatt tgtgcacaaa agtttaacgg ccttactgtt 2580

ttgccacctt tgctcacaga tgaaatgatt gctcaataca cttctgcact gttagcgggt 2640

acaatcactt ctggttggac ctttggtgca ggtgctgcat tacaaatacc atttgctatg 2700

caaatggctt ataggtttaa tggtattgga gttacacaga atgttctcta tgagaaccaa 2760

aaattgattg ccaaccaatt taatagtgct attggcaaaa ttcaagactc actttcttcc 2820

acagcaagtg cacttggaaa acttcaagat gtggtcaacc aaaatgcaca agctttaaac 2880

acgcttgtta aacaacttag ctccaatttt ggtgcaattt caagtgtttt aaatgatatc 2940

ctttcacgtc ttgacaaagt tgaggctgaa gtgcaaattg ataggttgat cacaggcaga 3000

cttcaaagtt tgcagacata tgtgactcaa caattaatta gagctgcaga aatcagagct 3060

tctgctaatc ttgctgctac taaaatgtca gagtgtgtac ttggacaatc aaaaagagtt 3120

gatttttgtg gaaagggcta tcatcttatg tccttccctc agtcagcacc tcatggtgta 3180

gtcttcttgc atgtgactta tgtccctgca caagaaaaga acttcacaac tgctcctgcc 3240

atttgtcatg atggaaaagc acactttcct cgtgaaggtg tctttgtttc aaatggcaca 3300

cactggtttg taacacaaag gaatttttat gaaccacaaa tcattactac agacaacaca 3360

tttgtgtctg gtaactgtga tgttgtaata ggaattgtca acaacacagt ttatgatcct 3420

ttgcaacctg aattagactc attcaaggag gagttagata aatattttaa gaatcataca 3480

tcaccagatg ttgatttagg tgacatctct ggcattaatg cttcagttgt aaacattcaa 3540

aaagaaattg accgcctcaa tgaggttgcc aagaatttaa atgaatctct catcgatctc 3600

caagaacttg gaaagtatga gcagtatata aaatggccat ggtacatttg gctaggtttt 3660

atagctggct tgattgccat agtaatggtg acaattatgc tttgctgtat gaccagttgc 3720

tgtagttgtc tcaagggctg ttgttcttgt ggatcctgct gcaaatttga tgaagacgac 3780

tctgagccag tgctcaaagg agtcaaatta cattacacat aa 3822

<210> 2
<211> 1273
<212> PRT
<213> SARS-CoV-2

<400> 2

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr

```
145                 150                 155                 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
                165                 170                 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
            180                 185                 190

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

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
    210                 215                 220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
225                 230                 235                 240

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
                245                 250                 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
            260                 265                 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
        275                 280                 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
    290                 295                 300

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

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
                325                 330                 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
            340                 345                 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
        355                 360                 365
```

```
Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
    370                 375                 380

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

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
                405                 410                 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
            420                 425                 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
        435                 440                 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
    450                 455                 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465                 470                 475                 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
                485                 490                 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
            500                 505                 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
        515                 520                 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
    530                 535                 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545                 550                 555                 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
                565                 570                 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
```

```
            580                 585                 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
        595                 600                 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
    610                 615                 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625                 630                 635                 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
                645                 650                 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
            660                 665                 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
        675                 680                 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
    690                 695                 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705                 710                 715                 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
                725                 730                 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
            740                 745                 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
        755                 760                 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
    770                 775                 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
785                 790                 795                 800
```

```
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
                805                 810                 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
            820                 825                 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
        835                 840                 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
    850                 855                 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
865                 870                 875                 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
                885                 890                 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
            900                 905                 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
        915                 920                 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
    930                 935                 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945                 950                 955                 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
                965                 970                 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
            980                 985                 990

Ile Asp Arg Leu Ile Thr Gly Arg  Leu Gln Ser Leu Gln  Thr Tyr Val
        995                 1000                1005

Thr Gln  Gln Leu Ile Arg Ala  Ala Glu Ile Arg Ala  Ser Ala Asn
```

```
    1010                1015                1020

Leu Ala  Ala Thr Lys Met Ser  Glu Cys Val Leu Gly  Gln Ser Lys
    1025                1030                1035

Arg Val  Asp Phe Cys Gly Lys  Gly Tyr His Leu Met  Ser Phe Pro
    1040                1045                1050

Gln Ser  Ala Pro His Gly Val  Val Phe Leu His Val  Thr Tyr Val
    1055                1060                1065

Pro Ala  Gln Glu Lys Asn Phe  Thr Thr Ala Pro Ala  Ile Cys His
    1070                1075                1080

Asp Gly  Lys Ala His Phe Pro  Arg Glu Gly Val Phe  Val Ser Asn
    1085                1090                1095

Gly Thr  His Trp Phe Val Thr  Gln Arg Asn Phe Tyr  Glu Pro Gln
    1100                1105                1110

Ile Ile  Thr Thr Asp Asn Thr  Phe Val Ser Gly Asn  Cys Asp Val
    1115                1120                1125

Val Ile  Gly Ile Val Asn Asn  Thr Val Tyr Asp Pro  Leu Gln Pro
    1130                1135                1140

Glu Leu  Asp Ser Phe Lys Glu  Glu Leu Asp Lys Tyr  Phe Lys Asn
    1145                1150                1155

His Thr  Ser Pro Asp Val Asp  Leu Gly Asp Ile Ser  Gly Ile Asn
    1160                1165                1170

Ala Ser  Val Val Asn Ile Gln  Lys Glu Ile Asp Arg  Leu Asn Glu
    1175                1180                1185

Val Ala  Lys Asn Leu Asn Glu  Ser Leu Ile Asp Leu  Gln Glu Leu
    1190                1195                1200

Gly Lys  Tyr Glu Gln Tyr Ile  Lys Trp Pro Trp Tyr  Ile Trp Leu
    1205                1210                1215
```

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
    1220   1225   1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
    1235   1240   1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
    1250   1255   1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
    1265   1270

<210> 3
<211> 2010
<212> DNA
<213> SARS-CoV-2

<400> 3
gttaatctta caaccagaac tcaattaccc cctgcataca ctaattcttt cacacgtggt 60

gtttattacc ctgacaaagt tttcagatcc tcagttttac attcaactca ggacttgttc 120

ttacctttct tttccaatgt tacttggttc catgctatac atgtctctgg gaccaatggt 180

actaagaggt ttgataaccc tgtcctacca tttaatgatg gtgtttattt tgcttccact 240

gagaagtcta acataataag aggctggatt tttggtacta ctttagattc gaagacccag 300

tccctactta ttgttaataa cgctactaat gttgttatta aagtctgtga atttcaattt 360

tgtaatgatc catttttggg tgtttattac cacaaaaaca acaaaagttg gatggaaagt 420

gagttcagag tttattctag tgcgaataat tgcacttttg aatatgtctc tcagcctttt 480

cttatggacc ttgaaggaaa acagggtaat ttcaaaaatc ttagggaatt tgtgtttaag 540

aatattgatg gttattttaa aatatattct aagcacacgc ctattaattt agtgcgtgat 600

ctccctcagg gtttttcggc tttagaacca ttggtagatt tgccaatagg tattaacatc 660

actaggtttc aaactttact tgctttacat agaagttatt tgactcctgg tgattcttct 720

tcaggttgga cagctggtgc tgcagcttat tatgtgggtt atcttcaacc taggactttt 780

ctattaaaat ataatgaaaa tggaaccatt acagatgctg tagactgtgc acttgaccct 840

ctctcagaaa caaagtgtac gttgaaatcc ttcactgtag aaaaaggaat ctatcaaact 900

tctaacttta gagtccaacc aacagaatct attgttagat ttcctaatat tacaaacttg 960

tgccctttg gtgaagtttt taacgccacc agatttgcat ctgtttatgc ttggaacagg 1020

aagagaatca gcaactgtgt tgctgattat tctgtcctat ataattccgc atcattttcc 1080

acttttaagt gttatggagt gtctcctact aaattaaatg atctctgctt tactaatgtc 1140

tatgcagatt catttgtaat tagaggtgat gaagtcagac aaatcgctcc agggcaaact 1200

ggaaagattg ctgattataa ttataaatta ccagatgatt ttacaggctg cgttatagct 1260

tggaattcta acaatcttga ttctaaggtt ggtggtaatt ataattacct gtatagattg 1320

tttaggaagt ctaatctcaa acctttgag agagatattt caactgaaat ctatcaggcc 1380

ggtagcacac cttgtaatgg tgttgaaggt tttaattgtt actttccttt acaatcatat 1440

ggtttccaac ccactaatgg tgttggttac caaccataca gagtagtagt actttctttt 1500

gaacttctac atgcaccagc aactgtttgt ggacctaaaa agtctactaa tttggttaaa 1560

aacaaatgtg tcaatttcaa cttcaatggt ttaacaggca caggtgttct tactgagtct 1620

aacaaaaagt ttctgccttt ccaacaattt ggcagagaca ttgctgacac tactgatgct 1680

gtccgtgatc cacagacact tgagattctt gacattacac catgttcttt tggtggtgtc 1740

agtgttataa caccaggaac aaatacttct aaccaggttg ctgttcttta tcaggatgtt 1800

aactgcacag aagtccctgt tgctattcat gcagatcaac ttactcctac ttggcgtgtt 1860

tattctacag gttctaatgt ttttcaaaca cgtgcaggct gtttaatagg ggctgaacat 1920

gtcaacaact catatgagtg tgacataccc attggtgcag gtatatgcgc tagttatcag 1980

actcagacta attctcctcg gcgggcacgt 2010

<210> 4
<211> 670
<212> PRT
<213> SARS-CoV-2

<400> 4

Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
1 5 10 15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
20 25 30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr

```
        35                  40                  45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
    50                  55                  60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
65                  70                  75                  80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
                85                  90                  95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
            100                 105                 110

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

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
    130                 135                 140

Tyr Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe
145                 150                 155                 160

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
                165                 170                 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
            180                 185                 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu
        195                 200                 205

Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
    210                 215                 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
225                 230                 235                 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
                245                 250                 255
```

```
Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
            260                 265                 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
        275                 280                 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
    290                 295                 300

Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu
305                 310                 315                 320

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
                325                 330                 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
            340                 345                 350

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

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
    370                 375                 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
385                 390                 395                 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
                405                 410                 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
            420                 425                 430

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
        435                 440                 445

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

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
```

```
465                 470                 475                 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
                485                 490                 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
            500                 505                 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
        515                 520                 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
    530                 535                 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
545                 550                 555                 560

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

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
            580                 585                 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
        595                 600                 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
    610                 615                 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His
625                 630                 635                 640

Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys
                645                 650                 655

Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg
            660                 665                 670
```

<210> 5
<211> 669
<212> DNA

<213> SARS-CoV-2

<400> 5
agagtccaac caacagaatc tattgttaga tttcctaata ttacaaactt gtgccctttt 60

ggtgaagttt ttaacgccac agatttgca tctgtttatg cttggaacag gaagagaatc 120

agcaactgtg ttgctgatta ttctgtccta tataattccg catcattttc cacttttaag 180

tgttatggag tgtctcctac taaattaaat gatctctgct ttactaatgt ctatgcagat 240

tcatttgtaa ttagaggtga tgaagtcaga caaatcgctc cagggcaaac tggaaagatt 300

gctgattata attataaatt accagatgat tttacaggct gcgttatagc ttggaattct 360

aacaatcttg attctaaggt tggtggtaat tataattacc tgtatagatt gtttaggaag 420

tctaatctca aacctttga gagagatatt tcaactgaaa tctatcaggc cggtagcaca 480

ccttgtaatg gtgttgaagg ttttaattgt tactttcctt tacaatcata tggtttccaa 540

cccactaatg gtgttggtta ccaaccatac agagtagtag tactttcttt tgaacttcta 600

catgcaccag caactgtttg tggacctaaa aagtctacta atttggttaa aaacaaatgt 660

gtcaatttc 669

<210> 6
<211> 223
<212> PRT
<213> SARS-CoV-2

<400> 6

Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
1 5 10 15

Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
20 25 30

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
35 40 45

Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
50 55 60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65 70 75 80

```
Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
                85                  90                  95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
            100                 105                 110

Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly
        115                 120                 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
    130                 135                 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
145                 150                 155                 160

Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190

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

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe
    210                 215                 220
```

<210> 7
<211> 2418
<212> DNA
<213> Homo sapiens

<400> 7

```
atgtcaagct cttcctggct ccttctcagc cttgttgctg taactgctgc tcagtccacc       60

attgaggaac aggccaagac atttttggac aagtttaacc acgaagccga agacctgttc      120

tatcaaagtt cacttgcttc ttggaattat aacaccaata ttactgaaga gaatgtccaa      180

aacatgaata atgctgggga caaatggtct gccttttaa aggaacagtc cacacttgcc       240

caaatgtatc cactacaaga aattcagaat ctcacagtca agcttcagct gcaggctctt      300

cagcaaaatg ggtcttcagt gctctcagaa gacaagagca aacggttgaa cacaattcta      360
```

aatacaatga gcaccatcta cagtactgga aaagtttgta acccagataa tccacaagaa 420

tgcttattac ttgaaccagg tttgaatgaa ataatggcaa acagtttaga ctacaatgag 480

aggctctggg cttgggaaag ctggagatct gaggtcggca agcagctgag gccattatat 540

gaagagtatg tggtcttgaa aaatgagatg gcaagagcaa atcattatga ggactatggg 600

gattattgga gaggagacta tgaagtaaat ggggtagatg gctatgacta cagccgcggc 660

cagttgattg aagatgtgga acataccttt gaagagatta aaccattata tgaacatctt 720

catgcctatg tgagggcaaa gttgatgaat gcctatcctt cctatatcag tccaattgga 780

tgcctccctg ctcatttgct tggtgatatg tggggtagat tttggacaaa tctgtactct 840

ttgacagttc cctttggaca gaaaccaaac atagatgtta ctgatgcaat ggtggaccag 900

gcctgggatg cacagagaat attcaaggag gccgagaagt tctttgtatc tgttggtctt 960

cctaatatga ctcaaggatt ctgggaaaat tccatgctaa cggacccagg aaatgttcag 1020

aaagcagtct gccatcccac agcttgggac ctggggaagg gcgacttcag gatccttatg 1080

tgcacaaagg tgacaatgga cgacttcctg acagctcatc atgagatggg gcatatccag 1140

tatgatatgg catatgctgc acaacctttt ctgctaagaa atggagctaa tgaaggattc 1200

catgaagctg ttggggaaat catgtcactt tctgcagcca cacctaagca tttaaaatcc 1260

attggtcttc tgtcacccga ttttcaagaa gacaatgaaa cagaaataaa cttcctgctc 1320

aaacaagcac tcacgattgt tgggactctg ccatttactt acatgttaga gaagtggagg 1380

tggatggtct ttaaagggga aattcccaaa gaccagtgga tgaaaaagtg gtgggagatg 1440

aagcgagaga tagttggggt ggtggaacct gtgccccatg atgaaacata ctgtgacccc 1500

gcatctctgt tccatgtttc taatgattac tcattcattc gatattacac aaggaccctt 1560

taccaattcc agtttcaaga agcactttgt caagcagcta aacatgaagg ccctctgcac 1620

aaatgtgaca tctcaaactc tacagaagct ggacagaaac tgttcaatat gctgaggctt 1680

ggaaaatcag aaccctggac cctagcattg gaaaatgttg taggagcaaa gaacatgaat 1740

gtaaggccac tgctcaacta ctttgagccc ttatttacct ggctgaaaga ccagaacaag 1800

aattcttttg tgggatggag taccgactgg agtccatatg cagaccaaag catcaaagtg 1860

aggataagcc taaaatcagc tcttggagat aaagcatatg aatggaacga caatgaaatg 1920

tacctgttcc gatcatctgt tgcatatgct atgaggcagt acttttaaa agtaaaaaat 1980

cagatgattc tttttgggga ggaggatgtg cgagtggcta atttgaaacc aagaatctcc 2040

tttaatttct ttgtcactgc acctaaaaat gtgtctgata tcattcctag aactgaagtt 2100

gaaaaggcca tcaggatgtc ccggagccgt atcaatgatg ctttccgtct gaatgacaac 2160

agcctagagt ttctggggat acagccaaca cttggacctc ctaaccagcc ccctgtttcc 2220

atatggctga ttgtttttgg agttgtgatg ggagtgatag tggttggcat tgtcatcctg 2280

atcttcactg ggatcagaga tcggaagaag aaaaataaag caagaagtgg agaaaatcct 2340

tatgcctcca tcgatattag caaaggagaa aataatccag gattccaaaa cactgatgat 2400

gttcagacct ccttttag 2418

<210> 8
<211> 805
<212> PRT
<213> Homo sapiens

<400> 8

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala
1 5 10 15

Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe
20 25 30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
50 55 60

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

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln
85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser

```
        115                 120                 125

Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu
    130                 135                 140

Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu
145                 150                 155                 160

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

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
            180                 185                 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
        195                 200                 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu
    210                 215                 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu
225                 230                 235                 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile
                245                 250                 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
            260                 265                 270

Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
        275                 280                 285

Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
    290                 295                 300

Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
305                 310                 315                 320

Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
                325                 330                 335
```

```
Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
            340                 345                 350

Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
        355                 360                 365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
    370                 375                 380

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
385                 390                 395                 400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
                405                 410                 415

His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
            420                 425                 430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
        435                 440                 445

Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
    450                 455                 460

Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
465                 470                 475                 480

Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
                485                 490                 495

Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
            500                 505                 510

Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
        515                 520                 525

Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
    530                 535                 540

Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu
```

```
545                 550                 555                 560

Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
                565                 570                 575

Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
            580                 585                 590

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
        595                 600                 605

Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
    610                 615                 620

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
625                 630                 635                 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
                645                 650                 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
            660                 665                 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
        675                 680                 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
    690                 695                 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
705                 710                 715                 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
                725                 730                 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
            740                 745                 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
        755                 760                 765
```

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
785 790 795 800

Val Gln Thr Ser Phe
805

<210> 9
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 HCDR1 DNA

<400> 9
gacgcctgga tgacc 15

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 HCDR1 PRT

<400> 10

Asp Ala Trp Met Thr
1 5

<210> 11
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 HCDR2 DNA

<400> 11
cgtattaaca gcaacacgga tcatgggaca acagactacg ctgcacccgt gaaaggc 57

<210> 12

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

<220>
<223> YU535-C09 HCDR2 PRT

<400> 12

Arg Ile Asn Ser Asn Thr Asp His Gly Thr Thr Asp Tyr Ala Ala Pro
1 5 10 15

Val Lys Gly

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 HCDR3 DNA

<400> 13
tcgtattacg attattggag tgctttcctg tac 33

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 HCDR3 PRT

<400> 14

Ser Tyr Tyr Asp Tyr Trp Ser Ala Phe Leu Tyr
1 5 10

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR1 DNA

<400> 15
cgggcaagtc agagcattag cagctattta aat 33

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR1 PRT

<400> 16

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR2 DNA

<400> 17
gctgcatcca gtttgcaaag t 21

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR2 PRT

<400> 18

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR3 DNA

<400> 19
caacaggctt acaatatccc gtacact 27

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 LCDR3 PRT

<400> 20

Gln Gln Ala Tyr Asn Ile Pro Tyr Thr
1 5

<210> 21
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 VL DNA

<400> 21
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagaatcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg gaacttacta ctgccaacag gcttacaata tcccgtacac ttttggccag 300

gggaccaagg tggaaatcaa a 321

<210> 22
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 VL PRT

<400> 22

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

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

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

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

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

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

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

<210> 23
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 VH DNA

<400> 23
gaggtgcagc tggtgcagtc tgggggaggc ttggtaaagc ctgggggGTC ccttagactc 60

tcctgtgcag cctctggatt ccctttcagt gacgcctgga tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaacagca acacggatca tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacaca 240

ctgtatctgc aaatgaatag cctgaaaacc gaggacacag gcgtttatta ctgtaccttc 300

tcgtattacg attattggag tgctttcctg tactggggtc agggcaccct ggtcaccgtg 360

tcctca 366

<210> 24
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 VH PRT

<400> 24
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Asp Ala
            20   25   30

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

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Gly Val Tyr
                85   90   95

Tyr Cys Thr Phe Ser Tyr Tyr Asp Tyr Trp Ser Ala Phe Leu Tyr Trp
            100   105   110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 25
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 VH complete DNA

<400> 25
gaggtgcagc tggtgcagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc   60

tcctgtgcag cctctggatt ccctttcagt gacgcctgga tgacctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggttggccgt attaacagca acacggatca tgggacaaca   180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacaca   240

ctgtatctgc aaatgaatag cctgaaaacc gaggacacag gcgtttatta ctgtaccttc   300

tcgtattacg attattggag tgctttcctg tactggggtc agggcaccct ggtcaccgtg 360

tcctcagcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tccagtggcc 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtgggcgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa cagctcccat cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaaa gcctctccct gtccccgggt 1350

<210> 26
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 VH complete PRT

<400> 26
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Asp Ala
20 25 30

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

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Gly Val Tyr
                85                  90                  95

Tyr Cys Thr Phe Ser Tyr Tyr Asp Tyr Trp Ser Ala Phe Leu Tyr Trp
            100                 105                 110

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

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

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

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

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

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

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240
```

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

Pro Gly
    450
```

<210> 27
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C09 VL complete DNA

<400> 27
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagaatcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg gaacttacta ctgccaacag gcttacaata tcccgtacac ttttggccag 300

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 28
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C09 VL complete PRT

<400> 28
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Ala Tyr Asn Ile Pro Tyr
                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> 29
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR1 DNA

<400> 29
ggctactata tgcac 15

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR1 PRT

<400> 30
Gly Tyr Tyr Met His
1 5

<210> 31
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR2 DNA

<400> 31
tggatcaacc ctatcagtgg tggcacaaac tatgcacaga agtttcaagg c 51

<210> 32
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR2 PRT

<400> 32
Trp Ile Asn Pro Ile Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 33
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR3 DNA

<400> 33

gtaccgtatt actatgatag tagtggtctc tggttcgacc cc 42

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 HCDR3 PRT

<400> 34
Val Pro Tyr Tyr Tyr Asp Ser Ser Gly Leu Trp Phe Asp Pro
1 5 10

<210> 35
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR1 DNA

<400> 35
actggaacca gcagtgacgt tggtggttat aactatgtct cc 42

<210> 36
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR1 PRT

<400> 36
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR2 DNA

<400> 37
gaggtcagta atcggccctc a 21

<210> 38
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR2 PRT

<400> 38
Glu Val Ser Asn Arg Pro Ser
1 5

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR3 DNA

<400> 39
agctcatata caagcagcag cacttgggtg 30

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 LCDR3 PRT

<400> 40
Ser Ser Tyr Thr Ser Ser Ser Thr Trp Val
1 5 10

<210> 41
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 VL DNA

<400> 41
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 42
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 VL PRT

<400> 42
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 43
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 VH DNA

<400> 43
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta tcagtggtgg cacaaactat 180

gcacagaagt ttcaaggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagtaccg 300

tattactatg atagtagtgg tctctggttc gacccctggg gccagggaac cctggtcacc 360

gtgtcctca 369

<210> 44
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 VH PRT

<400> 44
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 Gly Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 45
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 VH complete DNA

<400> 45
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta tcagtggtgg cacaaactat 180

gcacagaagt ttcaaggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagtaccg 300

tattactatg atagtagtgg tctctggttc gacccctggg gccagggaac cctggtcacc 360

gtgtcctcag ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctccagtg 720

gccggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtgggc gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaacagctcc catcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga aaagcctctc cctgtccccg ggt 1353

<210> 46
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 VH complete PRT

<400> 46
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 Gly Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

```
145                 150                 155                 160

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

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

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

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser
            260                 265                 270

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

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

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

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

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

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

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

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

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

Ser Pro Gly
450

<210> 47
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B05 VL complete DNA

<400> 47
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 48
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B05 VL complete PRT

<400> 48
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr

```
                165                 170                 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 49
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 HCDR1 DNA

<400> 49
ggctactata tgcac 15

<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 HCDR1 PRT

<400> 50
Gly Tyr Tyr Met His
1 5

<210> 51
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 HCDR2 DNA

<400> 51
tggatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcaggg c 51

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

<220>
<223> YU534-H01 HCDR2 PRT

<400> 52
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 53
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 HCDR3 DNA

<400> 53
gcccccatgt attactatga tagtagtggt tactttgact ac 42

<210> 54
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 HCDR3 PRT

<400> 54
Ala Pro Met Tyr Tyr Tyr Asp Ser Ser Gly Tyr Phe Asp Tyr
1 5 10

<210> 55
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 LCDR1 DNA

<400> 55
actggaacca gcagtgacgt tggtggttat aactatgtct cc 42

<210> 56

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

<220>
<223> YU534-H01 LCDR1 PRT

<400> 56
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 LCDR2 DNA

<400> 57
gaggtcagta atcggccctc a 21

<210> 58
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 LCDR2 PRT

<400> 58
Glu Val Ser Asn Arg Pro Ser
1 5

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 LCDR3 DNA

<400> 59
agctcatata caagcagcag cacttatgtc 30

<210> 60
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> YU534-H01 LCDR3 PRT

<400> 60
Ser Ser Tyr Thr Ser Ser Ser Thr Tyr Val
1 5 10

<210> 61
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 VL DNA

<400> 61
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc 240

caggctgagg atgaggctga ttattactgc agctcatata caagcagcag cacttatgtc 300

ttcggaactg ggaccaagct gaccgtccta 330

<210> 62
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 VL PRT

<400> 62
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

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

Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 63
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 VH DNA

<400> 63
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagccccc 300

atgtattact atgatagtag tggttacttt gactactggg gccagggaac cctggtcacc 360

gtgtcctca 369

<210> 64
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 VH PRT

<400> 64
Glu 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 Gly Tyr
            20   25   30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80

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

Ala Arg Ala Pro Met Tyr Tyr Tyr Asp Ser Ser Gly Tyr Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 65
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H01 VH complete DNA

<400> 65
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagccccc 300

atgtattact atgatagtag tggttacttt gactactggg gccagggaac cctggtcacc 360

gtgtcctcag ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctccagtg 720

gccggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtgggc gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaacagctcc catcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga aaagcctctc cctgtccccg ggt 1353

<210> 66
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 VH complete PRT

<400> 66
Glu 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 Gly Tyr
20 25 30

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

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

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Ala Pro Met Tyr Tyr Tyr Asp Ser Ser Gly Tyr Phe Asp Tyr
            100                 105                 110

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

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

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

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

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

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

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser
            260                 265                 270
```

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

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

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

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

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

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

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

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

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

Ser Pro Gly
    450
```

<210> 67
<211> 648
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-H01 VL complete DNA

<400> 67
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc 240

caggctgagg atgaggctga ttattactgc agctcatata caagcagcag cacttatgtc 300

ttcggaactg ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 68
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H01 VL complete PRT

<400> 68
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

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

Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 69
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR1 DNA

<400> 69
ggctactata tgcac 15

<210> 70
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR1 PRT

<400> 70
Gly Tyr Tyr Met His
1 5

<210> 71
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR2 DNA

<400> 71
tggatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcaggg c 51

<210> 72
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR2 PRT

<400> 72
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 73
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR3 DNA

<400> 73
ggaccccaat taaatatgat tacgtttggg ggagttggct atgcttttga tatc 54

<210> 74
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 HCDR3 PRT

<400> 74
Gly Pro Gln Leu Asn Met Ile Thr Phe Gly Gly Val Gly Tyr Ala Phe
1   5   10   15

Asp Ile

<210> 75
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR1 DNA

<400> 75
actggaacca gcagtgacgt tggtggttat aactatgtct cc   42

<210> 76
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR1 PRT

<400> 76
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1   5   10

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR2 DNA

<400> 77
gatgtcagta atcggccctc a   21

<210> 78
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR2 PRT

<400> 78
Asp Val Ser Asn Arg Pro Ser
1 5

<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR3 DNA

<400> 79
agctcatata caagcagcag cactgtggta 30

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 LCDR3 PRT

<400> 80
Ser Ser Tyr Thr Ser Ser Ser Thr Val Val
1 5 10

<210> 81
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 VL DNA

<400> 81
cagtctgccc tgactcagcc tgcctccgcg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cactgtggta 300

ttcggcggag ggaccaaggt caccgtccta 330

<210> 82
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 VL PRT

<400> 82
Gln Ser Ala Leu Thr Gln Pro Ala Ser Ala Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 83
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 VH DNA

<400> 83
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggctg ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtat tgttggaccc 300

caattaaata tgattacgtt tgggggagtt ggctatgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtgtcttc a 381

<210> 84
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 VH PRT

<400> 84
Glu Val Gln Leu Val Glu 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 Gly Tyr
20 25 30

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

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

Gln Gly Trp Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ile Val Gly Pro Gln Leu Asn Met Ile Thr Phe Gly Gly Val Gly Tyr
100 105 110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 85
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F11 VH complete DNA

<400> 85
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggctg ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtat tgttggaccc 300

caattaaata tgattacgtt tgggggagtt ggctatgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtgtcttc agctagcacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctccag tggccggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 780

atgatctccc ggaccctga ggtcacatgc gtggtggtgg gcgtgagcca cgaagaccct 840

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgg gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaacagct cccatccccc 1020

atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1260

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1320

ctgcacaacc actacacgca gaaaagcctc tccctgtccc cgggt 1365

<210> 86
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 VH complete PRT

<400> 86
Glu Val Gln Leu Val Glu 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 Gly Tyr
20 25 30

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

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

Gln Gly Trp Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ile Val Gly Pro Gln Leu Asn Met Ile Thr Phe Gly Gly Val Gly Tyr
100 105 110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala
115 120 125

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly

```
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

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

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

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

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305                 310                 315                 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln
                325                 330                 335

Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            340                 345                 350

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    370                 375                 380
```

```
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385                 390                 395                 400


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


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            420                 425                 430


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445


Ser Leu Ser Leu Ser Pro Gly
    450                 455


<210>  87
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU534-F11 VL complete DNA

<400>  87
cagtctgccc tgactcagcc tgcctccgcg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa      120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcaggggtt      180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cactgtggta      300

ttcggcggag ggaccaaggt caccgtccta ggtcagccca aggctgcacc aagtgtcact      360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata      420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag      480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc      540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg      600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca                   648
```

<210> 88
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F11 VL complete PRT

<400> 88
Gln Ser Ala Leu Thr Gln Pro Ala Ser Ala Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His

180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 89
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR1 DNA

<400> 89
aactatgcca tgagc 15

<210> 90
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR1 PRT

<400> 90
Asn Tyr Ala Met Ser
1 5

<210> 91
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR2 DNA

<400> 91
gcttttagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 92
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR2 PRT

<400> 92
Ala Phe Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

<210> 93
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR3 DNA

<400> 93
ggggcccggg gtggctacga ttacggggac tac   33

<210> 94
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 HCDR3 PRT

<400> 94
Gly Ala Arg Gly Gly Tyr Asp Tyr Gly Asp Tyr
1   5   10

<210> 95
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR1 DNA

<400> 95
cgggccagtc agagtattag tagctggttg gcc   33

<210> 96
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR1 PRT

<400> 96
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1   5   10

<210> 97
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR2 DNA

<400> 97
gatgcctcca gtttggaaag t   21

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR2 PRT

<400> 98
Asp Ala Ser Ser Leu Glu Ser
1   5

<210> 99
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR3 DNA

<400> 99
caacagtata atagttattc tcccacg   27

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 LCDR3 PRT

<400> 100
Gln Gln Tyr Asn Ser Tyr Ser Pro Thr
1 5

<210> 101
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 VL DNA

<400> 101
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggttcgatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctcccac gttcggccaa 300

gggaccaagc tggagatcaa a 321

<210> 102
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 VL PRT

<400> 102
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Arg Ser Arg Phe Ser Gly
50 55 60

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


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


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  103
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU536-C01 VH DNA

<400>  103
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc aactatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct tttagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggcc      300

cggggtggct acgattacgg ggactactgg ggccagggaa ccctggtcac cgtgtcctca      360

                                                                       360



<210>  104
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU536-C01 VH PRT

<400>  104
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


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

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

Ser Ala Phe Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

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

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

Ala Lys Gly Ala Arg Gly Gly Tyr Asp Tyr Gly Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 105
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 VH complete DNA

<400> 105
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc aactatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct tttagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggcc 300

cggggtggct acgattacgg ggactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 106
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 VH complete PRT

<400> 106
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Ala Phe Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Ala Arg Gly Gly Tyr Asp Tyr Gly 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 107
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C01 VL complete DNA

<400> 107
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggttcgatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctcccac gttcggccaa 300

gggaccaagc tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 108
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C01 VL complete PRT

<400> 108
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Arg Ser Arg Phe Ser Gly
50 55 60

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210

<210> 109
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR1 DNA

<400> 109
agctatgcca tgagc   15

<210> 110
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR1 PRT

<400> 110
Ser Tyr Ala Met Ser
1   5

<210> 111
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR2 DNA

<400> 111
gctattggtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 112
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR2 PRT

<400> 112
Ala Ile Gly Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 113
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR3 DNA

<400> 113
ggcccccgct cttccgggga ctactttgac tac 33

<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 HCDR3 PRT

<400> 114
Gly Pro Arg Ser Ser Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 115
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR1 DNA

<400> 115
cgggccagtc agagtattag tagctggttg gcc 33

<210> 116
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR1 PRT

<400> 116
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 117
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR2 DNA

<400> 117
gatgcctcca gtttggaaag t 21

<210> 118
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR2 PRT

<400> 118
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 119

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR3 DNA

<400> 119
caacagtata atagttattg ggggacg 27

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 LCDR3 PRT

<400> 120
Gln Gln Tyr Asn Ser Tyr Trp Gly Thr
1 5

<210> 121
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 VL DNA

<400> 121
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attgggggac gttcggccaa 300

gggaccaagg tggagatcaa a 321

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> YU535-A06 VL PRT

<400> 122
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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

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

<210> 123
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 VH DNA

<400> 123
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attggtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcccc   300

cgctcttccg gggactactt tgactactgg ggccagggaa ccacggtcac cgtgtcctca   360

                                                                       360

<210> 124
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 VH PRT

<400> 124
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 125
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 VH complete DNA

<400> 125
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attggtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcccc 300

cgctcttccg gggactactt tgactactgg ggccagggaa ccacggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 126
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 VH complete PRT

<400> 126
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

```
    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 127
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A06 VL complete DNA

<400> 127
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attgggggac gttcggccaa 300

gggaccaagg tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 128
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A06 VL complete PRT

<400> 128
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Trp Gly
                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> 129
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 HCDR1 DNA

<400> 129
agatatgcca tgagc 15

<210> 130
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 HCDR1 PRT

<400> 130
Arg Tyr Ala Met Ser
1 5

<210> 131
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 HCDR2 DNA

<400> 131
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 HCDR2 PRT

<400> 132
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 133
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> YU535-D12 HCDR3 DNA

<400> 133
ggaccccgca gtggctggga ctactttgac tac 33

<210> 134
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 HCDR3 PRT

<400> 134
Gly Pro Arg Ser Gly Trp Asp Tyr Phe Asp Tyr
1 5 10

<210> 135
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR1 DNA

<400> 135
cgggccagtc agagtattag tagctggttg gcc 33

<210> 136
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR1 PRT

<400> 136
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 137
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR2 DNA

<400> 137
gatgcctcca gtttggaaag t 21

<210> 138
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR2 PRT

<400> 138
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 139
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR3 DNA

<400> 139
caacagtata atagttatcc gatgtacact 30

<210> 140
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 LCDR3 PRT

<400> 140
Gln Gln Tyr Asn Ser Tyr Pro Met Tyr Thr
1 5 10

<210> 141
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 VL DNA

<400> 141
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt atccgatgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 142
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 VL PRT

<400> 142
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 143
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 VH DNA

<400> 143
caggtgcagc tggtggagtc tgggggaggc ttggtgcacc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agatatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggaccc 300

cgcagtggct gggactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

                                                                  360

<210> 144
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 VH PRT

<400> 144
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1   5   10   15

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 145
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 VH complete DNA

<400> 145
caggtgcagc tggtggagtc tgggggaggc ttggtgcacc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agatatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggaccc 300

cgcagtggct gggactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 146
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 VH complete PRT

<400> 146
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Pro Arg Ser Gly Trp Asp Tyr Phe 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220


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


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


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


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


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


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


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


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

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

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

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

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

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

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

<210> 147
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D12 VL complete DNA

<400> 147
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt atccgatgta cacttttggc 300

caggggacca agctggagat caaacgtacg gtggctgcac catctgtgtt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 148
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D12 VL complete PRT

<400> 148
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 149
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 HCDR1 DNA

<400> 149
aattatgctg tcagc 15

<210> 150
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 HCDR1 PRT

<400> 150
Asn Tyr Ala Val Ser
1 5

<210> 151
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 HCDR2 DNA

<400> 151
agaatcatcc ccaatcttgg tcttacaaag tacgcgcaaa acttccaggg c 51

<210> 152

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

<220>
<223> YU534-C09 HCDR2 PRT

<400> 152
Arg Ile Ile Pro Asn Leu Gly Leu Thr Lys Tyr Ala Gln Asn Phe Gln
1 5 10 15

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 HCDR3 DNA

<400> 153
gggttgggcg cttaccccga ttac 24

<210> 154
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 HCDR3 PRT

<400> 154
Gly Leu Gly Ala Tyr Pro Asp Tyr
1 5

<210> 155
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR1 DNA

<400> 155
tctggaagca gctccaacat cggaaataat gctgtaaac 39

<210> 156
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR1 PRT

<400> 156
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Ala Val Asn
1 5 10

<210> 157
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR2 DNA

<400> 157
tatgatgatc tgctgccctc a 21

<210> 158
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR2 PRT

<400> 158
Tyr Asp Asp Leu Leu Pro Ser
1 5

<210> 159
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR3 DNA

<400> 159
gcagcatggg atgacagcct gagtggtccg gtg 33

<210> 160
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 LCDR3 PRT

<400> 160
Ala Ala Trp Asp Asp Ser Leu Ser Gly Pro Val
1   5   10

<210> 161
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 VL DNA

<400> 161
cagtctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc   60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc   120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct   180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag   240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgag tggtccggtg   300

ttcggcggag ggaccaagct gaccgtccta   330

<210> 162
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 VL PRT

<400> 162
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1   5   10   15

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

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

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 163
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 VH DNA

<400> 163
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagg cttctggagc cacttccacg aattatgctg tcagctgggt gcgacaggcc 120

cctggacaag gacttcaata catgggaaga atcatcccca atcttggtct tacaaagtac 180

gcgcaaaact tccagggcgg ggtcacaatt accgcggaca catccacgag cacagtgtat 240

atggagttgc gcagcctgag atctgaagac acggccgtct attattgtgt gagagggttg 300

ggcgcttacc ccgattactg gggccaggga accctggtca ccgtgtcctc a 351

<210> 164
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 VH PRT

<400> 164
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ala Thr Ser Thr Asn Tyr
20 25 30

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

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

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

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

Val Arg Gly Leu Gly Ala Tyr Pro Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 165
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 VH complete DNA

<400> 165
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagg cttctggagc cacttccacg aattatgctg tcagctgggt gcgacaggcc 120

cctggacaag gacttcaata catgggaaga atcatcccca atcttggtct tacaaagtac 180

gcgcaaaact tccagggcgg ggtcacaatt accgcggaca catccacgag cacagtgtat 240

atggagttgc gcagcctgag atctgaagac acggccgtct attattgtgt gagagggttg 300

ggcgcttacc ccgattactg gggccaggga accctggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 166
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 VH complete PRT

<400> 166
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ala Thr Ser Thr Asn Tyr
20 25 30

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

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

Gln Gly Gly Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Val Tyr

```
65                  70                  75                  80

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

Val Arg Gly Leu Gly Ala Tyr Pro Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
```

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

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

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
325 330 335

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

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

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

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

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

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

<210> 167
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C09 VL complete DNA

<400> 167
cagtctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc 120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgag tggtccggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 168
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C09 VL complete PRT

<400> 168
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

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

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

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln

100 105 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 169
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR1 DNA

<400> 169
aactactata tgcac 15

<210> 170
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR1 PRT

<400> 170
Asn Tyr Tyr Met His

1 5

<210> 171
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR2 DNA

<400> 171
ataatcaacc ctagtggtgg tagcacaagc tacgcacaga agttccaggg c 51

<210> 172
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR2 PRT

<400> 172
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 173
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR3 DNA

<400> 173
gatctttatg cgatttttgg agtggttatt gac 33

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 HCDR3 PRT

<400> 174
Asp Leu Tyr Ala Ile Phe Gly Val Val Ile Asp
1 5 10

<210> 175
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR1 DNA

<400> 175
gctggaacca gcagtgacgt tggcggttat aactatgtct ca 42

<210> 176
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR1 PRT

<400> 176
Ala Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 177
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR2 DNA

<400> 177
gatgtcacta atcggccctc a 21

<210> 178
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR2 PRT

<400> 178
Asp Val Thr Asn Arg Pro Ser
1 5

<210> 179
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR3 DNA

<400> 179
agctcatata caagcagcag cacttgggtg 30

<210> 180
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 LCDR3 PRT

<400> 180
Ser Ser Tyr Thr Ser Ser Ser Thr Trp Val
1 5 10

<210> 181
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 VL DNA

<400> 181
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcgctg gaaccagcag tgacgttggc ggttataact atgtctcatg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca ctaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaaggt caccgtccta 330

<210> 182
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 VL PRT

<400> 182
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

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

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

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

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 183
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 VH DNA

<400> 183
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt   60

tcctgcaagg catctggata caccttcacc aactactata tgcactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac   180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac   240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatctt   300

tatgcgattt ttggagtggt tattgactgg ggccagggaa ccctggtcac cgtgtcctca   360

                                                                       360

<210> 184
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 VH PRT

<400> 184
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 Asn Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Asp Leu Tyr Ala Ile Phe Gly Val Val Ile Asp Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 185
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 VH complete DNA

<400> 185
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc aactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatctt 300

tatgcgattt ttggagtggt tattgactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 186
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 VH complete PRT

<400> 186

```
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 Asn Tyr
            20                  25                  30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

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

Ala Arg Asp Leu Tyr Ala Ile Phe Gly Val Val Ile Asp 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 187
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C12 VL complete DNA

<400> 187
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcgctg gaaccagcag tgacgttggc ggttataact atgtctcatg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca ctaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaaggt caccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 188
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C12 VL complete PRT

<400> 188
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
            100                 105                 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 189
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR1 DNA

<400> 189
agcaatgcta tgcat   15

<210> 190
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR1 PRT

<400> 190
Ser Asn Ala Met His
1   5

<210> 191
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR2 DNA

<400> 191
tggatcaacg ctggcaatgg taacacaaaa tattcacaga agttccaggg c   51

<210> 192
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR2 PRT

<400> 192
Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
1   5   10   15

<210> 193
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR3 DNA

<400> 193
ggtcgagatg gctacaatgt ggactacttt gaatac 36

<210> 194
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 HCDR3 PRT

<400> 194
Gly Arg Asp Gly Tyr Asn Val Asp Tyr Phe Glu Tyr
1 5 10

<210> 195
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR1 DNA

<400> 195
cgggccagtc agagtattag tagctggttg gcc 33

<210> 196
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR1 PRT

<400> 196
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 197
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR2 DNA

<400> 197
gatgcctcca gtttggaaag t 21

<210> 198
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR2 PRT

<400> 198
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 199
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR3 DNA

<400> 199
caacagtata atagttaccc gtggacg 27

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 LCDR3 PRT

<400> 200
Gln Gln Tyr Asn Ser Tyr Pro Trp Thr
1 5

<210> 201
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 VL DNA

<400> 201

gacatcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag tctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt acccgtggac gttcggccaa 300

gggaccaaag tggatatcaa a 321

<210> 202
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 VL PRT

<400> 202
Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 203
<211> 363
<212> DNA

<213> Artificial Sequence

<220>
<223> YU535-A02 VH DNA

<400> 203
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agcaatgcta tgcattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat 180

tcacagaagt tccagggcag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaggtcga 300

gatggctaca atgtggacta ctttgaatac tggggccagg gaaccctggt caccgtgtcc 360

tca 363

<210> 204
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 VH PRT

<400> 204
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 Ser Asn
20 25 30

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

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

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Asp Gly Tyr Asn Val Asp Tyr Phe Glu Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 205
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 VH complete DNA

<400> 205
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agcaatgcta tgcattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat 180

tcacagaagt tccagggcag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaggtcga 300

gatggctaca atgtggacta ctttgaatac tggggccagg gaaccctggt caccgtgtcc 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 206
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 VH complete PRT

<400> 206
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 Ser Asn
20 25 30

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

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

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Asp Gly Tyr Asn Val Asp Tyr Phe Glu Tyr Trp Gly
100 105 110

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

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

```
    130                 135                 140

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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
```

<210> 207
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A02 VL complete DNA

<400> 207

```
gacatcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca      180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag tctgcagcct      240

gatgattttg caacttatta ctgccaacag tataatagtt acccgtggac gttcggccaa      300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag      480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
```

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 208
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A02 VL complete PRT

<400> 208
Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Asp 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> 209
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 HCDR1 DNA

<400> 209
agcaatgtta tgcat 15

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

<220>
<223> YU535-E07 HCDR1 PRT

<400> 210
Ser Asn Val Met His
1 5

<210> 211
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 HCDR2 DNA

<400> 211
tggatcaacg ctggcaatgg taacacaaaa tattcacaga agttccaggg c 51

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

<220>
<223> YU535-E07 HCDR2 PRT

<400> 212
Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
1   5   10   15

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

<220>
<223> YU535-E07 HCDR3 DNA

<400> 213
ggtcgagatg gctacaatgt ggactacttt gactac   36

<210> 214
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 HCDR3 PRT

<400> 214
Gly Arg Asp Gly Tyr Asn Val Asp Tyr Phe Asp Tyr
1   5   10

<210> 215
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR1 DNA

<400> 215
cgggccagtc agagtattag tagctggttg gcc   33

<210> 216
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR1 PRT

<400> 216
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 217
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR2 DNA

<400> 217
gatgcctcca gtttggaaag t 21

<210> 218
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR2 PRT

<400> 218
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 219
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR3 DNA

<400> 219
caacagtata atagttatcc ctggacg 27

<210> 220
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 LCDR3 PRT

<400> 220
Gln Gln Tyr Asn Ser Tyr Pro Trp Thr
1   5

<210> 221
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 VL DNA

<400> 221
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca   180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct   240

gatgattttg caacttatta ctgccaacag tataatagtt atccctggac gttcggccaa   300

gggaccaagc tggagatcaa a   321

<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 VL PRT

<400> 222
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 223
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 VH DNA

<400> 223
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggct 60

tcctgcaagg cttctggata caccttcact agcaatgtta tgcattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat 180

tcacagaagt tccagggcag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaggtcga 300

gatggctaca atgtggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tca   363

<210> 224
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 VH PRT

<400> 224
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

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

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

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 225
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 VH complete DNA

<400> 225
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggct 60

tcctgcaagg cttctggata caccttcact agcaatgtta tgcattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat 180

tcacagaagt tccagggcag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaggtcga 300

gatggctaca atgtggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 226
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 VH complete PRT

<400> 226
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

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

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

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

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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
```

<210> 227
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-E07 VL complete DNA

<400> 227
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt atccctggac gttcggccaa 300

gggaccaagc tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 228
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-E07 VL complete PRT

<400> 228
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 229
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 HCDR1 DNA

<400> 229
agcaactaca tgagc 15

<210> 230
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 HCDR1 PRT

<400> 230
Ser Asn Tyr Met Ser
1   5

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

<220>
<223> YU536-E12 HCDR2 DNA

<400> 231
cttatttata gcggtggtag cacatactac gcagactccg tgaagggc   48

<210> 232
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 HCDR2 PRT

<400> 232
Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1   5   10   15

<210> 233
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 HCDR3 DNA

<400> 233
gccctcgagg tcaatacagc tggggactac tttgactac   39

<210> 234
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 HCDR3 PRT

<400> 234
Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 235
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR1 DNA

<400> 235
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 236
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR1 PRT

<400> 236
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 237
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR2 DNA

<400> 237
ggtaacagca atcggccctc a 21

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR2 PRT

<400> 238

Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 239
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR3 DNA

<400> 239
cagtcctatg acagcagcct gagtggttgg gtg 33

<210> 240
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 LCDR3 PRT

<400> 240
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val
1 5 10

<210> 241
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 VL DNA

<400> 241
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttgg 300

gtgttcggcg gagggaccaa gctgaccgtc cta 333

<210> 242

<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 VL PRT

<400> 242
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 243
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 VH DNA

<400> 243
gaggtgcagc tggtgcagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgagtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcgag 300

gtcaatacag ctggggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tca 363

<210> 244
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 VH PRT

<400> 244
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Val Ser Ser Asn
20 25 30

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

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 245
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>

<223> YU536-E12 VH complete DNA

<400> 245
gaggtgcagc tggtgcagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgagtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcgag 300

gtcaatacag ctggggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 246
<211> 448
<212> PRT

<213> Artificial Sequence

<220>
<223> YU536-E12 VH complete PRT

<400> 246
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Val Ser Ser Asn
20 25 30

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

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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

<210> 247
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E12 VL complete DNA

<400> 247
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc agggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttgg 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 248
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E12 VL complete PRT

<400> 248
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

```
1               5                   10                  15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

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

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

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 249
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 HCDR1 DNA

<400> 249
agcaactaca tgagc 15

<210> 250
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 HCDR1 PRT

<400> 250
Ser Asn Tyr Met Ser
1 5

<210> 251
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 HCDR2 DNA

<400> 251
cttatttata gcggtggtag cacatactac gcagactccg tgaagggc 48

<210> 252
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 HCDR2 PRT

<400> 252
Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 253

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

<220>
<223> YU537-E03 HCDR3 DNA

<400> 253
gccctcgagg tcaatacagc tggggactac tttgactac 39

<210> 254
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 HCDR3 PRT

<400> 254
Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 255
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR1 DNA

<400> 255
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 256
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR1 PRT

<400> 256
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 257
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR2 DNA

<400> 257
ggtaacagca atcggccctc a 21

<210> 258
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR2 PRT

<400> 258
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 259
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR3 DNA

<400> 259
cagtcctatg acagcagcct gagtggttat gtc 33

<210> 260
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 LCDR3 PRT

<400> 260
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 261
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 VL DNA

<400> 261
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtcttcggaa ctgggaccaa gctgaccgtc cta 333

<210> 262
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 VL PRT

<400> 262
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 263
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 VH DNA

<400> 263
caggtgcagc tggtgcagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgagtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcgag 300

gtcaatacag ctggggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tca 363

<210> 264
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 VH PRT

<400> 264
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Val Ser Ser Asn
            20 25 30

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

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50 55 60

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

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

Arg Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 265
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 VH complete DNA

<400> 265
caggtgcagc tggtgcagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgagtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcgag 300

gtcaatacag ctggggacta ctttgactac tggggccagg gaaccctggt caccgtgtcc 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 266
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 VH complete PRT

<400> 266
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Val Ser Ser Asn
20 25 30

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

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Ala Leu Glu Val Asn Thr Ala Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

```
        115                 120                 125

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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

<210> 267
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-E03 VL complete DNA

<400> 267
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtcttcggaa ctgggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 268
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-E03 VL complete PRT

<400> 268
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

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

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

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 269
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR1 DNA

<400> 269
agcaactaca tgagc 15

<210> 270
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR1 PRT

<400> 270
Ser Asn Tyr Met Ser
1 5

<210> 271
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR2 DNA

<400> 271
gttatttata gcggtggtag cacattctac gcagactccg tgaagggc 48

<210> 272
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR2 PRT

<400> 272
Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 273
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR3 DNA

<400> 273
gatgggtatt acgatatttt gactggttat tattcagaga attcttttga tatc 54

<210> 274
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 HCDR3 PRT

<400> 274
Asp Gly Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Ser Glu Asn Ser Phe
1 5 10 15

Asp Ile

<210> 275
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-D06 LCDR1 DNA

<400> 275
actggaacca gcagtgacgt tggtggttat aactatgtct cc 42

<210> 276
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 LCDR1 PRT

<400> 276
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 277
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 LCDR2 DNA

<400> 277
gaggtcagta atcggccctc a 21

<210> 278
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 LCDR2 PRT

<400> 278
Glu Val Ser Asn Arg Pro Ser
1 5

<210> 279
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 LCDR3 DNA

<400> 279
agctcatata caagcagcag cacttatgtg gta 33

<210> 280
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 LCDR3 PRT

<400> 280
Ser Ser Tyr Thr Ser Ser Ser Thr Tyr Val Val
1 5 10

<210> 281
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 VL DNA

<400> 281
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttatgtg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 282
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 VL PRT

<400> 282
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

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

Ser Thr Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 283
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 VH DNA

<400> 283
caggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caactgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatgggtat 300

tacgatattt tgactggtta ttattcagag aattcttttg atatctgggg ccaagggaca 360

atggtcaccg tgtcttca   378

<210> 284
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 VH PRT

<400> 284
Gln 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 Thr Val Ser Ser Asn
            20   25   30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50   55   60

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

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

Arg Asp Gly Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Ser Glu Asn Ser
            100   105   110

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120   125

<210> 285
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 VH complete DNA

<400> 285
caggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca   180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt   240

caactgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatgggtat   300

tacgatattt tgactggtta ttattcagag aattcttttg atatctgggg ccaagggaca 360

atggtcaccg tgtcttcagc tagcaccaag ggcccatcgg tcttcccccc ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 720

cctccagtgg ccggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtgggcg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aacagctccc atcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa aagcctctcc ctgtccccgg gt 1362

<210> 286
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 VH complete PRT

<400> 286
Gln 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 Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

Arg Asp Gly Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Ser Glu Asn Ser
            100                 105                 110

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
        115                 120                 125

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

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

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

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

```
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu
                325                 330                 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Leu Ser Leu Ser Pro Gly
    450
```

<210> 287
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D06 VL complete DNA

<400> 287
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cacttatgtg 300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 288
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D06 VL complete PRT

<400> 288
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

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

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

```
Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Ser Thr Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

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

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

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 289
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR1 DNA

<400> 289

agcaactaca tgagc 15

<210> 290
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR1 PRT

<400> 290
Ser Asn Tyr Met Ser
1 5

<210> 291
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR2 DNA

<400> 291
gttatttata gcggtggtag cacattctac gcagactccg tgaagggc 48

<210> 292
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR2 PRT

<400> 292
Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 293
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR3 DNA

<400> 293
gacttaggcc cctacggtat ggacgtc 27

<210> 294
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 HCDR3 PRT

<400> 294
Asp Leu Gly Pro Tyr Gly Met Asp Val
1   5

<210> 295
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR1 DNA

<400> 295
cgggccagtc agggcattag cagttattta gcc   33

<210> 296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR1 PRT

<400> 296
Arg Ala Ser Gln Gly Ile Ser Ser Tyr Leu Ala
1   5   10

<210> 297
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR2 DNA

<400> 297
gctgcatcca ctttgcaaag t   21

<210> 298
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR2 PRT

<400> 298
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 299
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR3 DNA

<400> 299
caacagctta atagttaccc tccgtacact 30

<210> 300
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 LCDR3 PRT

<400> 300
Gln Gln Leu Asn Ser Tyr Pro Pro Tyr Thr
1 5 10

<210> 301
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 VL DNA

<400> 301
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctccgta cactttggc 300

caggggacca agctggagat caaa 324

<210> 302
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 VL PRT

<400> 302
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 303
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 VH DNA

<400> 303

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctc 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttaggc 300

ccctacggta tggacgtctg gggccaaggg accctggtca ccgtgtcctc a 351

<210> 304
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 VH PRT

<400> 304
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 Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 305
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-E07 VH complete DNA

<400> 305
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctc 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttaggc 300

ccctacggta tggacgtctg gggccaaggg accctggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 306
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-E07 VH complete PRT

<400> 306
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 Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser

```
                165                 170                 175

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

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

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

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

```
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400


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


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430


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


<210>  307
<211>  645
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU536-E07 VL complete DNA

<400>  307
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca      120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca      180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct      240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctccgta cacttttggc      300

caggggacca agctggagat caaacgtacg gtggctgcac catctgtgtt catcttcccg      360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt                      645


<210>  308
<211>  215
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> YU536-E07 VL complete PRT

<400> 308
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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

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

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

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

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

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

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

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

195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 309
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR1 DNA

<400> 309
agcaactaca tgagc 15

<210> 310
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR1 PRT

<400> 310
Ser Asn Tyr Met Ser
1 5

<210> 311
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR2 DNA

<400> 311
gttatttata gcggtggtag cacattctac gcagactccg tgaagggc 48

<210> 312
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR2 PRT

<400> 312
Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 313
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR3 DNA

<400> 313
gacttaggcc cctacggtat ggacgtc 27

<210> 314
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 HCDR3 PRT

<400> 314
Asp Leu Gly Pro Tyr Gly Met Asp Val
1 5

<210> 315
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR1 DNA

<400> 315
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 316
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR1 PRT

<400> 316
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His

1 5 10

<210> 317
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR2 DNA

<400> 317
ggtagcagca atcggccctc a 21

<210> 318
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR2 PRT

<400> 318
Gly Ser Ser Asn Arg Pro Ser
1 5

<210> 319
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR3 DNA

<400> 319
gcagcatggg atgacagttt gagtgtcgac gtg 33

<210> 320
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 LCDR3 PRT

<400> 320
Ala Ala Trp Asp Asp Ser Leu Ser Val Asp Val
1 5 10

<210> 321
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 VL DNA

<400> 321
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtagca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgt gcagcatggg atgacagttt gagtgtcgac 300

gtgttcggcg gagggaccaa gctgaccgtc cta 333

<210> 322
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 VL PRT

<400> 322
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser

85 90 95

Leu Ser Val Asp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 323
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 VH DNA

<400> 323
caggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttaggc 300

ccctacggta tggacgtctg gggccaaggg accctggtca ccgtgtcctc a 351

<210> 324
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 VH PRT

<400> 324
Gln 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 Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 325
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 VH complete DNA

<400> 325
caggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttaggc 300

ccctacggta tggacgtctg gggccaaggg accctggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 326
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 VH complete PRT

<400> 326
Gln 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 Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu

```
            100                 105                 110

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
325 330 335

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

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

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

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

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

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

<210> 327
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B03 VL complete DNA

<400> 327
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtagca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgt gcagcatggg atgacagttt gagtgtcgac 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 328
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B03 VL complete PRT

<400> 328
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
85 90 95

Leu Ser Val Asp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe

130 135 140

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

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

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 329
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR1 DNA

<400> 329
agcaactaca tgagc 15

<210> 330
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR1 PRT

<400> 330
Ser Asn Tyr Met Ser
1 5

<210> 331
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR2 DNA

<400> 331
gttatttata gcggtggtag cacatactac gcagactccg tgaagggc 48

<210> 332
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR2 PRT

<400> 332
Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 333
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR3 DNA

<400> 333
gatttggtta actggggaat ggactac 27

<210> 334
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 HCDR3 PRT

<400> 334
Asp Leu Val Asn Trp Gly Met Asp Tyr
1 5

<210> 335
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR1 DNA

<400> 335
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 336
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR1 PRT

<400> 336
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 337
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR2 DNA

<400> 337
ggtaacagca atcggccctc a 21

<210> 338
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR2 PRT

<400> 338
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 339
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR3 DNA

<400> 339

cagtcctatg acagcagcct gagtggttat gtc 33

<210> 340
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 LCDR3 PRT

<400> 340
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 341
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 VL DNA

<400> 341
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtcttcggaa ctgggaccaa gctgaccgtc cta 333

<210> 342
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 VL PRT

<400> 342
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 343
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 VH DNA

<400> 343
gaggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggagt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatttggtt 300

aactggggaa tggactactg gggccaggga accctggtca ccgtgtcctc a 351

<210> 344
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 VH PRT

<400> 344
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Asp Leu Val Asn Trp Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 345
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 VH complete DNA

<400> 345
gaggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggagt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatttggtt 300

aactggggaa tggactactg gggccaggga accctggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 346
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 VH complete PRT

<400> 346
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```
        35                  40                  45

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

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

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

Arg Asp Leu Val Asn Trp Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

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

```
Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

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

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

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

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

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

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

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

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

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 347
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D10 VL complete DNA

<400> 347
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtcttcggaa ctgggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 348
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D10 VL complete PRT

<400> 348
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

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

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

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

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

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 349
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR1 DNA

<400> 349
agcaactaca tgagc 15

<210> 350
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR1 PRT

<400> 350
Ser Asn Tyr Met Ser
1 5

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR2 DNA

<400> 351
gttatttata gcggtggtag cacatactac gcagactccg tgaagggc 48

<210> 352
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR2 PRT

<400> 352
Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 353
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR3 DNA

<400> 353
gatcttgttg taatgggcct ggacgtc 27

<210> 354
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 HCDR3 PRT

<400> 354
Asp Leu Val Val Met Gly Leu Asp Val
1   5

<210> 355
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 LCDR1 DNA

<400> 355
cgggccagtc agggcattag cagttattta gcc   33

<210> 356
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 LCDR1 PRT

<400> 356
Arg Ala Ser Gln Gly Ile Ser Ser Tyr Leu Ala
1   5   10

<210> 357
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 LCDR2 DNA

<400> 357
gctgcatcca ctttgcaaag t   21

<210> 358
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> YU536-D04 LCDR2 PRT

<400> 358
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 359
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 LCDR3 DNA

<400> 359
caacagctta atagttaccc aatcacc 27

<210> 360
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 LCDR3 PRT

<400> 360
Gln Gln Leu Asn Ser Tyr Pro Ile Thr
1 5

<210> 361
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 VL DNA

<400> 361
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt acccaatcac cttcggccaa 300

gggaccaagc tggagatcaa a 321

<210> 362
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 VL PRT

<400> 362
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 363
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 VH DNA

<400> 363
caggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggact caccgtcagt agcaactaca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca   180

gactccgtga agggcagatt catcatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcttgtt 300

gtaatgggcc tggacgtctg gggcaaaggg accctggtca ccgtgtcctc a 351

<210> 364
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 VH PRT

<400> 364
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Asp Leu Val Val Met Gly Leu Asp Val Trp Gly Lys Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 365
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 VH complete DNA

<400> 365
caggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt catcatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcttgtt 300

gtaatgggcc tggacgtctg gggcaaaggg accctggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 366
<211> 445

<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 VH complete PRT

<400> 366
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Asp Leu Val Val Met Gly Leu Asp Val Trp Gly Lys Gly Thr Leu
100 105 110

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

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

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

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
```

405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

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

<210> 367
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-D04 VL complete DNA

<400> 367
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt acccaatcac cttcggccaa 300

gggaccaagc tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 368
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-D04 VL complete PRT

<400> 368
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

```
1               5                   10                  15

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 369
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 HCDR1 DNA

<400> 369
agcaactaca tgagc 15

<210> 370
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 HCDR1 PRT

<400> 370
Ser Asn Tyr Met Ser
1 5

<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 HCDR2 DNA

<400> 371
gttatttata gcggtggtag cacatactac gcagactccg tgaagggc 48

<210> 372
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 HCDR2 PRT

<400> 372
Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 373

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

<220>
<223> YU537-B08 HCDR3 DNA

<400> 373
ggggagatac agccatacta ctactacggt atggacgtc 39

<210> 374
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 HCDR3 PRT

<400> 374
Gly Glu Ile Gln Pro Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 375
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR1 DNA

<400> 375
actggaacca gcggtgacgt tggtggttat aactatgtct cc 42

<210> 376
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR1 PRT

<400> 376
Thr Gly Thr Ser Gly Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 377
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR2 DNA

<400> 377
gatgtcagta atcggccctc a 21

<210> 378
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR2 PRT

<400> 378
Asp Val Ser Asn Arg Pro Ser
1 5

<210> 379
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR3 DNA

<400> 379
agctcatata caagcagcag cactcctgtg gta 33

<210> 380
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 LCDR3 PRT

<400> 380
Ser Ser Tyr Thr Ser Ser Ser Thr Pro Val Val
1 5 10

<210> 381
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 VL DNA

<400> 381
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcgg tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cactcctgtg 300

gtattcggcg aagggaccaa gctgaccgtc cta 333

<210> 382
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 VL PRT

<400> 382
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Pro Val Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu
            100 105 110

<210> 383
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 VH DNA

<400> 383
caggtgcagc tggtgcagtc tgggggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgcgcgag aggggagata 300

cagccatact actactacgg tatggacgtc tggggccaag ggacaatggt caccgtgtct 360

tca 363

<210> 384
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 VH PRT

<400> 384
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Gly Glu Ile Gln Pro Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 385
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 VH complete DNA

<400> 385
caggtgcagc tggtgcagtc tgggggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgcgcgag aggggagata 300

cagccatact actactacgg tatggacgtc tggggccaag ggacaatggt caccgtgtct 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 386
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 VH complete PRT

<400> 386
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Gly Glu Ile Gln Pro Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

```
        115                 120                 125

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

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

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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

<210> 387
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-B08 VL complete DNA

<400> 387
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcgg tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cactcctgtg 300

gtattcggcg aagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 388
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-B08 VL complete PRT

<400> 388

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

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

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

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

Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65				70					75					80	

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

Ser	Thr	Pro	Val	Val	Phe	Gly	Glu	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly
		100					105					110			

Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu
		115					120					125			

Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe
	130					135					140				

```
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160


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


Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190


His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205


Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 389
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR1 DNA

<400> 389
agcaactaca tgagc 15

<210> 390
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR1 PRT

<400> 390
```
Ser Asn Tyr Met Ser
1               5
```

<210> 391
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR2 DNA

<400> 391
gttatttata gcggtggtag cacatactac gcagactccg tgaagggc 48

<210> 392
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR2 PRT

<400> 392
Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 393
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR3 DNA

<400> 393
ggagaaagtg ggagcccgta cggtatggac gtc 33

<210> 394
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 HCDR3 PRT

<400> 394
Gly Glu Ser Gly Ser Pro Tyr Gly Met Asp Val
1 5 10

<210> 395
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR1 DNA

<400> 395
tctggaagca gctccaacat tgggaataat tatgtatcc 39

<210> 396
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR1 PRT

<400> 396
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser
1 5 10

<210> 397
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR2 DNA

<400> 397
gacactaata agcgaccctc g 21

<210> 398
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR2 PRT

<400> 398
Asp Thr Asn Lys Arg Pro Ser
1 5

<210> 399
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR3 DNA

<400> 399
gcaacatggg atagcagcct gagtgttggg gtg 33

<210> 400
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 LCDR3 PRT

<400> 400
Ala Thr Trp Asp Ser Ser Leu Ser Val Gly Val
1   5   10

<210> 401
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 VL DNA

<400> 401
cagtctgtgc tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc   60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc   120

ccaggaacag cccccaaact cctcatttat gacactaata agcgaccctc ggggattcct   180

gaccgatttt ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag   240

actggggacg aggccgatta ttactgcgca acatgggata gcagcctgag tgttggggtg   300

ttcggcggag ggaccaagct gaccgtccta   330

<210> 402
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 VL PRT

<400> 402
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1   5   10   15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20   25   30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65   70   75   80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Ser Ser Leu
                85   90   95

Ser Val Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 403
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 VH DNA

<400> 403
gaggtgcagc tgttggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacgc gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag aggagaaagt 300

gggagcccgt acggtatgga cgtctggggc caagggaccc tggtcaccgt gtcctca 357

<210> 404
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 VH PRT

<400> 404
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1   5   10   15

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

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

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

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

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

Arg Gly Glu Ser Gly Ser Pro Tyr Gly Met Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 405
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 VH complete DNA

<400> 405
gaggtgcagc tgttggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc   60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca   180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacgc gctgtatctt   240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag aggagaaagt   300

gggagcccgt acggtatgga cgtctggggc caagggaccc tggtcaccgt gtcctcagct   360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc   420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg   480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctccagtggc cggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtgggcgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgggtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa acagctccca tcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaaa 1320

agcctctccc tgtccccggg t 1341

<210> 406
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 VH complete PRT

<400> 406
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

```
Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

Arg Gly Glu Ser Gly Ser Pro Tyr Gly Met Asp Val Trp Gly Gln Gly
            100                 105                 110

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

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

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

Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro
            260                 265                 270
```

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

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

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

Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr
                325                 330                 335

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

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

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

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

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

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 407
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H11 VL complete DNA

<400> 407
cagtctgtgc tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatttat gacactaata agcgaccctc ggggattcct 180

gaccgatttt ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgca acatgggata gcagcctgag tgttggggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 408
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H11 VL complete PRT

<400> 408
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Ser Ser Leu
85 90 95

Ser Val Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 409
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR1 DNA

<400> 409
agcaactaca tgagc 15

<210> 410
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR1 PRT

<400> 410
Ser Asn Tyr Met Ser
1   5

<210> 411
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR2 DNA

<400> 411
gttatttata gcggtggtag cacatactac gcagactccg tgaagggc   48

<210> 412
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR2 PRT

<400> 412
Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1   5   10   15

<210> 413
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR3 DNA

<400> 413
ggcaagagta ttactatggt tcggggagtg ccaactgggg tgcctcccta catggacgtc   60

<210> 414
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 HCDR3 PRT

<400> 414

Gly Lys Ser Ile Thr Met Val Arg Gly Val Pro Thr Gly Val Pro Pro
1 5 10 15

Tyr Met Asp Val
20

<210> 415
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR1 DNA

<400> 415
tctggaagca gctccaacat cggaaataat gctgtaaac 39

<210> 416
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR1 PRT

<400> 416
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Ala Val Asn
1 5 10

<210> 417
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR2 DNA

<400> 417
tatgatgatc tgctgccctc a 21

<210> 418
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR2 PRT

<400> 418
Tyr Asp Asp Leu Leu Pro Ser
1 5

<210> 419
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR3 DNA

<400> 419
gcagcatggg atgacagcct gaatggtgtg gta 33

<210> 420
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 LCDR3 PRT

<400> 420
Ala Ala Trp Asp Asp Ser Leu Asn Gly Val Val
1 5 10

<210> 421
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 VL DNA

<400> 421
cagtctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc 120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtgtggta 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 422
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 VL PRT

<400> 422
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

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

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

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 423
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 VH DNA

<400> 423
gaggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggcaagagt 300

attactatgg ttcggggagt gccaactggg gtgcctccct acatggacgt ctggggcaaa 360

gggaccacgg tcaccgtgtc ctca 384

<210> 424
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 VH PRT

<400> 424
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Gly Lys Ser Ile Thr Met Val Arg Gly Val Pro Thr Gly Val Pro
100 105 110

Pro Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 425
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 VH complete DNA

<400> 425
gaggtgcagc tggtgcagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggcaagagt 300

attactatgg ttcggggagt gccaactggg gtgcctccct acatggacgt ctggggcaaa 360

gggaccacgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt ccccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 426

<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 VH complete PRT

<400> 426
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Gly Lys Ser Ile Thr Met Val Arg Gly Val Pro Thr Gly Val Pro
100 105 110

Pro Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145 150 155 160

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
180 185 190

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400
```

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


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445


Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 427
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-A11 VL complete DNA

<400> 427

```
cagtctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc       60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc      120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtgtggta      300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact      360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata      420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag      480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc      540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg      600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca                   648
```

<210> 428
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-A11 VL complete PRT

<400> 428
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1   5   10   15

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

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

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100   105   110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130   135   140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145   150   155   160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180   185   190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195   200   205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 429
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR1 DNA

<400> 429
agttatgcta tcacc 15

<210> 430
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR1 PRT

<400> 430
Ser Tyr Ala Ile Thr
1 5

<210> 431
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR2 DNA

<400> 431
gggatcatcc ctatctttgg tacaccaaac tacgcacaga agttccagga c 51

<210> 432
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR2 PRT

<400> 432

Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 433
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR3 DNA

<400> 433
gataaagggt tcggggaggg gaaaggttac cactactacg gtctggacgt c 51

<210> 434
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 HCDR3 PRT

<400> 434
Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly Leu Asp
1 5 10 15

<210> 435
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR1 DNA

<400> 435
actggaacca gcagtgacgt tggtagttat aactttgtct cc 42

<210> 436
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR1 PRT

<400> 436

Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Phe Val Ser
1 5 10

<210> 437
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR2 DNA

<400> 437
gaggtcaata atcggccctc a 21

<210> 438
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR2 PRT

<400> 438
Glu Val Asn Asn Arg Pro Ser
1 5

<210> 439
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR3 DNA

<400> 439
agctcatata caagcagcag cgtggta 27

<210> 440
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 LCDR3 PRT

<400> 440
Ser Ser Tyr Thr Ser Ser Ser Val Val
1 5

<210> 441
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 VL DNA

<400> 441
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt agttataact ttgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca ataatcggcc ctcaggggtt 180

tcttatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cgtggtattc 300

ggcggaggga ccaaggtcac cgtccta 327

<210> 442
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 VL PRT

<400> 442
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

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

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

Met Ile Tyr Glu Val Asn Asn Arg Pro Ser Gly Val Ser Tyr Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95


Ser Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  443
<211>  378
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU534-G06 VH DNA

<400>  443
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcacc agttatgcta tcacctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac      180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa      300

gggttcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc      360

ctggtcaccg tgtcctca                                                    378



<210>  444
<211>  126
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU534-G06 VH PRT

<400>  444
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


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


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

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe
    50                  55                  60

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

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

Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly
            100                 105                 110

Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 445
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 VH complete DNA

<400> 445

```
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcacc agttatgcta tcacctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac      180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa      300

gggttcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc      360

ctggtcaccg tgtcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcaccctcc      420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc      480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg      540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc      600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg      660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca      720

cctccagtgg ccggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg      780
```

atctcccgga cccctgaggt cacatgcgtg gtggtgggcg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aacagctccc atcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa aagcctctcc ctgtccccgg gt 1362

<210> 446
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 VH complete PRT

<400> 446
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

```
Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly
            100                 105                 110

Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
        115                 120                 125

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

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

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300
```

```
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu
                325                 330                 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Leu Ser Leu Ser Pro Gly
    450
```

<210> 447
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G06 VL complete DNA

<400> 447

```
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt agttataact ttgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatgatt tatgaggtca ataatcggcc ctcaggggtt      180
```

tcttatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag cgtggtattc 300

ggcggaggga ccaaggtcac cgtcctaggt cagcccaagg ctgcaccaag tgtcactctg 360

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 420

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 540

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 645

<210> 448
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G06 VL complete PRT

<400> 448
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Asn Asn Arg Pro Ser Gly Val Ser Tyr Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro
100 105 110

```
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
        115                 120                 125


Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
    130                 135                 140


Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145                 150                 155                 160


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


Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
            180                 185                 190


Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
        195                 200                 205


Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  449
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU534-H02 HCDR1 DNA

<400>  449
agctatgctc tcacc                                                    15



<210>  450
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU534-H02 HCDR1 PRT

<400>  450
Ser Tyr Ala Leu Thr
1               5
```

<210> 451
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 HCDR2 DNA

<400> 451
gggatcatcc ctatctttgg tacaccaaac tacgcacaga agttccagga c 51

<210> 452
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 HCDR2 PRT

<400> 452
Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 453
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 HCDR3 DNA

<400> 453
gataaagggt tcggggaggg gaaaggttac cacttctacg gtctggacgt c 51

<210> 454
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 HCDR3 PRT

<400> 454
Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Phe Tyr Gly Leu Asp
1 5 10 15

<210> 455
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR1 DNA

<400> 455
actggaacca gcagtgacgt tggtggttat aattttgtct cc 42

<210> 456
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR1 PRT

<400> 456
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Phe Val Ser
1 5 10

<210> 457
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR2 DNA

<400> 457
gaggtcagta atcggccctc a 21

<210> 458
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR2 PRT

<400> 458
Glu Val Ser Asn Arg Pro Ser
1 5

<210> 459
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR3 DNA

<400> 459
agctcatata caagcagcgg cagtctcata 30

<210> 460
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 LCDR3 PRT

<400> 460
Ser Ser Tyr Thr Ser Ser Gly Ser Leu Ile
1 5 10

<210> 461
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 VL DNA

<400> 461
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgtactg gaaccagcag tgacgttggt ggttataatt ttgtctcctg gtatcaacaa 120

tacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctgatcgct tctcgggctc caagtctggc gacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcgg cagtctcata 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 462
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 VL PRT

<400> 462
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

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

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

<210> 463
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 VH DNA

<400> 463
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttctggagg caccttcagc agctatgctc tcacctgggt gcgacaggcc   120

cctggacaag gacttgagtg gatgggaggg atcatcccta tctttggtac accaaactac   180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac   240

atggagctga gcagcctgag atctgaagac acggccgtgt attactgtgc gaatgataaa   300

gggttcgggg aggggaaagg ttaccacttc tacggtctgg acgtctgggg ccaagggacc   360

acggtcaccg tgtcctca   378

<210> 464
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 VH PRT

<400> 464
Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

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

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

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

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

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

Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Phe Tyr Gly
            100   105   110

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

<210> 465
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 VH complete DNA

<400> 465
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttctggagg caccttcagc agctatgctc tcacctgggt gcgacaggcc 120

cctggacaag gacttgagtg gatgggaggg atcatcccta tctttggtac accaaactac 180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggccgtgt attactgtgc gaatgataaa 300

gggttcgggg aggggaaagg ttaccacttc tacggtctgg acgtctgggg ccaagggacc 360

acggtcaccg tgtcctcagc tagcaccaag ggcccatcgg tcttcccccct ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 720

cctccagtgg ccggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtgggcg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aacagctccc atcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa aagcctctcc ctgtccccgg gt 1362

<210> 466
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 VH complete PRT

<400> 466
Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Phe Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser
115 120 125

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

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

```
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
    210                 215                 220

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu
                325                 330                 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430
```

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Pro Gly
450

<210> 467
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-H02 VL complete DNA

<400> 467
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgtactg gaaccagcag tgacgttggt ggttataatt ttgtctcctg gtatcaacaa 120

tacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctgatcgct tctcgggctc caagtctggc gacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcgg cagtctcata 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 468
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-H02 VL complete PRT

<400> 468
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

```
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Gly Ser Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 469
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR1 DNA

<400> 469
agttatgcta tcacc 15

<210> 470
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR1 PRT

<400> 470
Ser Tyr Ala Ile Thr
1 5

<210> 471
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR2 DNA

<400> 471
gggatcatcc ctatctttgg tacaccaaac tacgcacaga agttccagga c 51

<210> 472
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR2 PRT

<400> 472
Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 473

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR3 DNA

<400> 473
gataaagggt tcggggaggg gaaaggttac cactactacg gtctggacgt c 51

<210> 474
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 HCDR3 PRT

<400> 474
Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly Leu Asp
1 5 10 15

<210> 475
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR1 DNA

<400> 475
actggaacca gcagtgatgt tgggagttat aaccttgtct cc 42

<210> 476
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR1 PRT

<400> 476
Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Leu Val Ser
1 5 10

<210> 477
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR2 DNA

<400> 477
gaggtcagta agcggccctc a 21

<210> 478
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR2 PRT

<400> 478
Glu Val Ser Lys Arg Pro Ser
1 5

<210> 479
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR3 DNA

<400> 479
agctcatatg caggcagcaa caatgtggta 30

<210> 480
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 LCDR3 PRT

<400> 480
Ser Ser Tyr Ala Gly Ser Asn Asn Val Val
1 5 10

<210> 481
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 VL DNA

<400> 481
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgatgttggg agttataacc ttgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc 240

caggctgagg atgaggctga ttattactgc agctcatatg caggcagcaa caatgtggta 300

ttcggcggag gcacccagct gaccgtcctc 330

<210> 482
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 VL PRT

<400> 482
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
    50 55 60

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

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

Asn Asn Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100 105 110

<210> 483
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 VH DNA

<400> 483
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcacc agttatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac 180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa 300

gggttcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc 360

ctggtcaccg tgtcctca 378

<210> 484
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 VH PRT

<400> 484
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly
100 105 110

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

<210> 485
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 VH complete DNA

<400> 485
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcacc agttatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac 180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa 300

gggttcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc 360

ctggtcaccg tgtcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 720

cctccagtgg ccggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtgggcg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aacagctccc atcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa aagcctctcc ctgtccccgg gt 1362

<210> 486
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 VH complete PRT

<400> 486
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Asn Asp Lys Gly Phe Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly
100 105 110

```
Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
        115                 120                 125

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

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

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu
                325                 330                 335
```

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


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


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400


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


Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445


Leu Ser Leu Ser Pro Gly
    450
```

<210> 487
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-F06 VL complete DNA

<400> 487

```
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgatgttggg agttataacc ttgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaagcggcc ctcaggggtt      180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc      240

caggctgagg atgaggctga ttattactgc agctcatatg caggcagcaa caatgtggta      300

ttcggcggag gcacccagct gaccgtcctc ggtcagccca aggctgcacc aagtgtcact      360
```

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 488
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-F06 VL complete PRT

<400> 488
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Asn Asn Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly Gln
100 105 110

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

```
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 489
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR1 DNA

<400> 489
agctatgcta tcagc 15

<210> 490
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR1 PRT

<400> 490
```
Ser Tyr Ala Ile Ser
1               5
```

<210> 491
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR2 DNA

<400> 491
tggatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcaggg c 51

<210> 492
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR2 PRT

<400> 492
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 493
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR3 DNA

<400> 493
ggaccactac cgtataactg gaactacgaa ggacactggt tcgacccc 48

<210> 494
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 HCDR3 PRT

<400> 494
Gly Pro Leu Pro Tyr Asn Trp Asn Tyr Glu Gly His Trp Phe Asp Pro
1 5 10 15

<210> 495
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR1 DNA

<400> 495
tctggaagca gctccaacat tgggaataat tatgtatcc 39

<210> 496
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR1 PRT

<400> 496
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser
1 5 10

<210> 497
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR2 DNA

<400> 497
ggtaacagca atcggccctc a 21

<210> 498
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR2 PRT

<400> 498
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 499
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR3 DNA

<400> 499
cagtcctatg acagcagcct gagtggttcg gta 33

<210> 500
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 LCDR3 PRT

<400> 500
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val
1 5 10

<210> 501
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 VL DNA

<400> 501
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatctat ggtaacagca atcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcac tgggctccag 240

gctgaggatg aggctgatta ttactgccag tcctatgaca gcagcctgag tggttcggta 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 502
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 VL PRT

<400> 502
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20   25   30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

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

Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 503
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 VH DNA

<400> 503
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaggacca 300

ctaccgtata actggaacta cgaaggacac tggttcgacc cctggggcca gggaaccctg 360

gtcaccgtgt cctca   375

<210> 504
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 VH PRT

<400> 504
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Pro Leu Pro Tyr Asn Trp Asn Tyr Glu Gly His Trp Phe
            100   105   110

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 505
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 VH complete DNA

<400> 505
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaggacca 300

ctaccgtata actggaacta cgaaggacac tggttcgacc cctggggcca gggaaccctg 360

gtcaccgtgt cctcagctag caccaagggc ccatcggtct tccccctggc accctcctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720

ccagtggccg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 780

tcccggaccc ctgaggtcac atgcgtggtg gtgggcgtga gccacgaaga ccctgaggtc 840

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900

gagcagtaca acagcacgta ccgggtggtc agcgtcctca ccgtcctgca ccaggactgg 960

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaac agctcccatc ccccatcgag 1020

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1140

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1260

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320

aaccactaca cgcagaaaag cctctccctg tccccgggt 1359

<210> 506
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 VH complete PRT

<400> 506
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr

```
            20                  25                  30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gly Pro Leu Pro Tyr Asn Trp Asn Tyr Glu Gly His Trp Phe
            100                 105                 110

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

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240
```

```
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

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

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

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

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

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

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

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

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

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

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

Ser Leu Ser Pro Gly
```

450

<210> 507
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C05 VL complete DNA

<400> 507
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatctat ggtaacagca atcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcac tgggctccag 240

gctgaggatg aggctgatta ttactgccag tcctatgaca gcagcctgag tggttcggta 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 508
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C05 VL complete PRT

<400> 508
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

```
        35                  40                  45

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

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

Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  509
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU534-D09 HCDR1 DNA
```

<400> 509
agttatgcta tcacc 15

<210> 510
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 HCDR1 PRT

<400> 510
Ser Tyr Ala Ile Thr
1 5

<210> 511
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 HCDR2 DNA

<400> 511
gggatcatcc ctatctttgg tacaccaaac tacgcacaga agttccagga c 51

<210> 512
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 HCDR2 PRT

<400> 512
Gly Ile Ile Pro Ile Phe Gly Thr Pro Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 513
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 HCDR3 DNA

<400> 513
gataaagggc tcggggaggg gaaaggttac cactactacg gtctggacgt c 51

<210> 514
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 HCDR3 PRT

<400> 514
Asp Lys Gly Leu Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly Leu Asp
1 5 10 15

<210> 515
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR1 DNA

<400> 515
actggaacca gcagtgacgt tggtggttat aactatgtct cc 42

<210> 516
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR1 PRT

<400> 516
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 517
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR2 DNA

<400> 517

gaggtcagta atcggccctc a 21

<210> 518
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR2 PRT

<400> 518
Glu Val Ser Asn Arg Pro Ser
1 5

<210> 519
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR3 DNA

<400> 519
acctcatata caagtaacag caatctcgcc 30

<210> 520
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 LCDR3 PRT

<400> 520
Thr Ser Tyr Thr Ser Asn Ser Asn Leu Ala
1 5 10

<210> 521
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 VL DNA

<400> 521
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc acctcatata caagtaacag caatctcgcc 300

ttcggatctg ggaccaagct gaccgtccta 330

<210> 522
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 VL PRT

<400> 522
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Thr Ser Tyr Thr Ser Asn
85 90 95

Ser Asn Leu Ala Phe Gly Ser Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 523
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 VH DNA

<400> 523
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agttatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac 180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa 300

gggctcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc 360

ctggtcaccg tgtcctca 378

<210> 524
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 VH PRT

<400> 524
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

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

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

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

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

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

Ala Asn Asp Lys Gly Leu Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly

100 105 110

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

<210> 525
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 VH complete DNA

<400> 525
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agttatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac accaaactac 180

gcacagaagt tccaggacag agtcacgatt accgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaatgataaa 300

gggctcgggg aggggaaagg ttaccactac tacggtctgg acgtctgggg ccaagggacc 360

ctggtcaccg tgtcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 720

cctccagtgg ccggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtgggcg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgggtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aacagctccc atcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa aagcctctcc ctgtccccgg gt 1362

<210> 526
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 VH complete PRT

<400> 526

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

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

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

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

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

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

Ala Asn Asp Lys Gly Leu Gly Glu Gly Lys Gly Tyr His Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

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

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

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

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu
                325                 330                 335

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
```

```
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Leu Ser Leu Ser Pro Gly
    450
```

<210> 527
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D09 VL complete DNA

<400> 527

```
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatgatt tatgaggtca gtaatcggcc ctcaggggtt      180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga ttattactgc acctcatata caagtaacag caatctcgcc      300

ttcggatctg ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact      360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata      420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag      480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc      540
```

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 528
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D09 VL complete PRT

<400> 528
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Thr Ser Tyr Thr Ser Asn
85 90 95

Ser Asn Leu Ala Phe Gly Ser Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 529
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR1 DNA

<400> 529
agctatgcta tgcat 15

<210> 530
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR1 PRT

<400> 530
Ser Tyr Ala Met His
1 5

<210> 531
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR2 DNA

<400> 531
tggatcaacg ctggcaatgg taacacaaaa tattcacaga agttccaggg c 51

<210> 532
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR2 PRT

<400> 532
Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
1 5 10 15

<210> 533
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR3 DNA

<400> 533
tcgttcgatt cggggagtta ttataacgta gatgcttttg atatc 45

<210> 534
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 HCDR3 PRT

<400> 534
Ser Phe Asp Ser Gly Ser Tyr Tyr Asn Val Asp Ala Phe Asp Ile
1 5 10 15

<210> 535
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR1 DNA

<400> 535
cgggccagtc agagtattag tagctggttg gcc 33

<210> 536
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR1 PRT

<400> 536
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 537
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR2 DNA

<400> 537
gatgcctcca gtttggaaag t 21

<210> 538
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR2 PRT

<400> 538
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 539
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR3 DNA

<400> 539
caacagtata atagttattc gtggacg 27

<210> 540

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 LCDR3 PRT

<400> 540
Gln Gln Tyr Asn Ser Tyr Ser Trp Thr
1 5

<210> 541
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 VL DNA

<400> 541
gacatcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attcgtggac gttcggccaa 300

gggaccaagg tggagatcaa a 321

<210> 542
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 VL PRT

<400> 542
Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Trp
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 543
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 VH DNA

<400> 543
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agctatgcta tgcattgggt gcgccaggcc 120

cccggacaaa ggcctgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat 180

tcacagaagt tccagggcag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagatcgttc 300

gattcgggga gttattataa cgtagatgct tttgatatct ggggccaagg gacaatggtc 360

accgtgtctt ca   372

<210> 544
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 VH PRT

<400> 544
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 Ser Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Phe Asp Ser Gly Ser Tyr Tyr Asn Val Asp Ala Phe Asp
            100                 105                 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 545
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 VH complete DNA

<400> 545

```
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt       60

tcctgcaagg cttctggata caccttcact agctatgcta tgcattgggt gcgccaggcc      120

cccggacaaa ggcctgagtg gatgggatgg atcaacgctg gcaatggtaa cacaaaatat      180

tcacagaagt tccagggcag agtcaccatt accagggaca tccgcgagg cacagcctac       240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagatcgttc      300

gattcgggga gttattataa cgtagatgct tttgatatct ggggccaagg gacaatggtc      360

accgtgtctt cagctagcac caagggccca tcggtcttcc ccctggcacc ctcctccaag      420

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg      480
```

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctcca 720

gtggccggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg ggcgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg ggtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaacagc tcccatcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaaaagcct ctccctgtcc ccgggt 1356

<210> 546
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 VH complete PRT

<400> 546
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 Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp Met
35 40 45

```
Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Phe Asp Ser Gly Ser Tyr Tyr Asn Val Asp Ala Phe Asp
            100                 105                 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 547
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-C06 VL complete DNA

<400> 547
gacatcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attcgtggac gttcggccaa 300

gggaccaagg tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 548
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-C06 VL complete PRT

<400> 548
Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 549
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR1 DNA

<400> 549
agctatgcca tgagc 15

<210> 550

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR1 PRT

<400> 550
Ser Tyr Ala Met Ser
1 5

<210> 551
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR2 DNA

<400> 551
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 552
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR2 PRT

<400> 552
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 553
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR3 DNA

<400> 553
ggtccgaggg ggtctgctga ctacgttgac tac 33

<210> 554
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 HCDR3 PRT

<400> 554
Gly Pro Arg Gly Ser Ala Asp Tyr Val Asp Tyr
1 5 10

<210> 555
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR1 DNA

<400> 555
cgggccagtc acagtattag tagctggttg gcc 33

<210> 556
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR1 PRT

<400> 556
Arg Ala Ser His Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 557
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR2 DNA

<400> 557
gatgcctcca gtttggaaag t 21

<210> 558
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR2 PRT

<400> 558
Asp Ala Ser Ser Leu Glu Ser
1   5

<210> 559
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR3 DNA

<400> 559
caacagtata atacttattc agggacg   27

<210> 560
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 LCDR3 PRT

<400> 560
Gln Gln Tyr Asn Thr Tyr Ser Gly Thr
1   5

<210> 561
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 VL DNA

<400> 561
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc gggccagtca cagtattagt agctggttgg cctggtatca gcagaaacca   120

gggaaagccc ctcagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca   180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct   240

gatgattttg caacttatta ctgccaacag tataatactt attcagggac gttcggccaa   300

gggaccaaag tggatatcaa a 321

<210> 562
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 VL PRT

<400> 562
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Ser Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 563
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 VH DNA

<400> 563
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccg 300

agggggtctg ctgactacgt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

360

<210> 564
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 VH PRT

<400> 564
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Pro Arg Gly Ser Ala Asp Tyr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 565

<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 VH complete DNA

<400> 565
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccg 300

agggggtctg ctgactacgt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 566
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-A09 VH complete PRT

<400> 566
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Pro Arg Gly Ser Ala Asp Tyr Val 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
```

385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 567
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-A09 VL complete DNA

<400> 567
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca cagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctcagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatactt attcagggac gttcggccaa 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 568
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> YU535-A09 VL complete PRT

<400> 568

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                  10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Ser Ile Ser Ser Trp
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Ser Gly
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Asp 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> 569
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR1 DNA

<400> 569
agctatgcca tgagc   15

<210> 570
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR1 PRT

<400> 570
Ser Tyr Ala Met Ser
1   5

<210> 571
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR2 DNA

<400> 571
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c   51

<210> 572
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR2 PRT

<400> 572
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

<210> 573
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR3 DNA

<400> 573
ggtccgaggg ggtctgctga ctacgttgac tac 33

<210> 574
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 HCDR3 PRT

<400> 574
Gly Pro Arg Gly Ser Ala Asp Tyr Val Asp Tyr
1 5 10

<210> 575
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR1 DNA

<400> 575
cgggccagtc agagtattag tagctggttg gcc 33

<210> 576
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR1 PRT

<400> 576
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 577
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR2 DNA

<400> 577
gatgcctcca gtttggaaag t 21

<210> 578
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR2 PRT

<400> 578
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 579
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR3 DNA

<400> 579
caacagtata atagttattc gtacact 27

<210> 580
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 LCDR3 PRT

<400> 580
Gln Gln Tyr Asn Ser Tyr Ser Tyr Thr
1 5

<210> 581
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 VL DNA

<400> 581
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attcgtacac ttttggccag 300

gggacacgac tggagattaa a 321

<210> 582
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 VL PRT

<400> 582
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 583
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 VH DNA

<400> 583
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccg 300

agggggtctg ctgactacgt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

360

<210> 584
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 VH PRT

<400> 584
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Pro Arg Gly Ser Ala Asp Tyr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 585
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 VH complete DNA

<400> 585
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccg 300

agggggtctg ctgactacgt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 586
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 VH complete PRT

<400> 586
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Lys Gly Pro Arg Gly Ser Ala Asp Tyr Val 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
```

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 587
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G09 VL complete DNA

<400> 587
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attcgtacac ttttggccag 300

gggacacgac tggagattaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 588
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G09 VL complete PRT

<400> 588
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 589
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR1 DNA

<400> 589
agctatgcca tgagc 15

<210> 590
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR1 PRT

<400> 590
Ser Tyr Ala Met Ser
1 5

<210> 591
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR2 DNA

<400> 591
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 592
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR2 PRT

<400> 592
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 593
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR3 DNA

<400> 593
ggggtccgat ataactccga ctactttgac tac 33

<210> 594
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 HCDR3 PRT

<400> 594
Gly Val Arg Tyr Asn Ser Asp Tyr Phe Asp Tyr
1 5 10

<210> 595
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR1 DNA

<400> 595
cgggccagtc agagtattag tagctggttg gcc 33

<210> 596
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR1 PRT

<400> 596
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 597
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR2 DNA

<400> 597
gatgcctcca gtttggaaag t 21

<210> 598
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR2 PRT

<400> 598
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 599
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR3 DNA

<400> 599
caacagtata atagtgttct cggggtcact 30

<210> 600
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 LCDR3 PRT

<400> 600
Gln Gln Tyr Asn Ser Val Leu Gly Val Thr
1 5 10

<210> 601
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 VL DNA

<400> 601
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtg ttctcggggt cactttcggc 300

ggagggacca agctggagat caaa 324

<210> 602
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 VL PRT

<400> 602
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Val Leu Gly
                85                  90                  95

Val Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 603
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 VH DNA

<400> 603

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtc      300

cgatataact ccgactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca      360

                                                                       360
```

<210> 604
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 VH PRT

<400> 604
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Gly Val Arg Tyr Asn Ser Asp Tyr Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 605
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 VH complete DNA

<400> 605
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtc 300

cgatataact ccgactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 606
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 VH complete PRT

<400> 606
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

```
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Val Arg Tyr Asn Ser Asp Tyr Phe 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240
```

```
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 607

<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H01 VL complete DNA

<400> 607
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtg ttctcggggt cactttcggc 300

ggagggacca agctggagat caaacgtacg gtggctgcac catctgtgtt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 608
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H01 VL complete PRT

<400> 608
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Val Leu Gly
85 90 95

Val Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 609
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR1 DNA

<400> 609
agctatgcca tgagc 15

<210> 610
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR1 PRT

<400> 610
Ser Tyr Ala Met Ser
1 5

<210> 611
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR2 DNA

<400> 611
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 612
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR2 PRT

<400> 612
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 613
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR3 DNA

<400> 613
ggggtcagat actcatcaga ctattttgag tac 33

<210> 614
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 HCDR3 PRT

<400> 614
Gly Val Arg Tyr Ser Ser Asp Tyr Phe Glu Tyr
1 5 10

<210> 615
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR1 DNA

<400> 615
cgggccagtc agagtattag tagctggttg gcc 33

<210> 616
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR1 PRT

<400> 616
Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 617
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR2 DNA

<400> 617
gatgcctcca gtttggaaag t 21

<210> 618

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR2 PRT

<400> 618
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 619
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR3 DNA

<400> 619
caacagtatg agacttattc tcagacg 27

<210> 620
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 LCDR3 PRT

<400> 620
Gln Gln Tyr Glu Thr Tyr Ser Gln Thr
1 5

<210> 621
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 VL DNA

<400> 621
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240

gatgattttg caacttatta ctgtcaacag tatgagactt attctcagac gttcggccaa 300

gggaccaagc tggagatcaa a 321

<210> 622
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 VL PRT

<400> 622
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Glu Thr Tyr Ser Gln
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 623
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 VH DNA

<400> 623
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtc 300

agatactcat cagactattt tgagtactgg ggccagggaa ccacggtcac cgtgtcctca 360

360

<210> 624
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 VH PRT

<400> 624
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Val Arg Tyr Ser Ser Asp Tyr Phe Glu Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 625
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 VH complete DNA

<400> 625
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtc 300

agatactcat cagactattt tgagtactgg ggccagggaa ccacggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 626
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-H05 VH complete PRT

<400> 626
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Val Arg Tyr Ser Ser Asp Tyr Phe Glu Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
```

```
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 627
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-H05 VL complete DNA

<400> 627

```
gacatccagt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca      180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagtct      240

gatgattttg caacttatta ctgtcaacag tatgagactt attctcagac gttcggccaa      300

gggaccaagc tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag      480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                         642
```

<210> 628
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> YU536-H05 VL complete PRT

<400> 628

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                  10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80


Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Glu Thr Tyr Ser Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
```

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205

Phe Asn Arg Gly Glu Cys
    210

<210> 629
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR1 DNA

<400> 629
agctatgcca tgagc   15

<210> 630
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR1 PRT

<400> 630
Ser Tyr Ala Met Ser
1   5

<210> 631
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR2 DNA

<400> 631
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c   51

<210> 632
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR2 PRT

<400> 632
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 633
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR3 DNA

<400> 633
ggtccccgta gtggtactga ctactttgac tac 33

<210> 634
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 HCDR3 PRT

<400> 634
Gly Pro Arg Ser Gly Thr Asp Tyr Phe Asp Tyr
1 5 10

<210> 635
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR1 DNA

<400> 635
cgggccagtg agagtattcg gagctggttg gcc 33

<210> 636
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR1 PRT

<400> 636
Arg Ala Ser Glu Ser Ile Arg Ser Trp Leu Ala
1 5 10

<210> 637
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR2 DNA

<400> 637
gatgcctcca atttggaaag t 21

<210> 638
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR2 PRT

<400> 638
Asp Ala Ser Asn Leu Glu Ser
1 5

<210> 639
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR3 DNA

<400> 639
caacagtatt atagttatcc gctcact 27

<210> 640
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 LCDR3 PRT

<400> 640
Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr

1 5

<210> 641
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 VL DNA

<400> 641
gacatccaga tgacccagtc tccttccatc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtga gagtattcgg agctggttgg cctggtatca gcagaaggca 120

gggaaagccc ctaacctcct aatctatgat gcctccaatt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggtcagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tattatagtt atccgctcac tttcggcgga 300

gggaccaaag tggatatcaa a 321

<210> 642
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 VL PRT

<400> 642
Asp Ile Gln Met Thr Gln Ser Pro Ser Ile Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Ile Arg Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

```
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  643
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU535-G02 VH DNA

<400>  643
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccc      300

cgtagtggta ctgactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca      360

                                                                       360



<210>  644
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU535-G02 VH PRT

<400>  644
Gln 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 Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Pro Arg Ser Gly Thr Asp Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 645
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G02 VH complete DNA

<400> 645

```
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtccc      300

cgtagtggta ctgactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca      360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc      600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg      720
```

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 646
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 VH complete PRT

<400> 646
Gln 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 Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

```
                85                  90                  95

Ala Lys Gly Pro Arg Ser Gly Thr Asp Tyr Phe 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
```

```
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320


Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335


Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350


Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365


Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380


Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400


Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415


Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430


Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445


<210>  647
<211>  642
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU535-G02 VL complete DNA

<400>  647
gacatccaga tgacccagtc tccttccatc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggccagtga gagtattcgg agctggttgg cctggtatca gcagaaggca      120

gggaaagccc ctaacctcct aatctatgat gcctccaatt tggaaagtgg ggtcccatca      180

aggttcagcg gcagtggatc tgggtcagaa ttcactctca ccatcagcag cctgcagcct      240
```

gatgattttg caacttatta ctgccaacag tattatagtt atccgctcac tttcggcgga 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 648
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G02 VL complete PRT

<400> 648
Asp Ile Gln Met Thr Gln Ser Pro Ser Ile Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Ile Arg Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp 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> 649
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR1 DNA

<400> 649
agctatgcca tgagc 15

<210> 650
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR1 PRT

<400> 650
Ser Tyr Ala Met Ser
1 5

<210> 651

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR2 DNA

<400> 651
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 652
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR2 PRT

<400> 652
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 653
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR3 DNA

<400> 653
ggaccgagaa gtggctacga ctatggggac tac 33

<210> 654
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 HCDR3 PRT

<400> 654
Gly Pro Arg Ser Gly Tyr Asp Tyr Gly Asp Tyr
1 5 10

<210> 655
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR1 DNA

<400> 655
cgggcgagtc agggtattag cagctggtta gcc 33

<210> 656
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR1 PRT

<400> 656
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 657
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR2 DNA

<400> 657
gatgcctcca gtttggaaag t 21

<210> 658
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR2 PRT

<400> 658
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 659
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR3 DNA

<400> 659
caacagttta atagttaccc tctcact 27

<210> 660
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 LCDR3 PRT

<400> 660
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 661
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 VL DNA

<400> 661
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatcg 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag tttaatagtt accctctcac tttcggcgga 300

gggaccaagg tggaaatcaa a 321

<210> 662
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 VL PRT

<400> 662

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 663
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 VH DNA

<400> 663

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggaccg      300

agaagtggct acgactatgg ggactactgg ggccagggaa ccctggtcac cgtgtcctca      360

                                                                       360
```

<210> 664

<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 VH PRT

<400> 664
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Pro Arg Ser Gly Tyr Asp Tyr Gly Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 665
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 VH complete DNA

<400> 665
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggaccg 300

agaagtggct acgactatgg ggactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 666
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 VH complete PRT

<400> 666
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Pro Arg Ser Gly Tyr Asp Tyr Gly 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 667
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-G11 VL complete DNA

<400> 667
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatcg 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag tttaatagtt accctctcac tttcggcgga 300

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 668
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-G11 VL complete PRT

<400> 668
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

```
Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Gly 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> 669
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR1 DNA

<400> 669
agctatgcca tgagc 15

<210> 670
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR1 PRT

<400> 670
Ser Tyr Ala Met Ser
1 5

<210> 671
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR2 DNA

<400> 671
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 672
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR2 PRT

<400> 672
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 673
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR3 DNA

<400> 673

tcggtgggtt actatgatag tagtggttat tatcactttg gggactactt tgactac 57

<210> 674
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 HCDR3 PRT

<400> 674
Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 675
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR1 DNA

<400> 675
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 676
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR1 PRT

<400> 676
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 677
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR2 DNA

<400> 677
ggtaacagca atcggccctc a 21

<210> 678
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR2 PRT

<400> 678
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 679
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR3 DNA

<400> 679
cagtcctatg acagcagcct gagtggttcg gta 33

<210> 680
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 LCDR3 PRT

<400> 680
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val
1 5 10

<210> 681
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 VL DNA

<400> 681

cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 682
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 VL PRT

<400> 682
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 683
<211> 384
<212> DNA

<213> Artificial Sequence

<220>
<223> YU534-B11 VH DNA

<400> 683
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc ccgctcggtg 300

ggttactatg atagtagtgg ttattatcac tttggggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 684
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 VH PRT

<400> 684
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 685
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 VH complete DNA

<400> 685
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc ccgctcggtg 300

ggttactatg atagtagtgg ttattatcac tttggggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt ccccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 686
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 VH complete PRT

<400> 686
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

```
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350
```

```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 687
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-B11 VL complete DNA

<400> 687

```
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc agggcagag ggtcaccatc       60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag      120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc      180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc      360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
```

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 688
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-B11 VL complete PRT

<400> 688
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val

145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 689
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR1 DNA

<400> 689
agctatgcca tgagc 15

<210> 690
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR1 PRT

<400> 690
Ser Tyr Ala Met Ser
1 5

<210> 691
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR2 DNA

<400> 691

gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 692
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR2 PRT

<400> 692
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 693
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR3 DNA

<400> 693
tcggtgggtt actatgatag tagtggttat tatcactttg gggactactt tgactac 57

<210> 694
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 HCDR3 PRT

<400> 694
Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 695
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-C10 LCDR1 DNA

<400> 695
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 696
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 LCDR1 PRT

<400> 696
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 697
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 LCDR2 DNA

<400> 697
ggtaacagca atcggccctc a 21

<210> 698
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 LCDR2 PRT

<400> 698
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 699
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 LCDR3 DNA

<400> 699
cagtcctatg acagcagcct gagtggagtg gta 33

<210> 700
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 LCDR3 PRT

<400> 700
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Val Val
1 5 10

<210> 701
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 VL DNA

<400> 701
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggagtg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 702
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 VL PRT

<400> 702
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 703
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 VH DNA

<400> 703
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc ccgctcggtg 300

ggttactatg atagtagtgg ttattatcac tttggggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca   384

<210> 704
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 VH PRT

<400> 704
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly
            100   105   110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 705
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 VH complete DNA

<400> 705
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc ccgctcggtg   300

ggttactatg atagtagtgg ttattatcac tttggggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 706
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 VH complete PRT

<400> 706
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Val Gly Tyr Tyr Asp Ser Ser Gly Tyr Tyr His Phe Gly
            100                 105                 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240
```

```
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 707
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C10 VL complete DNA

<400> 707
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc agggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggagtg 300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 708
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C10 VL complete PRT

<400> 708
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

```
Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 709
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR1 DNA

<400> 709
agctactgga tcggc 15

<210> 710
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR1 PRT

<400> 710
Ser Tyr Trp Ile Gly
1 5

<210> 711
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR2 DNA

<400> 711
atcatctatc ctggtgactc tgataccaga tacagcccgt ccttccaagg c 51

<210> 712
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR2 PRT

<400> 712
Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

<210> 713
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR3 DNA

<400> 713

caaaattact atgatagtag tggttattac tactttgact ac 42

<210> 714
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 HCDR3 PRT

<400> 714
Gln Asn Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 715
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR1 DNA

<400> 715
cgggcaagtc agagcattag cagctattta aat 33

<210> 716
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR1 PRT

<400> 716
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 717
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR2 DNA

<400> 717
gctgcatcca gtttgcaaag t 21

<210> 718
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR2 PRT

<400> 718
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 719
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR3 DNA

<400> 719
caacagagtt acagtaccca ttcgtggacg 30

<210> 720
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 LCDR3 PRT

<400> 720
Gln Gln Ser Tyr Ser Thr His Ser Trp Thr
1 5 10

<210> 721
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 VL DNA

<400> 721
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccattcgtg gacgttcggc 300

caagggacca aagtggatat caaa 324

<210> 722
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 VL PRT

<400> 722
Asp Ile Gln Leu 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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr His Ser
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 723
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 VH DNA

<400> 723
caggttcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagccaaaat 300

tactatgata gtagtggtta ttactacttt gactactggg gccagggaac cctggtcacc 360

gtgtcctca 369

<210> 724
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 VH PRT

<400> 724
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Ser Gln Asn Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 725
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 VH complete DNA

<400> 725
caggttcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagccaaaat 300

tactatgata gtagtggtta ttactacttt gactactggg gccagggaac cctggtcacc 360

gtgtcctcag ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctccagtg 720

gccggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtgggc gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaacagctcc catcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga aaagcctctc cctgtccccg ggt 1353

<210> 726
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 VH complete PRT

<400> 726
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Ser Gln Asn Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

```
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        355                 360                 365
```

```
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly
    450
```

<210> 727
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-D10 VL complete DNA

<400> 727

```
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagattttg caacttacta ctgtcaacag agttacagta cccattcgtg gacgttcggc      300

caagggacca aagtggatat caaacgtacg gtggctgcac catctgtgtt catcttcccg      360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
```

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 728
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-D10 VL complete PRT

<400> 728
Asp Ile Gln Leu 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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr His Ser
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

```
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 729
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR1 DNA

<400> 729
agctactgga tcggc 15

<210> 730
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR1 PRT

<400> 730
Ser Tyr Trp Ile Gly
1 5

<210> 731
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR2 DNA

<400> 731
atcatctatc ctggtgactc tgataccaga tacagcccgt ccttccaagg c 51

<210> 732
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR2 PRT

<400> 732
Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

<210> 733
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR3 DNA

<400> 733
agtcggagta gtgactactt tgactac 27

<210> 734
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 HCDR3 PRT

<400> 734
Ser Arg Ser Ser Asp Tyr Phe Asp Tyr
1 5

<210> 735
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR1 DNA

<400> 735
cgggcgagtc agggtattag cagctggtta gcc 33

<210> 736

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR1 PRT

<400> 736
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 737
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR2 DNA

<400> 737
gatgcatcca atttggaaac a 21

<210> 738
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR2 PRT

<400> 738
Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 739
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR3 DNA

<400> 739
caacagtatg ataatctccc tgtcact 27

<210> 740
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> YU535-B02 LCDR3 PRT

<400> 740
Gln Gln Tyr Asp Asn Leu Pro Val Thr
1 5

<210> 741
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 VL DNA

<400> 741
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctgtcac tttcggcgga 300

gggaccaaag tggatatcaa a 321

<210> 742
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 VL PRT

<400> 742
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

```
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Val
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 743
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 VH DNA

<400> 743
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtcgg 300

agtagtgact actttgacta ctggggccag ggaaccacgg tcaccgtgtc ctca 354

<210> 744
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 VH PRT

<400> 744
```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30
```

```
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60


Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80


Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Arg Ser Ser Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser
        115


<210>  745
<211>  1338
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU535-B02 VH complete DNA

<400>  745
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc       60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg      120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac      180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac      240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtcgg      300

agtagtgact actttgacta ctggggccag ggaaccacgg tcaccgtgtc ctcagctagc      360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca      420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac      480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc      540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc      600
```

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctc cagtggccgg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tgggcgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaaca gctcccatcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaaaagc 1320

ctctccctgt ccccgggt 1338

<210> 746
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 VH complete PRT

<400> 746
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

```
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Arg Ser Ser Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
```

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 747
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU535-B02 VL complete DNA

<400> 747
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctgtcac tttcggcgga 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 748
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU535-B02 VL complete PRT

<400> 748
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Val
85 90 95

```
Thr Phe Gly Gly Gly Thr Lys Val Asp 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>  749
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU534-D07 HCDR1 DNA

<400>  749
agctactgga tcggc                                                    15



<210>  750
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU534-D07 HCDR1 PRT

<400>  750
```

Ser Tyr Trp Ile Gly
1 5

<210> 751
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 HCDR2 DNA

<400> 751
atcatctatc ctggtgactc tgataccaga tacagcccgt ccttccaagg c 51

<210> 752
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 HCDR2 PRT

<400> 752
Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

<210> 753
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 HCDR3 DNA

<400> 753
tataacagtg gctggcttga ctac 24

<210> 754
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 HCDR3 PRT

<400> 754
Tyr Asn Ser Gly Trp Leu Asp Tyr

1 5

<210> 755
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR1 DNA

<400> 755
tctggaagca gctccaacat cggaagtaat cctgtaaac 39

<210> 756
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR1 PRT

<400> 756
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Pro Val Asn
1 5 10

<210> 757
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR2 DNA

<400> 757
agtaataatc agcggccctc a 21

<210> 758
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR2 PRT

<400> 758
Ser Asn Asn Gln Arg Pro Ser
1 5

<210> 759
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR3 DNA

<400> 759
gcagcatggg atgacagcct gaatggtaat gtgtta 36

<210> 760
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 LCDR3 PRT

<400> 760
Ala Ala Trp Asp Asp Ser Leu Asn Gly Asn Val Leu
1 5 10

<210> 761
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 VL DNA

<400> 761
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatcctg taaactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tggactccag 240

tctgaggatg aggctgacta ttactgtgca gcatgggatg acagcctgaa tggtaatgtg 300

ttatttggcg gagggaccaa gctgaccgtc cta 333

<210> 762
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 VL PRT

<400> 762
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Pro Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Asn Gly Asn Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 763
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 VH DNA

<400> 763
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc   60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg   120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac   180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac   240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc taggtataac   300

agtggctggc ttgactactg gggccaggga accacggtca ccgtgtcctc a   351

<210> 764
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 VH PRT

<400> 764
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Tyr Asn Ser Gly Trp Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 765
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 VH complete DNA

<400> 765
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc taggtataac 300

agtggctggc ttgactactg gggccaggga accacggtca ccgtgtcctc agctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 766
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 VH complete PRT

<400> 766
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Tyr Asn Ser Gly Trp Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His

```
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 767
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-D07 VL complete DNA

<400> 767
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatcctg taaactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tggactccag 240

tctgaggatg aggctgacta ttactgtgca gcatgggatg acagcctgaa tggtaatgtg 300

ttatttggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 768
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-D07 VL complete PRT

<400> 768
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

```
Pro Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Asn Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 769
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 HCDR1 DNA

<400> 769
agctactata tgcac   15

<210> 770
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 HCDR1 PRT

<400> 770
Ser Tyr Tyr Met His
1   5

<210> 771
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 HCDR2 DNA

<400> 771
ataatcaacc ctagtggtgg tagcacaagc tacgcacaga agttccaggg c   51

<210> 772
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 HCDR2 PRT

<400> 772
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1   5   10   15

<210> 773
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> YU537-H08 HCDR3 DNA

<400> 773
gcgagtcggg attactatga tagtagtggt tatttgcgtc gaatgggggg cgactac 57

<210> 774
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 HCDR3 PRT

<400> 774
Ala Ser Arg Asp Tyr Tyr Asp Ser Ser Gly Tyr Leu Arg Arg Met Gly
1 5 10 15

Gly Asp Tyr

<210> 775
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR1 DNA

<400> 775
gggggaaaca acattggaag taaaagtgtg cac 33

<210> 776
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR1 PRT

<400> 776
Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 777
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR2 DNA

<400> 777
gatgatagcg accggccctc a 21

<210> 778
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR2 PRT

<400> 778
Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 779
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR3 DNA

<400> 779
caggtgtggg acagcagcac tgcggta 27

<210> 780
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 LCDR3 PRT

<400> 780
Gln Val Trp Asp Ser Ser Thr Ala Val
1 5

<210> 781
<211> 318
<212> DNA
<213> Artificial Sequence

<220>

<223> YU537-H08 VL DNA

<400> 781
cagtctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gacagcagca ctgcggtatt cggcggaggg 300

accaagctga ccgtccta 318

<210> 782
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 VL PRT

<400> 782
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Thr Ala Val
                85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 783
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 VH DNA

<400> 783
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagcgagt 300

cgggattact atgatagtag tggttatttg cgtcgaatgg ggggcgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 784
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 VH PRT

<400> 784
Glu Val Gln Leu Val Glu 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 Ser Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Ser Arg Asp Tyr Tyr Asp Ser Ser Gly Tyr Leu Arg Arg
100 105 110

Met Gly Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 785
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 VH complete DNA

<400> 785
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagcgagt 300

cgggattact atgatagtag tggttatttg cgtcgaatgg ggggcgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 786
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 VH complete PRT

<400> 786
Glu Val Gln Leu Val Glu 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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Ser Arg Asp Tyr Tyr Asp Ser Ser Gly Tyr Leu Arg Arg
100 105 110

Met Gly Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

```
Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 787
<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> YU537-H08 VL complete DNA

<400> 787

```
cagtctgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg gacagcagca ctgcggtatt cggcggaggg      300

accaagctga ccgtcctagg tcagcccaag gctgcaccaa gtgtcactct gttcccgccc      360

tcctctgagg agcttcaagc caacaaggcc acactggtgt gtctcataag tgacttctac      420
```

ccgggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc gggagtggag 480

accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgagcctg 540

acgcctgagc agtggaagtc ccacagaagc tacagctgcc aggtcacgca tgaagggagc 600

accgtggaga agacagtggc ccctacagaa tgttca 636

<210> 788
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> YU537-H08 VL complete PRT

<400> 788
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Thr Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
195 200 205

Thr Glu Cys Ser
210

<210> 789
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 HCDR1 DNA

<400> 789
acctatgcca tgggc 15

<210> 790
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 HCDR1 PRT

<400> 790
Thr Tyr Ala Met Gly
1 5

<210> 791
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-E01 HCDR2 DNA

<400> 791
actattagtg gtactggtgg tatcacatac tacgcagact ccgtgaaggg c 51

<210> 792
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 HCDR2 PRT

<400> 792
Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 793
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 HCDR3 DNA

<400> 793
gtcggagata attactatga taggagtggt aattatcaca tggactactt tgactac 57

<210> 794
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 HCDR3 PRT

<400> 794
Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 795
<211> 39
<212> DNA

<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR1 DNA

<400> 795
tctggaagca gctccaacat tgggaataat tatgtatcc 39

<210> 796
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR1 PRT

<400> 796
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser
1 5 10

<210> 797
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR2 DNA

<400> 797
gaagataatg agcgaccctc a 21

<210> 798
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR2 PRT

<400> 798
Glu Asp Asn Glu Arg Pro Ser
1 5

<210> 799
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR3 DNA

<400> 799
ggaacatggg atagcagcct gagtgttatg tta 33

<210> 800
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 LCDR3 PRT

<400> 800
Gly Thr Trp Asp Ser Ser Leu Ser Val Met Leu
1 5 10

<210> 801
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 VL DNA

<400> 801
cagtctgtgt tgacgccgcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccaacacctc 120

ccaggaacag cccccaaact cctcatctat gaagataatg agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tccgccaccc tgggcatcac cggactccag 240

actggggacg agggcgattt ttactgcgga acatgggata gcagcctgag tgttatgtta 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 802
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 VL PRT

<400> 802
Gln Ser Val Leu Thr Pro Pro Pro Ser Val Ser Ala Ala Pro Gly Gln

1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Tyr Val Ser Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Glu Asp Asn Glu Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Gly Asp Phe Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Val Met Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 803
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 VH DNA

<400> 803
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgggctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 804
<211> 128

<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 VH PRT

<400> 804
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
            100   105   110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 805
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 VH complete DNA

<400> 805
caggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgggctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 806
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 VH complete PRT

<400> 806
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
            100                 105                 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
```

```
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445
```

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 807
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-E01 VL complete DNA

<400> 807
cagtctgtgt tgacgccgcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccaacacctc 120

ccaggaacag cccccaaact cctcatctat gaagataatg agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tccgccaccc tgggcatcac cggactccag 240

actggggacg agggcgattt ttactgcgga acatgggata gcagcctgag tgttatgtta 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 808
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-E01 VL complete PRT

<400> 808
Gln Ser Val Leu Thr Pro Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

```
Tyr Val Ser Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Glu Asp Asn Glu Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80

Thr Gly Asp Glu Gly Asp Phe Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Ser Val Met Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 809
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 HCDR1 DNA

<400> 809
acctatgcca tgagc 15

<210> 810
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 HCDR1 PRT

<400> 810
Thr Tyr Ala Met Ser
1 5

<210> 811
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 HCDR2 DNA

<400> 811
actattagtg gtactggtgg tatcacatac tacgcagact ccgtgaaggg c 51

<210> 812
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 HCDR2 PRT

<400> 812
Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 813
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-C02 HCDR3 DNA

<400> 813
gtcggagata attactatga taggagtggt aattatcaca tggactactt tgactac 57

<210> 814
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 HCDR3 PRT

<400> 814
Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 815
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR1 DNA

<400> 815
actgggagca gctccaacat cggggcagct tatgatgtac ac 42

<210> 816
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR1 PRT

<400> 816
Thr Gly Ser Ser Ser Asn Ile Gly Ala Ala Tyr Asp Val His
1 5 10

<210> 817
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR2 DNA

<400> 817
gaaaacaaca agcggccctc a 21

<210> 818
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR2 PRT

<400> 818
Glu Asn Asn Lys Arg Pro Ser
1 5

<210> 819
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR3 DNA

<400> 819
ggaacgtggg atggcagcct gagtgtt 27

<210> 820
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 LCDR3 PRT

<400> 820
Gly Thr Trp Asp Gly Ser Leu Ser Val
1 5

<210> 821
<211> 327
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-C02 VL DNA

<400> 821
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcagcttatg atgtacactg gtaccagcag 120

cttccaggaa cggcccccaa actcctcatc tatgaaaaca acaagcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acgtcagcca ccctgggcat caccggactc 240

cagactgggg acgaggccga ttatttctgc ggaacgtggg atggcagcct gagtgttttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 822
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 VL PRT

<400> 822
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Ala
            20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35 40 45

Leu Ile Tyr Glu Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu
65 70 75 80

Gln Thr Gly Asp Glu Ala Asp Tyr Phe Cys Gly Thr Trp Asp Gly Ser
                85 90 95

Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 823
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 VH DNA

<400> 823
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 824
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 VH PRT

<400> 824
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 825
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 VH complete DNA

<400> 825
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 826
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 VH complete PRT

<400> 826
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

```
Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 827
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C02 VL complete DNA

<400> 827

```
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc       60

tcctgcactg ggagcagctc caacatcggg gcagcttatg atgtacactg gtaccagcag      120

cttccaggaa cggcccccaa actcctcatc tatgaaaaca acaagcggcc ctcaggggtc      180

cctgaccgat tctctggctc caagtctggc acgtcagcca ccctgggcat caccggactc      240

cagactgggg acgaggccga ttatttctgc ggaacgtggg atggcagcct gagtgttttc      300

ggcggaggga ccaagctgac cgtcctaggt cagcccaagg ctgcaccaag tgtcactctg      360

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt      420
```

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 540

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 645

<210> 828
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C02 VL complete PRT

<400> 828
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Ala
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Glu Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu
65 70 75 80

Gln Thr Gly Asp Glu Ala Asp Tyr Phe Cys Gly Thr Trp Asp Gly Ser
85 90 95

Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Thr Glu Cys Ser
210 215

<210> 829
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 HCDR1 DNA

<400> 829
acctatgcca tgagc 15

<210> 830
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 HCDR1 PRT

<400> 830
Thr Tyr Ala Met Ser
1 5

<210> 831
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-C06 HCDR2 DNA

<400> 831
actattagtg gtactggtgg tatcacatac tacgcagact ccgtgaaggg c 51

<210> 832
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 HCDR2 PRT

<400> 832
Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 833
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 HCDR3 DNA

<400> 833
gtcggagata attactatga taggagtggt aattatcaca tggactactt tgactac 57

<210> 834
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 HCDR3 PRT

<400> 834
Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 835
<211> 42
<212> DNA

<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR1 DNA

<400> 835
actgggagca cctccaacat cggggcaggt tatgatgttc ag 42

<210> 836
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR1 PRT

<400> 836
Thr Gly Ser Thr Ser Asn Ile Gly Ala Gly Tyr Asp Val Gln
1 5 10

<210> 837
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR2 DNA

<400> 837
gaggacaaca atcggccctc a 21

<210> 838
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR2 PRT

<400> 838
Glu Asp Asn Asn Arg Pro Ser
1 5

<210> 839
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR3 DNA

<400> 839
cagtcctctg tcagcagcct gagtgctgtg gta 33

<210> 840
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 LCDR3 PRT

<400> 840
Gln Ser Ser Val Ser Ser Leu Ser Ala Val Val
1 5 10

<210> 841
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 VL DNA

<400> 841
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcacctc caacatcggg gcaggttatg atgttcagtg gtaccagcag 120

cttccaggaa aagcccccaa actcctcgtc tatgaggaca acaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggccgagg atgaggctga ttattactgc cagtcctctg tcagcagcct gagtgctgtg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 842
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 VL PRT

<400> 842
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val Gln Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu
35 40 45

Leu Val Tyr Glu Asp Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Val Ser Ser
85 90 95

Leu Ser Ala Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 843
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 VH DNA

<400> 843
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 844
<211> 128

<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 VH PRT

<400> 844
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 845
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 VH complete DNA

<400> 845
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 846
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 VH complete PRT

<400> 846
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
            100                 105                 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
```

```
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445
```

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 847
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-C06 VL complete DNA

<400> 847
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcacctc caacatcggg gcaggttatg atgttcagtg gtaccagcag 120

cttccaggaa aagcccccaa actcctcgtc tatgaggaca acaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggccgagg atgaggctga ttattactgc cagtcctctg tcagcagcct gagtgctgtg 300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 848
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-C06 VL complete PRT

<400> 848
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn Ile Gly Ala Gly
20 25 30

```
Tyr Asp Val Gln Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Leu Val Tyr Glu Asp Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Val Ser Ser
                85                  90                  95

Leu Ser Ala Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 849
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 HCDR1 DNA

<400> 849
acctatgcca tgagc 15

<210> 850
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 HCDR1 PRT

<400> 850
Thr Tyr Ala Met Ser
1 5

<210> 851
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 HCDR2 DNA

<400> 851
actattagtg gtactggtgg tatcacatac tacgcagact ccgtgaaggg c 51

<210> 852
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 HCDR2 PRT

<400> 852
Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 853
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> YU536-C12 HCDR3 DNA

<400> 853
gtcggagata attactatga taggagtggt aattatcaca tggactactt tgactac 57

<210> 854
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 HCDR3 PRT

<400> 854
Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 855
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR1 DNA

<400> 855
actggaacca gcagtgacct tggtgcttat gactatgtct cc 42

<210> 856
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR1 PRT

<400> 856
Thr Gly Thr Ser Ser Asp Leu Gly Ala Tyr Asp Tyr Val Ser
1 5 10

<210> 857
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR2 DNA

<400> 857
gatgtcaata atcggccctc a 21

<210> 858
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR2 PRT

<400> 858
Asp Val Asn Asn Arg Pro Ser
1 5

<210> 859
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR3 DNA

<400> 859
aactcatata caagcagcag cacttgggtg 30

<210> 860
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 LCDR3 PRT

<400> 860
Asn Ser Tyr Thr Ser Ser Ser Thr Trp Val
1 5 10

<210> 861
<211> 330
<212> DNA
<213> Artificial Sequence

<220>

<223> YU536-C12 VL DNA

<400> 861
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc ggtcaccatc 60

tcctgcactg gaaccagcag tgaccttggt gcttatgact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca ataatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc aactcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 862
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 VL PRT

<400> 862
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Leu Gly Ala Tyr
            20 25 30

Asp Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35 40 45

Met Ile Tyr Asp Val Asn Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Tyr Thr Ser Ser
                85 90 95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105 110

<210> 863
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 VH DNA

<400> 863
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 864
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 VH PRT

<400> 864
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 865
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 VH complete DNA

<400> 865
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 866
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 VH complete PRT

<400> 866
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
340 345 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
355 360 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 867
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU536-C12 VL complete DNA

<400> 867
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc ggtcaccatc 60

tcctgcactg gaaccagcag tgaccttggt gcttatgact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca ataatcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc aactcatata caagcagcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 868
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU536-C12 VL complete PRT

<400> 868

```
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                  10                  15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Leu Gly Ala Tyr
            20                  25                  30

Asp Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Asn Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Tyr Thr Ser Ser
                85                  90                  95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140
```

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 869
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 HCDR1 DNA

<400> 869
acctatgcca tgagc 15

<210> 870
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 HCDR1 PRT

<400> 870
Thr Tyr Ala Met Ser
1 5

<210> 871
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> YU534-G10 HCDR2 DNA

<400> 871
actattagtg gtactggtgg tatcacatac tacgcagact ccgtgaaggg c 51

<210> 872
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 HCDR2 PRT

<400> 872
Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 873
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 HCDR3 DNA

<400> 873
gtcggagata attactatga taggagtggt aattatcaca tggactactt tgactac 57

<210> 874
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 HCDR3 PRT

<400> 874
Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 875
<211> 42
<212> DNA

<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR1 DNA

<400> 875
actggaacca gcagtgatgt tgggagttat aaccttgtct cc 42

<210> 876
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR1 PRT

<400> 876
Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr Asn Leu Val Ser
1 5 10

<210> 877
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR2 DNA

<400> 877
gagggcagtc agcggccctc a 21

<210> 878
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR2 PRT

<400> 878
Glu Gly Ser Gln Arg Pro Ser
1 5

<210> 879
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR3 DNA

<400> 879
agctcatata caagcagcag caccgtggta 30

<210> 880
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 LCDR3 PRT

<400> 880
Ser Ser Tyr Thr Ser Ser Ser Thr Val Val
1 5 10

<210> 881
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 VL DNA

<400> 881
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacaggc gatcaccatc 60

tcctgcactg gaaccagcag tgatgttggg agttataacc ttgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actgatgatt tatgagggca gtcagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag caccgtggta 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 882
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 VL PRT

<400> 882
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln

1 5 10 15

Ala Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
20 25 30

Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Glu Gly Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 883
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 VH DNA

<400> 883
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 884
<211> 128

<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 VH PRT

<400> 884
Gln 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 Thr Phe Ser Thr Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
            100   105   110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 885
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 VH complete DNA

<400> 885
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc acctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcaact attagtggta ctggtggtat cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtcgga 300

gataattact atgataggag tggtaattat cacatggact actttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 886
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 VH complete PRT

<400> 886
Gln 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 Thr Phe Ser Thr Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Thr Ile Ser Gly Thr Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Gly Asp Asn Tyr Tyr Asp Arg Ser Gly Asn Tyr His Met
            100                 105                 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
```

```
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445
```

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 887
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU534-G10 VL complete DNA

<400> 887
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacaggc gatcaccatc 60

tcctgcactg gaaccagcag tgatgttggg agttataacc ttgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actgatgatt tatgagggca gtcagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caagcagcag caccgtggta 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 888
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU534-G10 VL complete PRT

<400> 888
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ala Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
20 25 30

```
Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Glu Gly Ser Gln Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 889
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 HCDR1 DNA

<400> 889
agctactata tgcac 15

<210> 890
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 HCDR1 PRT

<400> 890
Ser Tyr Tyr Met His
1 5

<210> 891
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 HCDR2 DNA

<400> 891
ataatcaacc ctagtggtgg tagcacaagc tacgcacaga agttccaggg c 51

<210> 892
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 HCDR2 PRT

<400> 892
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 893
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> YU505-A01 HCDR3 DNA

<400> 893
gaccgccatt actatgatag tagtggttct tcccaggcca cctttctctt tgactac 57

<210> 894
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 HCDR3 PRT

<400> 894
Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr Phe Leu
1 5 10 15

Phe Asp Tyr

<210> 895
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR1 DNA

<400> 895
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 896
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR1 PRT

<400> 896
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 897
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR2 DNA

<400> 897
ggtaacagca atcggccctc a 21

<210> 898
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR2 PRT

<400> 898
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 899
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR3 DNA

<400> 899
cagtcctatg acagcagcct gaatgtc 27

<210> 900
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 LCDR3 PRT

<400> 900
Gln Ser Tyr Asp Ser Ser Leu Asn Val
1 5

<210> 901
<211> 327
<212> DNA
<213> Artificial Sequence

<220>

<223> YU505-A01 VL DNA

<400> 901
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gaatgtcttc 300

ggaactggga ccaagctgac cgtccta 327

<210> 902
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 VL PRT

<400> 902
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Asn Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105

<210> 903
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 VH DNA

<400> 903
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaccgc 300

cattactatg atagtagtgg ttcttcccag gccacctttc tctttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 904
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 VH PRT

<400> 904
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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr
100 105 110

Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 905
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 VH complete DNA

<400> 905
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaccgc 300

cattactatg atagtagtgg ttcttcccag gccacctttc tctttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 906
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 VH complete PRT

<400> 906
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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr
100 105 110

Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

```
Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 907
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A01 VL complete DNA

<400> 907

```
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc       60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag      120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc      180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gaatgtcttc      300

ggaactggga ccaagctgac cgtcctaggt cagcccaagg ctgcaccaag tgtcactctg      360

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt      420
```

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 540

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 645

<210> 908
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A01 VL complete PRT

<400> 908
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Asn Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Thr Glu Cys Ser
210 215

<210> 909
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 HCDR1 DNA

<400> 909
agctatgcta tcagc 15

<210> 910
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 HCDR1 PRT

<400> 910
Ser Tyr Ala Ile Ser
1 5

<210> 911
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> YU505-A02 HCDR2 DNA

<400> 911
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 912
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 HCDR2 PRT

<400> 912
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 913
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 HCDR3 DNA

<400> 913
caaatctggg cttatgatag tagtggttac cccgtcccgg ccgaatactt ccagcac 57

<210> 914
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 HCDR3 PRT

<400> 914
Gln Ile Trp Ala Tyr Asp Ser Ser Gly Tyr Pro Val Pro Ala Glu Tyr
1 5 10 15

Phe Gln His

<210> 915
<211> 42
<212> DNA

<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR1 DNA

<400> 915
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 916
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR1 PRT

<400> 916
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 917
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR2 DNA

<400> 917
ggtaacagca atcggccctc a 21

<210> 918
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR2 PRT

<400> 918
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 919
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR3 DNA

<400> 919
cagtcctatg acagcagcct gagtggtgtg gta 33

<210> 920
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 LCDR3 PRT

<400> 920
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Val Val
1 5 10

<210> 921
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 VL DNA

<400> 921
cagtctgtgt tgacgcagcc gccctcggtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggtgtg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 922
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 VL PRT

<400> 922
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 923
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 VH DNA

<400> 923
caggtgcagc tggtggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc acgtcaaatc 300

tgggcttatg atagtagtgg ttaccccgtc ccggccgaat acttccagca ctggggccag 360

ggcaccctgg tcaccgtgtc ctca 384

<210> 924
<211> 128

<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 VH PRT

<400> 924
Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Ile Trp Ala Tyr Asp Ser Ser Gly Tyr Pro Val Pro Ala
100 105 110

Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 925
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 VH complete DNA

<400> 925
caggtgcagc tggtggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc acgtcaaatc 300

tgggcttatg atagtagtgg ttaccccgtc ccggccgaat acttccagca ctggggccag 360

ggcaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 926
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 VH complete PRT

<400> 926
Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gln Ile Trp Ala Tyr Asp Ser Ser Gly Tyr Pro Val Pro Ala
            100                 105                 110

Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
    130                 135                 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
```

```
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445
```

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 927
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A02 VL complete DNA

<400> 927
cagtctgtgt tgacgcagcc gccctcggtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggtgtg 300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 928
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A02 VL complete PRT

<400> 928
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

```
Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 929
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 HCDR1 DNA

<400> 929
agctatgcta tcagc 15

<210> 930
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 HCDR1 PRT

<400> 930
Ser Tyr Ala Ile Ser
1 5

<210> 931
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 HCDR2 DNA

<400> 931
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 932
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 HCDR2 PRT

<400> 932
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 933
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> YU505-A05 HCDR3 DNA

<400> 933
agtgactccg gatatagtgg ctacgggtac tttgactac 39

<210> 934
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 HCDR3 PRT

<400> 934
Ser Asp Ser Gly Tyr Ser Gly Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 935
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR1 DNA

<400> 935
actggaacca gcagcgacgt tggtcgttat aactatgtct cc 42

<210> 936
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR1 PRT

<400> 936
Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr Asn Tyr Val Ser
1 5 10

<210> 937
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR2 DNA

<400> 937
gatgtcacta atcggccctc a 21

<210> 938
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR2 PRT

<400> 938
Asp Val Thr Asn Arg Pro Ser
1 5

<210> 939
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR3 DNA

<400> 939
acctcatata caagcagtaa cactcttgtg ata 33

<210> 940
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 LCDR3 PRT

<400> 940
Thr Ser Tyr Thr Ser Ser Asn Thr Leu Val Ile
1 5 10

<210> 941
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 VL DNA

<400> 941
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ccggacagtc gatctccatc 60

tcctgcactg gaaccagcag cgacgttggt cgttataact atgtctcctg gtaccaacag 120

cacccaggca aagcccccaa actcatgatt tatgatgtca ctaatcggcc ctcaggggtt 180

tctagtcgct tctctggctc caagtctggc aacgcggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga gtattattgc acctcatata caagcagtaa cactcttgtg 300

atattcggcg gagggaccaa ggtcaccgtc cta 333

<210> 942
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 VL PRT

<400> 942
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Ser Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Thr Asn Arg Pro Ser Gly Val Ser Ser Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Ala Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Ser Tyr Thr Ser Ser
85 90 95

Asn Thr Leu Val Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 943
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 VH DNA

<400> 943
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaagtgac 300

tccggatata gtggctacgg gtactttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctca 366

<210> 944
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 VH PRT

<400> 944
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85 90 95

Ala Arg Ser Asp Ser Gly Tyr Ser Gly Tyr Gly Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 945
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 VH complete DNA

<400> 945
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaagtgac 300

tccggatata gtggctacgg gtactttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctcagcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tccagtggcc 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtgggcgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa cagctcccat cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaaa gcctctccct gtccccgggt 1350

<210> 946
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 VH complete PRT

<400> 946

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5				10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
		20					25					30			
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35					40					45				
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
50					55					60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65				70					75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Ser	Asp	Ser	Gly	Tyr	Ser	Gly	Tyr	Gly	Tyr	Phe	Asp	Tyr	Trp
		100					105					110			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
	115					120					125				
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
130					135					140					

```
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

```
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly
    450
```

<210> 947
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-A05 VL complete DNA

<400> 947

```
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ccggacagtc gatctccatc       60

tcctgcactg gaaccagcag cgacgttggt cgttataact atgtctcctg gtaccaacag      120

cacccaggca aagcccccaa actcatgatt tatgatgtca ctaatcggcc ctcaggggtt      180

tctagtcgct tctctggctc caagtctggc aacgcggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga gtattattgc acctcatata caagcagtaa cactcttgtg      300

atattcggcg gagggaccaa ggtcaccgtc ctaggtcagc ccaaggctgc accaagtgtc      360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc      540
```

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 948
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-A05 VL complete PRT

<400> 948
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Ser Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Thr Asn Arg Pro Ser Gly Val Ser Ser Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Ala Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Ser Tyr Thr Ser Ser
85 90 95

Asn Thr Leu Val Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 949
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR1 DNA

<400> 949
agtagtaact ggtggagt 18

<210> 950
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR1 PRT

<400> 950
Ser Ser Asn Trp Trp Ser
1 5

<210> 951
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR2 DNA

<400> 951
agtatctatc atagtgggag cacctactac aacccgtccc tcaagagt 48

<210> 952
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR2 PRT

<400> 952
Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 953
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR3 DNA

<400> 953
gttcgccccg agaggaggtt tccttactac tactacatgg acgtc 45

<210> 954
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 HCDR3 PRT

<400> 954
Val Arg Pro Glu Arg Arg Phe Pro Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 955
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR1 DNA

<400> 955
tctggaagca actccaacat cggaactaat actgtaaac 39

<210> 956
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR1 PRT

<400> 956
Ser Gly Ser Asn Ser Asn Ile Gly Thr Asn Thr Val Asn
1 5 10

<210> 957
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR2 DNA

<400> 957
actaatgatc agcggccctc a 21

<210> 958
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR2 PRT

<400> 958
Thr Asn Asp Gln Arg Pro Ser
1 5

<210> 959
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR3 DNA

<400> 959
gcagcatggg atgacagcct gagtcgttgg gtg 33

<210> 960

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 LCDR3 PRT

<400> 960
Ala Ala Trp Asp Asp Ser Leu Ser Arg Trp Val
1 5 10

<210> 961
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 VL DNA

<400> 961
cagtctgtgc tgacgcagcc gccctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcaactc caacatcgga actaatactg taaactggta ccagcaactc 120

ccaggaacgg cccccaaact cctcatctat actaatgatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tccgacgatg aggctgatta ttactgtgca gcatgggatg acagcctgag tcgttgggtg 300

ttcggcggag ggaccaaggt caccgtccta 330

<210> 962
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 VL PRT

<400> 962
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile Gly Thr Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Thr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Ser Arg Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105   110

<210> 963
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 VH DNA

<400> 963
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60

acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag 120

cccccaggga aggggctgga gtggattggg agtatctatc atagtgggag cacctactac 180

aacccgtccc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc cagagttcgc 300

cccgagagga ggtttcctta ctactactac atggacgtct ggggcaaagg gaccacggtc 360

accgtgtcct ca 372

<210> 964
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 VH PRT

<400> 964
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1   5   10   15

```
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Arg Pro Glu Arg Arg Phe Pro Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 965
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 VH complete DNA

<400> 965

```
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc       60

acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag      120

cccccaggga aggggctgga gtggattggg agtatctatc atagtgggag cacctactac      180

aacccgtccc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc      240

ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc cagagttcgc      300

cccgagagga ggtttcctta ctactactac atggacgtct ggggcaaagg gaccacggtc      360

accgtgtcct cagctagcac caagggccca tcggtcttcc ccctggcacc ctcctccaag      420

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg      480
```

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctcca 720

gtggccggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg ggcgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg ggtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaacagc tcccatcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaaaagcct ctccctgtcc ccgggt 1356

<210> 966
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 VH complete PRT

<400> 966
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

```
Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Arg Pro Glu Arg Arg Phe Pro Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 967
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B03 VL complete DNA

<400> 967
cagtctgtgc tgacgcagcc gccctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcaactc caacatcgga actaatactg taaactggta ccagcaactc 120

ccaggaacgg cccccaaact cctcatctat actaatgatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tccgacgatg aggctgatta ttactgtgca gcatgggatg acagcctgag tcgttgggtg 300

ttcggcggag ggaccaaggt caccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 968
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B03 VL complete PRT

<400> 968
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile Gly Thr Asn
            20   25   30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Thr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Arg Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 969
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR1 DNA

<400> 969
agctactata tgcac 15

<210> 970

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR1 PRT

<400> 970
Ser Tyr Tyr Met His
1 5

<210> 971
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR2 DNA

<400> 971
ataatcaacc ctagtggtgg tagcacaagc tacgcacaga agttccaggg c 51

<210> 972
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR2 PRT

<400> 972
Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 973
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR3 DNA

<400> 973
gaccgccatt actatgatag tagtggttct tcccaggcca cctttctctt tgactac 57

<210> 974
<211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 HCDR3 PRT

<400> 974
Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr Phe Leu
1 5 10 15

Phe Asp Tyr

<210> 975
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR1 DNA

<400> 975
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 976
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR1 PRT

<400> 976
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 977
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR2 DNA

<400> 977
ggtaacagca atcggccctc a 21

<210> 978
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR2 PRT

<400> 978
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 979
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR3 DNA

<400> 979
cagtcctatg acagcagcct gagtggttcg ttg 33

<210> 980
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 LCDR3 PRT

<400> 980
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Leu
1 5 10

<210> 981
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 VL DNA

<400> 981
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

ttgttcggcg gaggcaccca ggtgaccgtc ctc 333

<210> 982
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 VL PRT

<400> 982
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Leu Phe Gly Gly Gly Thr Gln Val Thr Val Leu
100 105 110

<210> 983
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 VH DNA

<400> 983

caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaccgc 300

cattactatg atagtagtgg ttcttcccag gccacctttc tctttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctca 384

<210> 984
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 VH PRT

<400> 984
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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr
100 105 110

Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 985
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 VH complete DNA

<400> 985
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaccgc 300

cattactatg atagtagtgg ttcttcccag gccacctttc tctttgacta ctggggccag 360

ggaaccctgg tcaccgtgtc ctcagctagc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctc cagtggccgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tgggcgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgggtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaaca gctcccatcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaaaagc ctctccctgt ccccgggt 1368

<210> 986
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 VH complete PRT

<400> 986
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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg His Tyr Tyr Asp Ser Ser Gly Ser Ser Gln Ala Thr
100 105 110

Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
130 135 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145 150 155 160

```
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 987
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B04 VL complete DNA

<400> 987
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

ttgttcggcg gaggcaccca ggtgaccgtc ctcggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 988
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B04 VL complete PRT

<400> 988
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Ser Leu Phe Gly Gly Gly Thr Gln Val Thr Val Leu Gly
            100   105   110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115   120   125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130   135   140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145   150   155   160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165   170   175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 989
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR1 DNA

<400> 989
agctatgcca tgagc 15

<210> 990
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR1 PRT

<400> 990
Ser Tyr Ala Met Ser
1 5

<210> 991
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR2 DNA

<400> 991
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 992
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR2 PRT

<400> 992
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 993
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR3 DNA

<400> 993
cctattgacc acgggatttt tgactac 27

<210> 994
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 HCDR3 PRT

<400> 994
Pro Ile Asp His Gly Ile Phe Asp Tyr
1 5

<210> 995
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR1 DNA

<400> 995
gggggaaaca acattggaag taaaagtgtg cac 33

<210> 996
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR1 PRT

<400> 996
Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 997
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR2 DNA

<400> 997
tatgatagcg accggccctc a 21

<210> 998
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR2 PRT

<400> 998
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 999
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR3 DNA

<400> 999
caggtgtggg atagtagtag tgatcatgtg gta 33

<210> 1000
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 LCDR3 PRT

<400> 1000
Gln Val Trp Asp Ser Ser Ser Asp His Val Val
1   5   10

<210> 1001
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 VL DNA

<400> 1001
tcctatgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt   60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc   120

caggcccctg tgctggtcat ctattatgat agcgaccggc cctcagggat ccctgagcga   180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg   240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatgt ggtattcggc   300

ggagggacca agctgaccgt ccta   324

<210> 1002
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 VL PRT

<400> 1002
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1   5   10   15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20   25   30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

```
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
                85                  90                  95


Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  1003
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-B06 VH DNA

<400>  1003
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacctatt      300

gaccacggga tttttgacta ctggggccag ggaaccctgg tcaccgtgtc ctca            354



<210>  1004
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU505-B06 VH PRT

<400>  1004
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Pro Ile Asp His Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 1005
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 VH complete DNA

<400> 1005
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacctatt 300

gaccacggga tttttgacta ctggggccag ggaaccctgg tcaccgtgtc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctc cagtggccgg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tgggcgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaaca gctcccatcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaaaagc 1320

ctctccctgt ccccgggt 1338

<210> 1006
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 VH complete PRT

<400> 1006
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Pro Ile Asp His Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
```

```
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1007
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-B06 VL complete DNA

<400> 1007

```
tcctatgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tgctggtcat ctattatgat agcgaccggc cctcagggat ccctgagcga      180
```

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatgt ggtattcggc 300

ggagggacca agctgaccgt cctaggtcag cccaaggctg caccaagtgt cactctgttc 360

ccgccctcct ctgaggagct tcaagccaac aaggccacac tggtgtgtct cataagtgac 420

ttctacccgg gagccgtgac agtggcctgg aaggcagata gcagccccgt caaggcggga 480

gtggagacca ccacaccctc caaacaaagc aacaacaagt acgcggccag cagctatctg 540

agcctgacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggt cacgcatgaa 600

gggagcaccg tggagaagac agtggcccct acagaatgtt ca 642

<210> 1008
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-B06 VL complete PRT

<400> 1008
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

```
Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
        115                 120                 125


Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
    130                 135                 140


Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145                 150                 155                 160


Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
                165                 170                 175


Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180                 185                 190


Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
        195                 200                 205


Ala Pro Thr Glu Cys Ser
    210
```

<210> 1009
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR1 DNA

<400> 1009
agttatgata tcaac 15

<210> 1010
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR1 PRT

<400> 1010
```
Ser Tyr Asp Ile Asn
1               5
```

<210> 1011
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR2 DNA

<400> 1011
tggatgaacc ctaacagtgg taacacaggc tatgcacaga agttccaggg c 51

<210> 1012
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR2 PRT

<400> 1012
Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1013
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR3 DNA

<400> 1013
aactcgttag gagctgctac tggctggttc gacccc 36

<210> 1014
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 HCDR3 PRT

<400> 1014
Asn Ser Leu Gly Ala Ala Thr Gly Trp Phe Asp Pro
1 5 10

<210> 1015
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR1 DNA

<400> 1015
tctggaagca gctccaacat cggaagtaat tatgtatac 39

<210> 1016
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR1 PRT

<400> 1016
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr
1 5 10

<210> 1017
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR2 DNA

<400> 1017
aggaataatc agcggccctc a 21

<210> 1018
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR2 PRT

<400> 1018
Arg Asn Asn Gln Arg Pro Ser
1 5

<210> 1019

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR3 DNA

<400> 1019
gcagcatggg atgacagcct ggta 24

<210> 1020
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 LCDR3 PRT

<400> 1020
Ala Ala Trp Asp Asp Ser Leu Val
1 5

<210> 1021
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 VL DNA

<400> 1021
tcctatgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 240

tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctggt attcggcgga 300

gggaccaagg tcaccgtcct a 321

<210> 1022
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> YU505-D01 VL PRT

<400> 1022
Ser Tyr Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100   105

<210> 1023
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 VH DNA

<400> 1023
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc   60

tcctgcaagg cttctggata caccttcacc agttatgata tcaactgggt gcgacaggcc   120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtggtaa cacaggctat   180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac   240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaggaactcg   300

ttaggagctg ctactggctg gttcgacccc tggggccagg gaaccctggt caccgtgtcc   360

tca   363

<210> 1024
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 VH PRT

<400> 1024
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 Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Ser Leu Gly Ala Ala Thr Gly Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1025
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 VH complete DNA

<400> 1025
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaggaactcg 300

ttaggagctg ctactggctg gttcgacccc tggggccagg gaaccctggt caccgtgtcc 360

tcagctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctcc agtggccgga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt gggcgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaacag ctcccatccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc 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

cagaaaagcc tctccctgtc cccgggt 1347

<210> 1026
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 VH complete PRT

<400> 1026
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 Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Ser Leu Gly Ala Ala Thr Gly Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

```
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly 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 Gln Leu Pro Ser 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

<210> 1027
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D01 VL complete DNA

<400> 1027
tcctatgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 240

tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctggt attcggcgga 300

gggaccaagg tcaccgtcct aggtcagccc aaggctgcac caagtgtcac tctgttcccg 360

ccctcctctg aggagcttca agccaacaag gccacactgg tgtgtctcat aagtgacttc 420

tacccgggag ccgtgacagt ggcctggaag gcagatagca gccccgtcaa ggcgggagtg 480

gagaccacca caccctccaa acaaagcaac aacaagtacg cggccagcag ctatctgagc 540

ctgacgcctg agcagtggaa gtcccacaga agctacagct gccaggtcac gcatgaaggg 600

agcaccgtgg agaagacagt ggcccctaca gaatgttca 639

<210> 1028
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D01 VL complete PRT

<400> 1028
Ser Tyr Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

```
Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro Lys Ala
            100                 105                 110

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
        115                 120                 125

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
    130                 135                 140

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145                 150                 155                 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
                165                 170                 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
            180                 185                 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
        195                 200                 205

Pro Thr Glu Cys Ser
    210
```

<210> 1029
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR1 DNA

<400> 1029
agctatgcta tcagc 15

<210> 1030
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR1 PRT

<400> 1030
Ser Tyr Ala Ile Ser
1 5

<210> 1031
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR2 DNA

<400> 1031
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1032
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR2 PRT

<400> 1032
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1033
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR3 DNA

<400> 1033
gaaacctcca gtggctggag tttccttgac tac 33

<210> 1034
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 HCDR3 PRT

<400> 1034
Glu Thr Ser Ser Gly Trp Ser Phe Leu Asp Tyr
1 5 10

<210> 1035
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR1 DNA

<400> 1035
gggggaaaca acattggaag taaaagtgtg cac 33

<210> 1036
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR1 PRT

<400> 1036
Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 1037
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR2 DNA

<400> 1037
tatgatagcg accggccctc a 21

<210> 1038
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR2 PRT

<400> 1038
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 1039
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR3 DNA

<400> 1039
caggtgtggg atagtagtag tgatcatgtg gta 33

<210> 1040
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 LCDR3 PRT

<400> 1040
Gln Val Trp Asp Ser Ser Ser Asp His Val Val
1 5 10

<210> 1041
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 VL DNA

<400> 1041

tcctatgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctattatgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatgt ggtattcggc 300

ggagggacca aggtcaccgt ccta 324

<210> 1042
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 VL PRT

<400> 1042
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105

<210> 1043
<211> 360
<212> DNA

<213> Artificial Sequence

<220>
<223> YU505-D02 VH DNA

<400> 1043
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagaaacc 300

tccagtggct ggagtttcct tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

360

<210> 1044
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 VH PRT

<400> 1044
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Thr Ser Ser Gly Trp Ser Phe Leu Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1045
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 VH complete DNA

<400> 1045
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagaaacc 300

tccagtggct ggagtttcct tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 1046
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 VH complete PRT

<400> 1046
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Thr Ser Ser Gly Trp Ser Phe Leu 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
```

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 1047
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-D02 VL complete DNA

<400> 1047
tcctatgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctattatgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatgt ggtattcggc 300

ggagggacca aggtcaccgt cctaggtcag cccaaggctg caccaagtgt cactctgttc 360

ccgccctcct ctgaggagct tcaagccaac aaggccacac tggtgtgtct cataagtgac 420

ttctacccgg gagccgtgac agtggcctgg aaggcagata gcagccccgt caaggcggga 480

gtggagacca ccacaccctc caaacaaagc aacaacaagt acgcggccag cagctatctg 540

agcctgacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggt cacgcatgaa 600

gggagcaccg tggagaagac agtggcccct acagaatgtt ca 642

<210> 1048
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-D02 VL complete PRT

<400> 1048
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala

```
                165                 170                 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180                 185                 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
        195                 200                 205

Ala Pro Thr Glu Cys Ser
    210
```

<210> 1049
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR1 DNA

<400> 1049
agttatagta ttgtc 15

<210> 1050
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR1 PRT

<400> 1050
Ser Tyr Ser Ile Val
1 5

<210> 1051
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR2 DNA

<400> 1051
gggatcatcc ctatttttgg tactacaaac tatgcacaga agttccaggg c 51

<210> 1052
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR2 PRT

<400> 1052
Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1053
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR3 DNA

<400> 1053
tctctgggag ccactcgtga ctac 24

<210> 1054
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 HCDR3 PRT

<400> 1054
Ser Leu Gly Ala Thr Arg Asp Tyr
1 5

<210> 1055
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR1 DNA

<400> 1055
tctggaagca gctccaacat cggaaataat gctgtaaac 39

<210> 1056

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR1 PRT

<400> 1056
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Ala Val Asn
1 5 10

<210> 1057
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR2 DNA

<400> 1057
tatgatgatc tgctgccctc a 21

<210> 1058
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR2 PRT

<400> 1058
Tyr Asp Asp Leu Leu Pro Ser
1 5

<210> 1059
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR3 DNA

<400> 1059
gcagcatggg atgacagcct gaatggtccg gtg 33

<210> 1060
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> YU505-E01 LCDR3 PRT

<400> 1060
Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 1061
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 VL DNA

<400> 1061
tcctatgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc 120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtccggtg 300

ttcggcggag ggaccaaggt caccgtccta 330

<210> 1062
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 VL PRT

<400> 1062
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 1063
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 VH DNA

<400> 1063
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agttatagta ttgtctgggt gcgacaggcc 120

cctggacaag gacttgagtg gatgggaggg atcatcccta tttttggtac tacaaactat 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacaag cacagccttc 240

atggagctga gcaacctaaa atctgaggac acggccgtct atttctgtgc gagatctctg 300

ggagccactc gtgactactg gggccaggga accctggtca ccgtgtcctc a 351

<210> 1064
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 VH PRT

<400> 1064
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

```
Ser Ile Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Phe
65                  70                  75                  80


Met Glu Leu Ser Asn Leu Lys Ser Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95


Ala Arg Ser Leu Gly Ala Thr Arg Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  1065
<211>  1335
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-E01 VH complete DNA

<400>  1065
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagc agttatagta ttgtctgggt gcgacaggcc      120

cctggacaag gacttgagtg gatgggaggg atcatcccta tttttggtac tacaaactat      180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacaag cacagccttc      240

atggagctga gcaacctaaa atctgaggac acggccgtct atttctgtgc gagatctctg      300

ggagccactc gtgactactg gggccaggga accctggtca ccgtgtcctc agctagcacc      360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600
```

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctccag tggccggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg gcgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaacagct cccatccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaaaagcctc 1320

tccctgtccc cgggt 1335

<210> 1066
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 VH complete PRT

<400> 1066
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ser Ile Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Phe
65                  70                  75                  80

Met Glu Leu Ser Asn Leu Lys Ser Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Ser Leu Gly Ala Thr Arg Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
```

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 1067
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E01 VL complete DNA

<400> 1067
tcctatgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagctc 120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtccggtg 300

ttcggcggag ggaccaaggt caccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 1068
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E01 VL complete PRT

<400> 1068
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

```
Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
            100                 105                 110


Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125


Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140


Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160


Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175


Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190


Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205


Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  1069
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-E02 HCDR1 DNA

<400>  1069
agctatacta tcagc                                                    15



<210>  1070
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU505-E02 HCDR1 PRT

<400>  1070
```

Ser Tyr Thr Ile Ser
1 5

<210> 1071
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 HCDR2 DNA

<400> 1071
aggatcatcc ctatccttgg tatagcaaac tacgcacaga agttccaggg c 51

<210> 1072
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 HCDR2 PRT

<400> 1072
Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1073
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 HCDR3 DNA

<400> 1073
gatatggtct ctgtaggggc agctggacct tactactttg actac 45

<210> 1074
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 HCDR3 PRT

<400> 1074
Asp Met Val Ser Val Gly Ala Ala Gly Pro Tyr Tyr Phe Asp Tyr

1 5 10 15

<210> 1075
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR1 DNA

<400> 1075
actgggagca gctccaacat cggggcaggt tatgatgtac ac 42

<210> 1076
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR1 PRT

<400> 1076
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 1077
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR2 DNA

<400> 1077
ggtaacagca atcggccctc a 21

<210> 1078
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR2 PRT

<400> 1078
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 1079
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR3 DNA

<400> 1079
cagtcctatg acagcagcct gagtggttcg gta 33

<210> 1080
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 LCDR3 PRT

<400> 1080
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val
1 5 10

<210> 1081
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 VL DNA

<400> 1081
cagtctgtgt tgacgcagcc gccctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctgtc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

gtattcggcg gagggaccaa gctgaccgtc cta 333

<210> 1082
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 VL PRT

<400> 1082
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Val Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1083
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 VH DNA

<400> 1083
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc   60

tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac   180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac   240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatatg   300

gtctctgtag gggcagctgg accttactac tttgactact ggggccaggg aaccctggtc   360

accgtgtcct ca 372

<210> 1084
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 VH PRT

<400> 1084
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Met Val Ser Val Gly Ala Ala Gly Pro Tyr Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1085
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 VH complete DNA

<400> 1085

caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatatg 300

gtctctgtag gggcagctgg accttactac tttgactact ggggccaggg aaccctggtc 360

accgtgtcct cagctagcac caagggccca tcggtcttcc ccctggcacc ctcctccaag 420

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 480

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctcca 720

gtggccggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg ggcgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg ggtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaacagc tcccatcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaaaagcct ctccctgtcc ccgggt 1356

<210> 1086
<211> 452
<212> PRT
<213> Artificial Sequence

<220>

<223> YU505-E02 VH complete PRT

<400> 1086

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30


Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Met Val Ser Val Gly Ala Ala Gly Pro Tyr Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125


Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140


Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160


Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175


Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190


Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205
```

```
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
```

420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 1087
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E02 VL complete DNA

<400> 1087
cagtctgtgt tgacgcagcc gccctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctgtc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

gtattcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc accaagtgtc 360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1088
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E02 VL complete PRT

<400> 1088
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln

```
1               5                   10                  15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Val Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 1089
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR1 DNA

<400> 1089
agctatgcta tcagc 15

<210> 1090
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR1 PRT

<400> 1090
Ser Tyr Ala Ile Ser
1 5

<210> 1091
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR2 DNA

<400> 1091
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1092
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR2 PRT

<400> 1092
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1093
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR3 DNA

<400> 1093
ggacgtggat acagctatgg tcacgactac 30

<210> 1094
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 HCDR3 PRT

<400> 1094
Gly Arg Gly Tyr Ser Tyr Gly His Asp Tyr
1 5 10

<210> 1095
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR1 DNA

<400> 1095
tctggaagca gctccaacat cggaaataat gctgtaaac 39

<210> 1096
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR1 PRT

<400> 1096
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Ala Val Asn
1 5 10

<210> 1097
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR2 DNA

<400> 1097
tatgatgatc tgctgccctc a 21

<210> 1098
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR2 PRT

<400> 1098
Tyr Asp Asp Leu Leu Pro Ser
1 5

<210> 1099
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR3 DNA

<400> 1099
gcagcctggg atgacagcct gaatggttgg gtg 33

<210> 1100
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 LCDR3 PRT

<400> 1100
Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val
1 5 10

<210> 1101
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 VL DNA

<400> 1101
tcctatgagc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagttc 120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcctgggatg acagcctgaa tggttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 1102
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 VL PRT

<400> 1102
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20   25   30

Ala Val Asn Trp Tyr Gln Gln Phe Pro Gly Lys Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85   90   95

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1103
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 VH DNA

<400> 1103
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggacgt 300

ggatacagct atggtcacga ctactggggc cagggaaccc tggtcaccgt gtcctca 357

<210> 1104
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 VH PRT

<400> 1104
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Gly Tyr Ser Tyr Gly His Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 1105
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 VH complete DNA

<400> 1105
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggacgt 300

ggatacagct atggtcacga ctactggggc cagggaaccc tggtcaccgt gtcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctccagtggc cggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtgggcgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgggtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa acagctccca tcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaaa 1320

agcctctccc tgtccccggg t 1341

<210> 1106
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 VH complete PRT

<400> 1106
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Gly Tyr Ser Tyr Gly His Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

```
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr
                325                 330                 335
```

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1107
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-E04 VL complete DNA

<400> 1107

```
tcctatgagc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc       60

tcctgttctg gaagcagctc caacatcgga aataatgctg taaactggta ccagcagttc      120

ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgccctc aggggtctct      180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240

tctgaggatg aggctgatta ttactgtgca gcctgggatg acagcctgaa tggttgggtg      300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact      360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata      420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag      480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc      540
```

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 1108
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-E04 VL complete PRT

<400> 1108
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Phe Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Leu Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

```
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175


Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190


Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205


Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  1109
<211>  15
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-F03 HCDR1 DNA

<400>  1109
ggctactata tgcac                                                    15



<210>  1110
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU505-F03 HCDR1 PRT

<400>  1110
Gly Tyr Tyr Met His
1               5


<210>  1111
<211>  51
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-F03 HCDR2 DNA

<400>  1111
cagatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcaggg c             51
```

<210> 1112
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 HCDR2 PRT

<400> 1112
Gln Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 HCDR3 DNA

<400> 1113
ggggaaggct ttgactac 18

<210> 1114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 HCDR3 PRT

<400> 1114
Gly Glu Gly Phe Asp Tyr
1 5

<210> 1115
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR1 DNA

<400> 1115
tctggaagca gctccaacat cggaagtaat tatgtatac 39

<210> 1116
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR1 PRT

<400> 1116
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr
1 5 10

<210> 1117
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR2 DNA

<400> 1117
aggaataatc agcggccctc a 21

<210> 1118
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR2 PRT

<400> 1118
Arg Asn Asn Gln Arg Pro Ser
1 5

<210> 1119
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR3 DNA

<400> 1119
gcagcatggg atgacagcct gagtggtgtg gta 33

<210> 1120
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 LCDR3 PRT

<400> 1120
Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val
1 5 10

<210> 1121
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 VL DNA

<400> 1121
tcctatgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 240

tccgagggtg aggctgatta ttactgtgca gcatgggatg acagcctgag tggtgtggta 300

ttcggcggag ggaccaaggt caccgtccta 330

<210> 1122
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 VL PRT

<400> 1122
Ser Tyr Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

```
        35                  40                  45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Gly Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110
```

<210> 1123
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 VH DNA

<400> 1123
gaggtgcagc tgttggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggacag atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagggggaa 300

ggctttgact actggggcca gggaaccctg gtcaccgtgt cctca 345

<210> 1124
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 VH PRT

<400> 1124
```
Glu Val Gln Leu Leu Glu 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 Gly Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gln Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Glu Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ser
        115

<210> 1125
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 VH complete DNA

<400> 1125
gaggtgcagc tgttggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggacag atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagggggaa 300

ggctttgact actggggcca gggaaccctg gtcaccgtgt cctcagctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct ccagtggccg gaccgtcagt cttcctcttc 720

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 780

gtgggcgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 960

tccaacaaac agctcccatc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaaaag cctctccctg 1320

tccccgggt 1329

<210> 1126
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 VH complete PRT

<400> 1126
Glu Val Gln Leu Leu Glu 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 Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gln Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Glu Gly Phe Asp 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 Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe
            260                 265                 270
```

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275   280   285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290   295   300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305   310   315   320

Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala
                325   330   335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340   345   350

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355   360   365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370   375   380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385   390   395   400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405   410   415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420   425   430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440

<210> 1127
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F03 VL complete DNA

<400> 1127

tcctatgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 240

tccgagggtg aggctgatta ttactgtgca gcatgggatg acagcctgag tggtgtggta 300

ttcggcggag ggaccaaggt caccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 1128
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F03 VL complete PRT

<400> 1128
Ser Tyr Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Gly Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu

85 90 95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1129
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 HCDR1 DNA

<400> 1129
agctatgcta tcagc 15

<210> 1130
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> YU505-F04 HCDR1 PRT

<400> 1130
Ser Tyr Ala Ile Ser
1 5

<210> 1131
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 HCDR2 DNA

<400> 1131
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 HCDR2 PRT

<400> 1132
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1133
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 HCDR3 DNA

<400> 1133
ggagctgggg aaattgacta c 21

<210> 1134
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 HCDR3 PRT

<400> 1134
Gly Ala Gly Glu Ile Asp Tyr
1 5

<210> 1135
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR1 DNA

<400> 1135
actgggagca gctccaacat cggggcaggt tatgatgtac ag 42

<210> 1136
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR1 PRT

<400> 1136
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Gln
1 5 10

<210> 1137
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR2 DNA

<400> 1137
gctaacacct atcggccctc a 21

<210> 1138
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR2 PRT

<400> 1138

Ala Asn Thr Tyr Arg Pro Ser
1 5

<210> 1139
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR3 DNA

<400> 1139
tcaacacgag atgacaacct ggatggtgtg ata 33

<210> 1140
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 LCDR3 PRT

<400> 1140
Ser Thr Arg Asp Asp Asn Leu Asp Gly Val Ile
1 5 10

<210> 1141
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 VL DNA

<400> 1141
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacagtg gtaccaacaa 120

cttccaggaa cagcccccaa actcctcatc tatgctaaca cctatcggcc ctcaggggtc 180

cctgaccgat tctctgcctc caagtctggc acctcagcct ccctggccat cagtgggctc 240

cactctgagg atgaggctga ttattattgt tcaacacgag atgacaacct ggatggtgtg 300

atattcggcg gagggaccaa gttgaccgtc cta 333

<210> 1142

<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 VL PRT

<400> 1142
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Ala Asn Thr Tyr Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65 70 75 80

His Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Thr Arg Asp Asp Asn
85 90 95

Leu Asp Gly Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1143
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 VH DNA

<400> 1143
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgcgc gagaggagct 300

ggggaaattg actactgggg ccagggaacc ctggtcaccg tgtcctca 348

<210> 1144
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 VH PRT

<400> 1144
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Gly Glu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 1145
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F04 VH complete DNA

<400> 1145
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgcgc gagaggagct 300

ggggaaattg actactgggg ccagggaacc ctggtcaccg tgtcctcagc tagcaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctccagtgg ccggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtgggcg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgggtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aacagctccc atcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa aagcctctcc 1320

ctgtccccgg gt 1332

<210> 1146
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F04 VH complete PRT

<400> 1146
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Ala Gly Glu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115   120   125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130   135   140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145   150   155   160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165   170   175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180   185   190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195   200   205

```
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gly Val Ser His Glu Asp Pro Glu Val Lys
            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 Gln Leu Pro Ser 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

Arg Asp Glu Leu 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
```

```
Gln 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 Gly
        435                 440


<210>  1147
<211>  651
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  YU505-F04 VL complete DNA

<400>  1147
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc       60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacagtg gtaccaacaa      120

cttccaggaa cagccccaa actcctcatc tatgctaaca cctatcggcc ctcaggggtc      180

cctgaccgat tctctgcctc caagtctggc acctcagcct ccctggccat cagtgggctc      240

cactctgagg atgaggctga ttattattgt tcaacacgag atgacaacct ggatggtgtg      300

atattcggcg gagggaccaa gttgaccgtc ctaggtcagc ccaaggctgc accaagtgtc      360

actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc      540

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc      600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a               651


<210>  1148
<211>  217
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YU505-F04 VL complete PRT

<400>  1148
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

Tyr Asp Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

Leu Ile Tyr Ala Asn Thr Tyr Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

Ser Ala Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80

His Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Thr Arg Asp Asp Asn
                85                  90                  95

Leu Asp Gly Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 1149
<211> 15

<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR1 DNA

<400> 1149
agctatggca tgcac 15

<210> 1150
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR1 PRT

<400> 1150
Ser Tyr Gly Met His
1 5

<210> 1151
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR2 DNA

<400> 1151
gttatgtcat atgatggaag taaaaaatac tatgcagact ccgtgaaggg c 51

<210> 1152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR2 PRT

<400> 1152
Val Met Ser Tyr Asp Gly Ser Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1153
<211> 15
<212> DNA

<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR3 DNA

<400> 1153
cagggtatgg acgtc 15

<210> 1154
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 HCDR3 PRT

<400> 1154
Gln Gly Met Asp Val
1 5

<210> 1155
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR1 DNA

<400> 1155
gggggaaaca acattggaag taaaagtgtg cac 33

<210> 1156
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR1 PRT

<400> 1156
Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 1157
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR2 DNA

<400> 1157
tatattagcg accggccctc a 21

<210> 1158
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR2 PRT

<400> 1158
Tyr Ile Ser Asp Arg Pro Ser
1 5

<210> 1159
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR3 DNA

<400> 1159
cacgtgtggg atagtagtag tgatcatgtg gta 33

<210> 1160
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 LCDR3 PRT

<400> 1160
His Val Trp Asp Ser Ser Ser Asp His Val Val
1 5 10

<210> 1161
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 VL DNA

<400> 1161
cagtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgttggtcat ctattatatt agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240

gatgaggccg cctattactg tcacgtgtgg gatagtagta gtgatcatgt ggtattcggc 300

ggagggacca agctgaccgt ccta 324

<210> 1162
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 VL PRT

<400> 1162
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Ile Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Ala Tyr Tyr Cys His Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1163

<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 VH DNA

<400> 1163
gaggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atgtcatatg atggaagtaa aaaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgt cactcagggt 300

atggacgtct ggggccaagg gaccctggtc accgtgtcct ca 342

<210> 1164
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 VH PRT

<400> 1164
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Met Ser Tyr Asp Gly Ser Lys Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Thr Gln Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 1165
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 VH complete DNA

<400> 1165
gaggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atgtcatatg atggaagtaa aaaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgt cactcagggt 300

atggacgtct ggggccaagg gaccctggtc accgtgtcct cagctagcac caagggccca 360

tcggtcttcc ccctggcacc ctcctccaag agcacctctg ggggcacagc ggccctgggc 420

tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 540

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaatcttg tgacaaaact 660

cacacatgcc caccgtgccc agcacctcca gtggccggac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

ggcgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 960

aacaaacagc tcccatcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaaaagcct ctccctgtcc 1320

ccgggt 1326

<210> 1166
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 VH complete PRT

<400> 1166
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Met Ser Tyr Asp Gly Ser Lys Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Thr Gln Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys

```
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                165                 170                 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            180                 185                 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
            340                 345                 350
```

```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440
```

<210> 1167
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU505-F05 VL complete DNA

<400> 1167

```
cagtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tgttggtcat ctattatatt agcgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaggccggg      240

gatgaggccg cctattactg tcacgtgtgg gatagtagta gtgatcatgt ggtattcggc      300

ggagggacca agctgaccgt cctaggtcag cccaaggctg caccaagtgt cactctgttc      360

ccgccctcct ctgaggagct tcaagccaac aaggccacac tggtgtgtct cataagtgac      420

ttctacccgg gagccgtgac agtggcctgg aaggcagata gcagccccgt caaggcggga      480

gtggagacca ccacaccctc caaacaaagc aacaacaagt acgcggccag cagctatctg      540

agcctgacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggt cacgcatgaa      600
```

gggagcaccg tggagaagac agtggcccct acagaatgtt ca 642

<210> 1168
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU505-F05 VL complete PRT

<400> 1168
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Ile Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Ala Tyr Tyr Cys His Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala

```
                165                 170                 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180                 185                 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
        195                 200                 205

Ala Pro Thr Glu Cys Ser
    210
```

<210> 1169
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR1 DNA

<400> 1169
agctatgcca tgagc 15

<210> 1170
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR1 PRT

<400> 1170
Ser Tyr Ala Met Ser
1 5

<210> 1171
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR2 DNA

<400> 1171
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 1172
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR2 PRT

<400> 1172
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1173
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR3 DNA

<400> 1173
gatcgatttt tggagtggtt attcacggga ccatttgact ac 42

<210> 1174
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 HCDR3 PRT

<400> 1174
Asp Arg Phe Leu Glu Trp Leu Phe Thr Gly Pro Phe Asp Tyr
1 5 10

<210> 1175
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR1 DNA

<400> 1175
caggcgagtc aggacattag caactattta aat 33

<210> 1176

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR1 PRT

<400> 1176
Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 1177
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR2 DNA

<400> 1177
gatgcatcca atttggaaac a 21

<210> 1178
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR2 PRT

<400> 1178
Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 1179
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR3 DNA

<400> 1179
caccagtatg ataatttccc ctacact 27

<210> 1180
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> YU519-A01 LCDR3 PRT

<400> 1180
His Gln Tyr Asp Asn Phe Pro Tyr Thr
1 5

<210> 1181
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 VL DNA

<400> 1181
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggaaagat ttcactttta tcatcaacaa cctgcagcct 240

gatgacattg caacatatta ctgtcaccag tatgataatt tcccctacac ttttggccag 300

gggaccaaag tggatatcaa a 321

<210> 1182
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 VL PRT

<400> 1182
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Phe Thr Phe Ile Ile Asn Asn Leu Gln Pro
65 70 75 80

Asp Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Asp Asn Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1183
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 VH DNA

<400> 1183
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcga 300

ttttggagt ggttattcac gggaccattt gactactggg gccagggaac cctggtcacc 360

gtgtcctca 369

<210> 1184
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 VH PRT

<400> 1184
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Asp Arg Phe Leu Glu Trp Leu Phe Thr Gly Pro Phe Asp Tyr
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1185
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A01 VH complete DNA

<400> 1185
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcga 300

ttttggagt ggttattcac gggaccattt gactactggg gccagggaac cctggtcacc 360

gtgtcctcag ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctccagtg 720

gccggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtgggc gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgggt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaacagctcc catcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga aaagcctctc cctgtccccg ggt 1353

<210> 1186
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 VH complete PRT

<400> 1186
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Asp Arg Phe Leu Glu Trp Leu Phe Thr Gly Pro Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser
            260                 265                 270
```

```
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly
    450
```

<210> 1187
<211> 642
<212> DNA
<213> Artificial Sequence

<220>

<223> YU519-A01 VL complete DNA

<400> 1187
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggaaagat ttcactttta tcatcaacaa cctgcagcct 240

gatgacattg caacatatta ctgtcaccag tatgataatt tcccctacac ttttggccag 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1188
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A01 VL complete PRT

<400> 1188
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Phe Thr Phe Ile Ile Asn Asn Leu Gln Pro
65 70 75 80

Asp Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Asp Asn Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Asp 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> 1189
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR1 DNA

<400> 1189
agctatgcca tgagc 15

<210> 1190
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR1 PRT

<400> 1190
Ser Tyr Ala Met Ser
1 5

<210> 1191
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR2 DNA

<400> 1191
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 1192
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR2 PRT

<400> 1192
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1193
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR3 DNA

<400> 1193
caccttgggg acggtgacta cgtcaattac tactactact acggtatgga cgtc 54

<210> 1194
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 HCDR3 PRT

<400> 1194
His Leu Gly Asp Gly Asp Tyr Val Asn Tyr Tyr Tyr Tyr Tyr Gly Met
1   5   10   15

Asp Val

<210> 1195
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR1 DNA

<400> 1195
gggggaaaca acattggaag taaaaatgta cac   33

<210> 1196
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR1 PRT

<400> 1196
Gly Gly Asn Asn Ile Gly Ser Lys Asn Val His
1   5   10

<210> 1197
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR2 DNA

<400> 1197
gatgataacg tccggccctc a   21

<210> 1198
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR2 PRT

<400> 1198
Asp Asp Asn Val Arg Pro Ser
1   5

<210> 1199
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR3 DNA

<400> 1199
caggtgtggc ttaatagtag tgatgatgtg cta   33

<210> 1200
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 LCDR3 PRT

<400> 1200
Gln Val Trp Leu Asn Ser Ser Asp Asp Val Leu
1   5   10

<210> 1201
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 VL DNA

<400> 1201
tcctatgtgc tgactcagcc accctcggtg tcagtggccc cacgacagac ggccaggatt   60

acctgtgggg gaaacaacat tggaagtaaa aatgtacact ggtaccagca gaagccaggc   120

caggcccctg tgctggtcgt ctatgatgat aacgtccggc cctcagggat ccctgagcga   180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg   240

gatgaggccg actattactg tcaggtgtgg cttaatagta gtgatgatgt gctattcggc 300

ggaggcacca aggtgaccgt cctc 324

<210> 1202
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 VL PRT

<400> 1202
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Asn Val Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Leu Asn Ser Ser Asp Asp
85 90 95

Val Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105

<210> 1203
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 VH DNA

<400> 1203
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttggc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacacctt 300

ggggacggtg actacgtcaa ttactactac tactacggta tggacgtctg gggccaaggg 360

accctggtca ccgtgtcctc a 381

<210> 1204
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 VH PRT

<400> 1204
Gln 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 Thr Phe Gly Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Leu Gly Asp Gly Asp Tyr Val Asn Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1205
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 VH complete DNA

<400> 1205
caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttggc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacacctt 300

ggggacggtg actacgtcaa ttactactac tactacggta tggacgtctg gggccaaggg 360

accctggtca ccgtgtcctc agctagcacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctccag tggccggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 780

atgatctccc ggacccctga ggtcacatgc gtggtggtgg gcgtgagcca cgaagaccct 840

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgg gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaacagct cccatccccc 1020

atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1260

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1320

ctgcacaacc actacacgca gaaaagcctc tccctgtccc cgggt 1365

<210> 1206
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 VH complete PRT

<400> 1206
Gln 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 Thr Phe Gly Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Leu Gly Asp Gly Asp Tyr Val Asn Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
130 135 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly

```
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        275                 280                 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305                 310                 315                 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln
                325                 330                 335

Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            340                 345                 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
        355                 360                 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    370                 375                 380
```

```
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385                 390                 395                 400

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                405                 410                 415

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            420                 425                 430

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445

Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 1207
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-A09 VL complete DNA

<400> 1207

```
tcctatgtgc tgactcagcc accctcggtg tcagtggccc cacgacagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa aatgtacact ggtaccagca gaagccaggc      120

caggcccctg tgctggtcgt ctatgatgat aacgtccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg cttaatagta gtgatgatgt gctattcggc      300

ggaggcacca aggtgaccgt cctcggtcag cccaaggctg caccaagtgt cactctgttc      360

ccgccctcct ctgaggagct tcaagccaac aaggccacac tggtgtgtct cataagtgac      420

ttctacccgg gagccgtgac agtggcctgg aaggcagata gcagccccgt caaggcggga      480

gtggagacca ccacaccctc caaacaaagc aacaacaagt acgcggccag cagctatctg      540

agcctgacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggt cacgcatgaa      600

gggagcaccg tggagaagac agtggcccct acagaatgtt ca                         642
```

<210> 1208
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-A09 VL complete PRT

<400> 1208
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Asn Val Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Leu Asn Ser Ser Asp Asp
85 90 95

Val Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser

180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 1209
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR1 DNA

<400> 1209
agctatgcta tcagc 15

<210> 1210
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR1 PRT

<400> 1210
Ser Tyr Ala Ile Ser
1 5

<210> 1211
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR2 DNA

<400> 1211
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1212
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR2 PRT

<400> 1212
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1   5   10   15

<210> 1213
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR3 DNA

<400> 1213
ccccgagtcc cccgagtctg ggagctctgg atcgggtttg gtgcttttga tatc   54

<210> 1214
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 HCDR3 PRT

<400> 1214
Pro Arg Val Pro Arg Val Trp Glu Leu Trp Ile Gly Phe Gly Ala Phe
1   5   10   15

Asp Ile

<210> 1215
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR1 DNA

<400> 1215
agggccagtc agagtgttag cagcagctac ttagcc   36

<210> 1216

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR1 PRT

<400> 1216
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 1217
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR2 DNA

<400> 1217
ggtgcatcca gcagggccac t 21

<210> 1218
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR2 PRT

<400> 1218
Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 1219
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR3 DNA

<400> 1219
cagcagtatg gtagctcacc ctacagt 27

<210> 1220
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> YU519-B05 LCDR3 PRT

<400> 1220
Gln Gln Tyr Gly Ser Ser Pro Tyr Ser
1 5

<210> 1221
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 VL DNA

<400> 1221
gaaatagtga tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacccta cagttttggc 300

caggggacca agctggagat caaa 324

<210> 1222
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 VL PRT

<400> 1222
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1223
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 VH DNA

<400> 1223
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaggccccga 300

gtcccccgag tctgggagct ctggatcggg tttggtgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtgtcttc a 381

<210> 1224
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 VH PRT

<400> 1224
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Pro Arg Val Pro Arg Val Trp Glu Leu Trp Ile Gly Phe Gly
            100   105   110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120   125

<210> 1225
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-B05 VH complete DNA

<400> 1225
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaggccccga 300

gtcccccgag tctgggagct ctggatcggg tttggtgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtgtcttc agctagcacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctccag tggccggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 780

atgatctccc ggaccctga ggtcacatgc gtggtggtgg gcgtgagcca cgaagaccct 840

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgg gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaacagct cccatccccc 1020

atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1260

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1320

ctgcacaacc actacacgca gaaaagcctc tccctgtccc cgggt 1365

<210> 1226
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 VH complete PRT

<400> 1226
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Pro Arg Val Pro Arg Val Trp Glu Leu Trp Ile Gly Phe Gly
            100                 105                 110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270
```

```
Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        275                 280                 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305                 310                 315                 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln
                325                 330                 335

Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            340                 345                 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
        355                 360                 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385                 390                 395                 400

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                405                 410                 415

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            420                 425                 430

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445

Ser Leu Ser Leu Ser Pro Gly
    450                 455
```

<210> 1227
<211> 645
<212> DNA
<213> Artificial Sequence

<220>

<223> YU519-B05 VL complete DNA

<400> 1227
gaaatagtga tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacccta cagttttggc 300

caggggacca agctggagat caaacgtacg gtggctgcac catctgtgtt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 1228
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-B05 VL complete PRT

<400> 1228
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 1229
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR1 DNA

<400> 1229
agctatgcta tgcac 15

<210> 1230
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR1 PRT

<400> 1230
Ser Tyr Ala Met His
1 5

<210> 1231
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR2 DNA

<400> 1231
gttatatcat atgatggaag caataaatac tacgcagact ccgtgaaggg c 51

<210> 1232
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR2 PRT

<400> 1232
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1233
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR3 DNA

<400> 1233
gatcttttgg tgaac 15

<210> 1234
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 HCDR3 PRT

<400> 1234
Asp Leu Leu Val Asn
1   5

<210> 1235
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 LCDR1 DNA

<400> 1235
cgggcgagtc agggcattag caattattta gcc   33

<210> 1236
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 LCDR1 PRT

<400> 1236
Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
1   5   10

<210> 1237
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 LCDR2 DNA

<400> 1237
gctgcatcca ctttgcaatc a   21

<210> 1238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> YU519-C01 LCDR2 PRT

<400> 1238
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 1239
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 LCDR3 DNA

<400> 1239
caaaagtata acagtgcccc ccggact 27

<210> 1240
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 LCDR3 PRT

<400> 1240
Gln Lys Tyr Asn Ser Ala Pro Arg Thr
1 5

<210> 1241
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 VL DNA

<400> 1241
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaaag tataacagtg ccccccggac tttcggcgga 300

gggaccaaag tggatatcaa a 321

<210> 1242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 VL PRT

<400> 1242
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1243
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 VH DNA

<400> 1243
gaggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatctt 300

ttggtgaact ggggccaggg aaccctggtc accgtgtcct ca 342

<210> 1244
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 VH PRT

<400> 1244
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Leu Val Asn Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 1245
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 VH complete DNA

<400> 1245
gaggtgcagc tgttggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatctt 300

ttggtgaact ggggccaggg aaccctggtc accgtgtcct cagctagcac caagggccca 360

tcggtcttcc ccctggcacc ctcctccaag agcacctctg ggggcacagc ggccctgggc 420

tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 540

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaatcttg tgacaaaact 660

cacacatgcc caccgtgccc agcacctcca gtggccggac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

ggcgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 960

aacaaacagc tcccatcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaaaagcct ctccctgtcc 1320

ccgggt 1326

<210> 1246
<211> 442

<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 VH complete PRT

<400> 1246
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Leu Val Asn Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

```
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
            340                 345                 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
```

405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440

<210> 1247
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-C01 VL complete DNA

<400> 1247
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaaag tataacagtg ccccccggac tttcggcgga 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1248
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-C01 VL complete PRT

<400> 1248
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

```
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Asp 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> 1249
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR1 DNA

<400> 1249
agctatgcta tcagc 15

<210> 1250
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR1 PRT

<400> 1250
Ser Tyr Ala Ile Ser
1 5

<210> 1251
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR2 DNA

<400> 1251
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1252
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR2 PRT

<400> 1252
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1253
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR3 DNA

<400> 1253
ggtgggagct acttgcccctt tgactac 27

<210> 1254
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 HCDR3 PRT

<400> 1254
Gly Gly Ser Tyr Leu Pro Phe Asp Tyr
1 5

<210> 1255
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR1 DNA

<400> 1255
agggccagtc agagtgttag cagctactta gcc 33

<210> 1256
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR1 PRT

<400> 1256
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 1257
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR2 DNA

<400> 1257
gatgcatcca acagggccac t 21

<210> 1258
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR2 PRT

<400> 1258
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 1259
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR3 DNA

<400> 1259
cagcaacgta gcaactggcc tccgact 27

<210> 1260
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 LCDR3 PRT

<400> 1260
Gln Gln Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 1261
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 VL DNA

<400> 1261
gaaatagtga tgacgcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg ccgtttatta ctgtcagcaa cgtagcaact ggcctccgac tttcggcgga 300

gggaccaagc tggagatcaa a 321

<210> 1262
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 VL PRT

<400> 1262
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
                85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100 105

<210> 1263
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 VH DNA

<400> 1263
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggtggg 300

agctacttgc cctttgacta ctggggccag ggaaccctgg tcaccgtgtc ctca 354

<210> 1264
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 VH PRT

<400> 1264
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Ser Tyr Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1265
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 VH complete DNA

<400> 1265
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggtggg 300

agctacttgc cctttgacta ctggggccag ggaaccctgg tcaccgtgtc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctc agtggccgg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tgggcgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaaca gctcccatcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaaaagc 1320

ctctccctgt ccccgggt 1338

<210> 1266
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 VH complete PRT

<400> 1266
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Ser Tyr Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

```
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr Ile
                325                 330                 335
```

```
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1267
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E03 VL complete DNA

<400> 1267

```
gaaatagtga tgacgcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct      120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc      180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct      240

gaagattttg ccgtttatta ctgtcagcaa cgtagcaact ggcctccgac tttcggcgga      300

gggaccaagc tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag      480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540
```

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1268
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E03 VL complete PRT

<400> 1268
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1269
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR1 DNA

<400> 1269
agctatgcta tcagc 15

<210> 1270
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR1 PRT

<400> 1270
Ser Tyr Ala Ile Ser
1 5

<210> 1271
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR2 DNA

<400> 1271
gggatcatcc ctatctttgg tacagcaaac tacgcacaga agttccaggg c 51

<210> 1272
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR2 PRT

<400> 1272
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

<210> 1273
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR3 DNA

<400> 1273
gatttgtaca gctatggccc ctggtactac tttgactac 39

<210> 1274
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 HCDR3 PRT

<400> 1274
Asp Leu Tyr Ser Tyr Gly Pro Trp Tyr Tyr Phe Asp Tyr
1 5 10

<210> 1275
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR1 DNA

<400> 1275
cgggcaagtc agagcattga caactattta aat 33

<210> 1276
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR1 PRT

<400> 1276
Arg Ala Ser Gln Ser Ile Asp Asn Tyr Leu Asn
1 5 10

<210> 1277
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR2 DNA

<400> 1277
actgcatcca gtttgcaaag t 21

<210> 1278
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR2 PRT

<400> 1278
Thr Ala Ser Ser Leu Gln Ser
1 5

<210> 1279
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR3 DNA

<400> 1279
caacagagtt acaatacccc tcccact 27

<210> 1280
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 LCDR3 PRT

<400> 1280
Gln Gln Ser Tyr Asn Thr Pro Pro Thr
1 5

<210> 1281
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 VL DNA

<400> 1281
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattgac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgccaacag agttacaata ccctcccac tttcggccct 300

gggaccaagg tggaaatcaa a 321

<210> 1282
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 VL PRT

<400> 1282
Asp Ile Val 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 Ser Ile Asp Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1283
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 VH DNA

<400> 1283
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatttg 300

tacagctatg gcccctggta ctactttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctca 366

<210> 1284
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 VH PRT

<400> 1284
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Tyr Ser Tyr Gly Pro Trp Tyr Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1285
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> YU519-E12 VH complete DNA

<400> 1285
caggttcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatttg 300

tacagctatg gcccctggta ctactttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctcagcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tccagtggcc 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtgggcgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa cagctcccat cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaaa gcctctccct gtccccgggt 1350

<210> 1286
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 VH complete PRT

<400> 1286
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Tyr Ser Tyr Gly Pro Trp Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His
```

```
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly
    450
```

<210> 1287
<211> 642
<212> DNA

<213> Artificial Sequence

<220>
<223> YU519-E12 VL complete DNA

<400> 1287
gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattgac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgccaacag agttacaata cccctcccac tttcggccct 300

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1288
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> YU519-E12 VL complete PRT

<400> 1288
Asp Ile Val 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 Ser Ile Asp Asn Tyr
            20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro
                85                  90                  95


Thr Phe Gly Pro 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>  1289
<211>  123
<212>  PRT
<213>  artificial sequence

<220>
<223>  PHE162-D2

<400>  1289

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Arg Leu Asn Asn Trp Lys Thr Gln Pro Tyr Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  1290
<211>  10
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH PHE162-D2

<400>  1290

Gly Ser Ser Ile Ser Ser Gly Gly Tyr Tyr
1               5                   10


<210>  1291
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH PHE162-D2

<400>  1291

Ile Tyr Tyr Ser Gly Ser Thr
```

1 5

<210> 1292
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH PHE162-D2

<400> 1292

Ala Arg Arg Leu Asn Asn Trp Lys Thr Gln Pro Tyr Phe Asp Tyr
1 5 10 15

<210> 1293
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL PHE162-D2

<400> 1293

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Pro Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1294
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL PHE162-D2

<400> 1294

Ser Pro Asn Ile Gly Ala Gly Tyr Asp
1   5

<210> 1295
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL PHE162-D2

<400> 1295

Gly Asn Ser
1

<210> 1296
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL PHE162-D2

<400> 1296

Gln Ser Tyr Asp Ser Ser Leu Ser Asp Val Val
1   5   10

<210> 1297
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-A10

<400> 1297

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1298
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-A10

<400> 1298

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1299
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-A10

<400> 1299

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1300
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-A10

<400> 1300

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1301
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-A10

<400> 1301

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Lys Ala Ser Ser Leu Gly Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Asp Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr Asn Ser Tyr Pro Val
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1302
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 STE90-A10

<400> 1302

Gln Gly Ile Ser Ser Trp
1 5

<210> 1303
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-A10

<400> 1303

Lys Ala Ser
1

<210> 1304
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-A10

<400> 1304

Gln Gln Tyr Asn Ser Tyr Pro Val Thr
1 5

<210> 1305
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-C11

<400> 1305

```
Gln 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 Leu Thr Val Ser Ser Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  1306
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE90-C11

<400>  1306

Gly Leu Thr Val Ser Ser Asn Tyr
1               5


<210>  1307
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE90-C11
```

<400> 1307

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1308
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-C11

<400> 1308

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1309
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-C11

<400> 1309

Asp Ile Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1310
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-C11

<400> 1310

Gln Gly Ile Ser Ser Tyr
1 5

<210> 1311
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-C11

<400> 1311

Ala Ala Ser
1

<210> 1312
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-C11

<400> 1312

Gln Gln Leu Asn Ser Tyr Pro Pro Phe Thr
1 5 10

<210> 1313
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-D7

<400> 1313

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110


Thr Val Ser Ser
        115
```

<210> 1314
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-D7

<400> 1314

```
Gly Leu Thr Val Ser Ser Asn Tyr
1               5
```

<210> 1315
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-D7

<400> 1315

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1316
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-D7

<400> 1316

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1317
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-D7

<400> 1317

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Leu Pro Leu

85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1318
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-D7

<400> 1318

Gln Gly Ile Ser Ser Trp
1 5

<210> 1319
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-D7

<400> 1319

Ala Ala Ser
1

<210> 1320
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-D7

<400> 1320

Gln Gln Ala Asn Ser Leu Pro Leu Thr
1 5

<210> 1321
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-G2

<400> 1321

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1322
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-G2

<400> 1322

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1323
<211> 7
<212> PRT

<213> artificial sequence

<220>
<223> CDR2 VH STE90-G2

<400> 1323

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1324
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-G2

<400> 1324

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1325
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-G2

<400> 1325

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
85 90 95

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1326
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-G2

<400> 1326

Gln Gly Ile Ser Ser Trp
1 5

<210> 1327
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-G2

<400> 1327

Ala Ala Ser
1

<210> 1328
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-G2

<400> 1328

Gln Gln Ala Asn Ser Phe Pro Pro Leu Phe Thr
1 5 10

<210> 1329
<211> 116
<212> PRT

<213> artificial sequence

<220>
<223> VH STE90-B1-A10

<400> 1329

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1330
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B1-A10

<400> 1330

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1331

<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B1-A10

<400> 1331

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1332
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B1-A10

<400> 1332

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1333
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B1-A10

<400> 1333

Asp Val Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1334
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B1-A10

<400> 1334

Gln Ser Ile Gly Ser Trp
1 5

<210> 1335
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B1-A10

<400> 1335

Lys Ala Ser
1

<210> 1336
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B1-A10

<400> 1336

Gln Gln Tyr Asn Ser Tyr Pro Val Thr
1 5

<210> 1337

<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B1-B4

<400> 1337

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1338
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B1-B4

<400> 1338

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1339
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B1-B4

<400> 1339

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1340
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B1-B4

<400> 1340

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1341
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B1-B4

<400> 1341

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 Ser Ile Ser Thr Tyr
            20   25   30

Leu His Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35   40   45

Tyr Gly Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Arg Val Glu Ile Lys
100 105

<210> 1342
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B1-B4

<400> 1342

Gln Ser Ile Ser Thr Tyr
1 5

<210> 1343
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B1-B4

<400> 1343

Gly Ala Ser
1

<210> 1344
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B1-B4

<400> 1344

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> 1345
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B1-D1

<400> 1345

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1346
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B1-D1

<400> 1346

Gly Leu Thr Val Ser Ser Asn Tyr

1 5

<210> 1347
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B1-D1

<400> 1347

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1348
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B1-D1

<400> 1348

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1349
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B1-D1

<400> 1349

Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 1350
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B1-D1

<400> 1350

Gln Gly Ile Ser Ser Tyr
1 5

<210> 1351
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B1-D1

<400> 1351

Ala Ala Ser
1

<210> 1352
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B1-D1

<400> 1352

Gln Gln Leu Asn Ser Tyr Pro Ile Thr

1 5

<210> 1353
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B1-D6

<400> 1353

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Gly Leu Val Gly Ala Thr Thr Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1354
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B1-D6

<400> 1354

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1355
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B1-D6

<400> 1355

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1356
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B1-D6

<400> 1356

Ala Arg Glu Gly Leu Val Gly Ala Thr Thr Ala Phe Asp Tyr
1   5   10

<210> 1357
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B1-D6

<400> 1357

Asp Ile Val 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 Ser Ile Ser Ser Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Met Pro Pro
                85   90   95

Ser Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1358
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B1-D6

<400> 1358

Gln Ser Ile Ser Ser Tyr
1   5

<210> 1359
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B1-D6

<400> 1359

Ala Ala Ser
1

<210> 1360
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B1-D6

<400> 1360

Gln Gln Ser Tyr Ser Met Pro Pro Ser Thr
1 5 10

<210> 1361
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B1-F8

<400> 1361

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Gly Leu Val Gly Ala Thr Thr Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1362
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B1-F8

<400> 1362

Gly Phe Thr Val Ser Ser Asn Tyr
1 5

<210> 1363
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CD2 VH STE90-B1-F8

<400> 1363

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1364
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B1-F8

<400> 1364

Ala Arg Glu Gly Leu Val Gly Ala Thr Thr Ala Phe Asp Tyr
1 5 10

<210> 1365
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B1-F8

<400> 1365

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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
                85                  90                  95

Val Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 1366
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B1-F8

<400> 1366

```
Gln Ser Ile Ser Ser Tyr
1               5
```

<210> 1367
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B1-F8

<400> 1367

```
Ala Ala Ser
1
```

<210> 1368
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B1-F8

<400> 1368

Gln Gln Ser Tyr Ser Thr Pro Pro Val Thr
1 5 10

<210> 1369
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B2-A1

<400> 1369

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1370
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B2-A1

<400> 1370

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1371
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B2-A1

<400> 1371

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1372
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B2-A1

<400> 1372

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1373
<211> 103
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B2-A1

<400> 1373

Asp Ile Val 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 Ser Ile Ser Ser Tyr
            20   25   30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Asp Thr Phe Gly Gln
                85                  90                  95

Gly Thr Lys Leu Glu Ile Lys
            100
```

<210> 1374
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B2-A1

<400> 1374

```
Gln Ser Ile Ser Ser Tyr
1               5
```

<210> 1375
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B2-A1

<400> 1375

```
Ala Ala Ser
1
```

<210> 1376
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B2-A1

<400> 1376

Gln Gln Arg Asp Thr
1   5

<210> 1377
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B2-B3

<400> 1377

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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Val Ala Asp Val Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1378
<211> 8
<212> PRT

<213> artificial sequence

<220>
<223> CDR1 VH STE90-B2-B3

<400> 1378

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1379
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B2-B3

<400> 1379

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1380
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B2-B3

<400> 1380

Ala Arg Asp Val Ala Asp Val Phe Asp Ile
1 5 10

<210> 1381
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B2-B3

<400> 1381

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp

```
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 1382
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B2-B3

<400> 1382

```
Gln Ser Ile Ser Ser Trp
1               5
```

<210> 1383
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B2-B3

<400> 1383

```
Lys Ala Ser
1
```

<210> 1384
<211> 9
<212> PRT

<213> artificial sequence

<220>
<223> CDR3 VL STE90-B2-B3

<400> 1384

Gln Gln Tyr Asn Ser Tyr Pro Pro Thr
1 5

<210> 1385
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B2-C5

<400> 1385

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1386

<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B2-C5

<400> 1386

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1387
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B2-C5

<400> 1387

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1388
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B2-C5

<400> 1388

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1389
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B2-C5

<400> 1389

Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Val
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 1390
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B2-C5

<400> 1390

```
Gln Ser Ile Ser Ser Trp
1               5
```

<210> 1391
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B2-C5

<400> 1391

```
Lys Ala Ser
1
```

<210> 1392

<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B2-C5

<400> 1392

Gln Gln Tyr Asn Ser Tyr Pro Val Thr
1 5

<210> 1393
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B2-D12

<400> 1393

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1394
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> GLTVSSNY

<400> 1394

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1395
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B2-D12

<400> 1395

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1396
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B2-D12

<400> 1396

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1397
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B2-D12

<400> 1397

Asp Ile Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1398
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B2-D12

<400> 1398

Gln Gly Ile Ser Ser Tyr
1 5

<210> 1399
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B2-D12

<400> 1399

Ala Ala Ser
1

<210> 1400
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B2-D12

<400> 1400

Gln Gln Leu Asn Ser Tyr Pro Pro Tyr Thr
1 5 10

<210> 1401
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B2-E6

<400> 1401

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser

115

<210> 1402
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B2-E6

<400> 1402

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1403
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B2-E6

<400> 1403

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1404
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B2-E6

<400> 1404

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1405
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B2-E6

<400> 1405

```
Ala Ile Arg Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
                85                  90                  95

Ala Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 1406
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B2-E6

<400> 1406

```
Gln Gly Ile Ser Ser Tyr
1               5
```

<210> 1407
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B2-E6

<400> 1407

```
Ala Ala Ser
```

1

<210> 1408
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B2-E6

<400> 1408

Gln Gln Leu Asn Ser Tyr Pro Pro Ala
1 5

<210> 1409
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B3-B10

<400> 1409

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
        115

<210> 1410
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B3-B10

<400> 1410

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1411
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B3-B10

<400> 1411

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1412
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B3-B10

<400> 1412

Ala Arg Asp Val Ala Asp Ala Phe Asp Val
1   5   10

<210> 1413
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B3-B10

<400> 1413

Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1414
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B3-B10

<400> 1414

Gln Ser Ile Ser Ser Trp
1 5

<210> 1415
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B3-B10

<400> 1415

Lys Ala Ser
1

<210> 1416
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B3-B10

<400> 1416

Gln Gln Tyr Asn Ser Tyr Pro Val Thr
1 5

<210> 1417
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B3-H3

<400> 1417

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val

100 105 110

Thr Val Ser Ser
115

<210> 1418
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B3-H3

<400> 1418

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1419
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B3-H3

<400> 1419

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1420
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE90-B3-H3

<400> 1420

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1421
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> VL STE90-B3-H3

<400> 1421

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
                85   90   95

Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 1422
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B3-H3

<400> 1422

Gln Gly Ile Ser Ser Trp
1   5

<210> 1423
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B3-H3

<400> 1423

Ala Ala Ser
1

<210> 1424
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B3-H3

<400> 1424

Gln Gln Ala Asn Ser Phe Pro Pro Leu Phe Thr
1 5 10

<210> 1425
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE90-B3-H6

<400> 1425

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu His Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1426
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B3-H6

<400> 1426

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1427
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE90-B3-H6

<400> 1427

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1428
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE90-B3-H6

<400> 1428

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1429
<211> 108
<212> PRT

<213> artificial sequence

<220>
<223> VL STE90-B3-H6

<400> 1429

Ala Ile Arg Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1430
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE90-B3-H6

<400> 1430

Gln Gly Ile Ser Ser Tyr
1 5

<210> 1431
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE90-B3-H6

<400> 1431

Ala Ala Ser
1

<210> 1432
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE90-B3-H6

<400> 1432

Gln Gln Leu Asn Ser Tyr Pro Pro Trp Thr
1   5   10

<210> 1433
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-C4

<400> 1433

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1434
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE91-C4

<400> 1434

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1435
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE91-C4

<400> 1435

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1436
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE91-C4

<400> 1436

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1437

<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-C4

<400> 1437

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Thr
1 5 10 15

Thr Ala Thr Ile Thr Cys Ala Glu Asp Thr Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Ala Gly Gln Ala Pro Val Leu Val Ile Phe
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Lys Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Phe Cys Gln Val Trp Asp Ser Tyr Thr Asp Ala
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1438
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-C4

<400> 1438

Thr Ile Gly Ser Lys Ser
1 5

<210> 1439
<211> 3
<212> PRT

<213> artificial sequence

<220>
<223> CDR2 VL STE91-C4

<400> 1439

Tyr Asp Ser
1

<210> 1440
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-C4

<400> 1440

Gln Val Trp Asp Ser Tyr Thr Asp Ala Val Val
1 5 10

<210> 1441
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-D4

<400> 1441

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

```
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  1442
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE91-D4

<400>  1442

Gly Leu Thr Val Ser Ser Asn Tyr
1               5


<210>  1443
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE91-D4

<400>  1443

Ile Tyr Ser Gly Gly Ser Thr
1               5


<210>  1444
<211>  10
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR3 VH STE91-D4

<400>  1444

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1               5                   10
```

<210> 1445
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-D4

<400> 1445

Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Tyr Lys Leu Gly Asp Lys Tyr Val
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Phe Ala Phe Tyr
85 90 95

Ile Phe Gly Thr Gly Thr Arg Val Thr Val Leu
100 105

<210> 1446
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-D4

<400> 1446

Lys Leu Gly Asp Lys Tyr
1 5

<210> 1447

<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE91-D4

<400> 1447

Gln Asp Thr
1

<210> 1448
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-D4

<400> 1448

Gln Ala Trp Asp Ser Phe Ala Phe Tyr Ile
1 5 10

<210> 1449
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-F6

<400> 1449

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1450
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE91-F6

<400> 1450

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1451
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE91-F6

<400> 1451

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1452
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE91-F6

<400> 1452

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile

1 5 10

<210> 1453
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-F6

<400> 1453

Leu Pro Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Gly Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Gly Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 1454
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-F6

<400> 1454

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1 5

<210> 1455
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE91-F6

<400> 1455

Gly Asn Ser
1

<210> 1456
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-F6

<400> 1456

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Gly Val
1   5   10

<210> 1457
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-F10

<400> 1457

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1458
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE91-F10

<400> 1458

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1459
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE91-F10

<400> 1459

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1460
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE91-F10

<400> 1460

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1461
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-F10

<400> 1461

Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Ile Ala Ser Ile Thr Cys Ser Gly Tyr Lys Leu Gly Asp Lys Tyr Val
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Gly Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Phe Ala Phe Tyr
85 90 95

Val Phe Gly Thr Gly Thr Arg Val Thr Val Leu
100 105

<210> 1462
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-F10

<400> 1462

Lys Leu Gly Asp Lys Tyr

1 5

<210> 1463
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE91-F10

<400> 1463

Gln Gly Thr
1

<210> 1464
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-F10

<400> 1464

Gln Ala Trp Asp Ser Phe Ala Phe Tyr Val
1 5 10

<210> 1465
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-B1-A10

<400> 1465

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys

50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1466
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE91-B1-A10

<400> 1466

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1467
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE91-B1-A10

<400> 1467

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1468
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE91-B1-A10

<400> 1468

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1469
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-B1-A10

<400> 1469

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Tyr Lys Leu Gly Asp Lys Tyr Val
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Asp Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Phe Ala Phe Tyr
85 90 95

Val Phe Gly Thr Gly Thr Arg Val Thr Val Leu
100 105

<210> 1470
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-B1-A10

<400> 1470

Lys Leu Gly Asp Lys Tyr
1   5

<210> 1471
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE91-B1-A10

<400> 1471

Gln Asp Thr
1

<210> 1472
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-B1-A10

<400> 1472

Gln Ala Trp Asp Ser Phe Ala Phe Tyr Val
1   5   10

<210> 1473
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE91-B1-B3

<400> 1473

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

```
Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110


Thr Val Ser Ser
        115
```

<210> 1474
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE91-B1-B3

<400> 1474

```
Gly Leu Thr Val Ser Ser Asn Tyr
1               5
```

<210> 1475
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE91-B1-B3

<400> 1475

```
Ile Tyr Ser Gly Gly Ser Thr
1               5
```

<210> 1476
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE91-B1-B3

<400> 1476

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1477
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE91-B1-B3

<400> 1477

Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1   5   10   15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
            20   25   30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35   40   45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65   70   75   80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
                85   90   95

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105

<210> 1478
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE91-B1-B3

<400> 1478

Asn Ile Gly Ser Lys Ser
1 5

<210> 1479
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE91-B1-B3

<400> 1479

Asp Asp Ser
1

<210> 1480
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE91-B1-B3

<400> 1480

Gln Val Trp Asp Ser Ser Ser Asp His Tyr Val
1 5 10

<210> 1481
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-A1

<400> 1481

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110

Thr Val Ser Ser
        115
```

<210> 1482
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-A1

<400> 1482

```
Gly Leu Thr Val Ser Ser Asn Tyr
1               5
```

<210> 1483
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-A1

<400> 1483

```
Ile Tyr Ser Gly Gly Ser Thr
1               5
```

<210> 1484
<211> 10
<212> PRT

<213> artificial sequence

<220>
<223> CDR3 VH STE94-A1

<400> 1484

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1485
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-A1

<400> 1485

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1486
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-A1

<400> 1486

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1   5

<210> 1487
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-A1

<400> 1487

Gly Asn Ser
1

<210> 1488
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-A1

<400> 1488

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Leu Val
1   5   10

<210> 1489
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B2

<400> 1489

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1490
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-B2

<400> 1490

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1491
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B2

<400> 1491

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1492

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B2

<400> 1492

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1493
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B2

<400> 1493

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Asn Asp Arg Pro Ser Arg Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asp Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1494
<211> 6
<212> PRT

<213> artificial sequence

<220>
<223> CDR1 VL STE94-B2

<400> 1494

Asn Ile Gly Ser Lys Ser
1 5

<210> 1495
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B2

<400> 1495

Asp Asp Asn
1

<210> 1496
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-B2

<400> 1496

Gln Val Trp Asp Ser Ser Ser Asp His Val Val
1 5 10

<210> 1497
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-D3

<400> 1497

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn

```
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110

Thr Val Ser Ser
        115


<210>  1498
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE94-D3

<400>  1498

Gly Leu Thr Val Ser Ser Asn Tyr
1               5


<210>  1499
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE94-D3

<400>  1499

Ile Tyr Ser Gly Gly Ser Thr
1               5
```

<210> 1500
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-D3

<400> 1500

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1501
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-D3

<400> 1501

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Asn Asp Val Gly Ala Ala
            20   25   30

Asn Tyr Val Phe Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35   40   45

Met Ile Tyr Gly Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85   90   95

Gly Tyr Leu Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1502

<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-D3

<400> 1502

Ser Asn Asp Val Gly Ala Ala Asn Tyr
1 5

<210> 1503
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-D3

<400> 1503

Gly Val Ser
1

<210> 1504
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-D3

<400> 1504

Ser Ser Tyr Thr Ser Ser Gly Tyr Leu Gly Val
1 5 10

<210> 1505
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-E3

<400> 1505

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1506
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-E3

<400> 1506

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1507
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-E3

<400> 1507

Ile Tyr Ser Gly Gly Ser Thr

1 5

<210> 1508
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-E3

<400> 1508

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1509
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-E3

<400> 1509

Asp Ile Arg Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Arg
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1510
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-E3

<400> 1510

Gln Gly Ile Ser Ser Tyr
1   5

<210> 1511
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-E3

<400> 1511

Ala Ala Ser
1

<210> 1512
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-E3

<400> 1512

Gln Gln Leu Asn Ser Tyr Pro Arg Ser
1   5

<210> 1513
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-E9

<400> 1513

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1514
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-E9

<400> 1514

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1515
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-E9

<400> 1515

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1516
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-E9

<400> 1516

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1517
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-E9

<400> 1517

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Ser Ala Gly Ser Asn
85 90 95

Asn Leu Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 1518
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-E9

<400> 1518

Ser Ser Asn Ile Gly Ser Asn Tyr
1 5

<210> 1519
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-E9

<400> 1519

Arg Asn Asn
1

<210> 1520
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-E9

<400> 1520

Ser Ser Ser Ala Gly Ser Asn Asn Leu Leu
1 5 10

<210> 1521
<211> 128
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-F6

<400> 1521

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asn Asn Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Ala Val Gly Asp Tyr Tyr Tyr Asp Ser Ser Gly Tyr Ser Pro
            100                 105                 110


Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  1522
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE94-F6

<400>  1522

Gly Gly Thr Phe Asn Asn Tyr Ala
1               5


<210>  1523
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE94-F6
```

<400> 1523

Ile Ile Pro Ile Leu Gly Ile Ala
1   5

<210> 1524
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-F6

<400> 1524

Ala Thr Ala Val Gly Asp Tyr Tyr Tyr Asp Ser Ser Gly Tyr Ser Pro
1   5   10   15

Asn Trp Phe Asp Pro
            20

<210> 1525
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-F6

<400> 1525

Asp Ile Val 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 Ser Ile Ser Ser Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1526
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-F6

<400> 1526

Gln Ser Ile Ser Ser Tyr
1 5

<210> 1527
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-F6

<400> 1527

Ala Ala Ser
1

<210> 1528
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-F6

<400> 1528

Gln Gln Ser Tyr Ser Thr Leu Tyr Thr
1 5

<210> 1529
<211> 116
<212> PRT

<213> artificial sequence

<220>
<223> VH STE94-F7

<400> 1529

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1530
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-F7

<400> 1530

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1531

<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-F7

<400> 1531

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1532
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-F7

<400> 1532

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1533
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-F7

<400> 1533

Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Leu Gly Ser Asn
20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Asn Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Gly Ser Leu
85 90 95

Ser Gly Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1534
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-F7

<400> 1534

Ser Ser Asn Leu Gly Ser Asn Tyr
1 5

<210> 1535
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-F7

<400> 1535

Arg Asn Tyr
1

<210> 1536
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-F7

<400> 1536

Ala Ala Trp Asp Gly Ser Leu Ser Gly Val Leu
1 5 10

<210> 1537

<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-F12

<400> 1537

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1538
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-F12

<400> 1538

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1539
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-F12

<400> 1539

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1540
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-F12

<400> 1540

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1541
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-F12

<400> 1541

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1   5   10   15

Thr Ala Arg Ile Ile Cys Gly Gly Asn Asn Val Gly Ser Thr Ser Val
            20   25   30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35   40   45

Asp Asn Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

Thr Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Ala Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr His Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1542
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-F12

<400> 1542

Asn Asn Val Gly Ser Thr Ser
1 5

<210> 1543
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-F12

<400> 1543

Asp Asn Ser
1

<210> 1544
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-F12

<400> 1544

Gln Val Trp Asp Ser Ser Ser Asp His Val Val
1 5 10

<210> 1545
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-H2

<400> 1545

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1546
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-H2

<400> 1546

Gly Leu Thr Val Ser Ser Asn Tyr

1 5

<210> 1547
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-H2

<400> 1547

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1548
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-H2

<400> 1548

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1549
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-H2

<400> 1549

Asp Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

```
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
                85                  90                  95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 1550
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-H2

<400> 1550

```
Gln Gly Ile Ser Ser Tyr
1               5
```

<210> 1551
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-H2

<400> 1551

```
Ala Ala Ser
1
```

<210> 1552
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-H2

<400> 1552

```
Gln Gln Leu Asn Ser Tyr Pro Pro Tyr Thr
```

1 5 10

<210> 1553
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B1-D1

<400> 1553

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1554
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-B1-D1

<400> 1554

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1555
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B1-D1

<400> 1555

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1556
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B1-D1

<400> 1556

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1557
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B1-D1

<400> 1557

Leu Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1   5   10   15

Thr Ala Ser Ile Thr Cys Gly Gly Asp Tyr Ile Gly Ser Lys Ser Val
            20   25   30

His Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35   40   45

Asp Asp Ser Glu Trp Pro Pro Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Pro Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Glu Ser Gly Ser Asp His
85 90 95

Tyr Val Phe Gly Ser Gly Thr Lys Val Ala Val Leu
100 105

<210> 1558
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-B1-D1

<400> 1558

Tyr Ile Gly Ser Lys Ser
1 5

<210> 1559
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B1-D1

<400> 1559

Asp Asp Ser
1

<210> 1560
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-B1-D1

<400> 1560

Gln Val Trp Glu Ser Gly Ser Asp His Tyr Val
1 5 10

<210> 1561
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B1-E12

<400> 1561

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1562
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-B1-E12

<400> 1562

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1563
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B1-E12

<400> 1563

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1564
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B1-E12

<400> 1564

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1565
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B1-E12

<400> 1565

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Ile Ala Lys Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Asn Val
20 25 30

Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Leu Ile Tyr

```
        35                  40                  45

Gln Asp Leu Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Asn Ser Gly Ser Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Thr Met
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ile Ser Thr Ser Thr
                85                  90                  95

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105
```

<210> 1566
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-B1-E12

<400> 1566

```
Asn Leu Gly Asp Lys Asn
1               5
```

<210> 1567
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B1-E12

<400> 1567

```
Gln Asp Leu
1
```

<210> 1568
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-B1-E12

<400> 1568

Gln Ala Trp Asp Ile Ser Thr Ser Thr Tyr Val
1 5 10

<210> 1569
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B2-B1

<400> 1569

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1570
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-B2-B1

<400> 1570

Gly Leu Thr Val Ser Ser Asn Tyr
1   5

<210> 1571
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B2-B1

<400> 1571

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1572
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B2-B1

<400> 1572

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1   5   10

<210> 1573
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B2-B1

<400> 1573

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Leu Lys Leu
        35   40   45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1574
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-B2-B1

<400> 1574

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1   5

<210> 1575
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B2-B1

<400> 1575

Gly Asn Ser
1

<210> 1576
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-B2-B1

<400> 1576

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Val Val
1   5   10

<210> 1577
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B2-B6

<400> 1577

Gln 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 Leu Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100   105   110

Thr Val Ser Ser
        115

<210> 1578
<211> 8
<212> PRT

<213> artificial sequence

<220>
<223> CDR1 VH STE94-B2-B6

<400> 1578

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1579
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B2-B6

<400> 1579

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1580
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B2-B6

<400> 1580

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1581
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B2-B6

<400> 1581

Asp Val Val Leu 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 Ser Ile Ser Ser Tyr

```
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
                85                  90                  95

His Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 1582
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-B2-B6

<400> 1582

```
Gln Ser Ile Ser Ser Tyr
1               5
```

<210> 1583
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B2-B6

<400> 1583

```
Ala Ala Ser
1
```

<210> 1584
<211> 10
<212> PRT

<213> artificial sequence

<220>
<223> CDR3 VL STE94-B2-B6

<400> 1584

Gln Gln Ser Tyr Ser Thr Pro Pro His Thr
1 5 10

<210> 1585
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE94-B2-E11

<400> 1585

Gln 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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Ala Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 1586

<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE94-B2-E11

<400> 1586

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 1587
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE94-B2-E11

<400> 1587

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 1588
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE94-B2-E11

<400> 1588

Ala Arg Asp Val Ala Asp Ala Phe Asp Ile
1 5 10

<210> 1589
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE94-B2-E11

<400> 1589

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu
65   70   75   80

Gln Thr Gly Asp Glu Ala Thr Tyr Tyr Cys Gly Thr Trp Asp Ser Ser
                85   90   95

Leu Ile Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1590
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE94-B2-E11

<400> 1590

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1   5

<210> 1591
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE94-B2-E11

<400> 1591

Asp Asn Asn
1

<210> 1592

<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE94-B2-E11

<400> 1592

Gly Thr Trp Asp Ser Ser Leu Ile Gly Val Val
1 5 10

<210> 1593
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> VH STE70-1E12

<400> 1593

Gln Met 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 Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg Asp Gly Tyr Asn Phe Asn Asn Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1594
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE70-1E12

<400> 1594

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1   5

<210> 1595
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE70-1E12

<400> 1595

Ile Asn Pro Asn Ser Gly Gly Thr
1   5

<210> 1596
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE70-1E12

<400> 1596

Val Arg Asp Gly Tyr Asn Phe Asn Asn Trp Phe Asp Pro
1   5   10

<210> 1597
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE70-1E12

<400> 1597

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Gly Ser Pro Gly Glu

1 5 10 15

Thr Ile Thr Ile Ser Cys Thr Gly Ser Gly Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Arg Gln Arg Pro Gly Ser Ala Pro Thr Ile Val
35 40 45

Ile Tyr Glu Asp Thr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Glu Ser
85 90 95

Thr Asn His Val Met Phe Gly Gly Gly Ser Lys Leu Thr Val Leu
100 105 110

<210> 1598
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE70-1E12

<400> 1598

Gly Gly Ser Ile Ala Ser Asn Tyr
1 5

<210> 1599
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE70-1E12

<400> 1599

Glu Asp Thr
1

<210> 1600
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE70-1E12

<400> 1600

Gln Ser Ser Glu Ser Thr Asn His Val Met
1 5 10

<210> 1601
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-1B6

<400> 1601

Gln Val Lys Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ala Pro Tyr Gly Asp Phe Arg Gly Leu Trp Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1602
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-1B6

<400> 1602

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 1603
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-1B6

<400> 1603

Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 1604
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-1B6

<400> 1604

Ala Lys Ala Pro Tyr Gly Asp Phe Arg Gly Leu Trp Tyr Phe Asp Tyr
1 5 10 15

<210> 1605
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-1B6

<400> 1605

```
Asp Ile Val Met Thr Gln Ser Pro Phe Ser Val Ser Ala Ser Val Gly
1               5                  10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Ser Trp
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Val Pro Leu
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Gln
            100                 105


<210>  1606
<211>  6
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VL STE72-1B6

<400>  1606

Gln Asp Ile Arg Ser Trp
1               5


<210>  1607
<211>  3
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VL STE72-1B6

<400>  1607

Asp Ala Ser
```

1

<210> 1608
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-1B6

<400> 1608

Gln Gln Ala Asp Ser Val Pro Leu Thr
1 5

<210> 1609
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-1G5

<400> 1609

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 Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Gly Gly Val Gln Leu Trp Leu Thr Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
        115

<210> 1610
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-1G5

<400> 1610

Gly Gly Thr Phe Ser Ser Tyr Ala
1   5

<210> 1611
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-1G5

<400> 1611

Ile Ile Pro Ile Phe Gly Thr Ala
1   5

<210> 1612
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-1G5

<400> 1612

Ala Val Gly Gly Val Gln Leu Trp Leu Thr Tyr
1   5   10

<210> 1613
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-1G5

<400> 1613

Glu Thr Thr Leu Thr Gln Ser Pro Gly Ala Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Val Ser Gln Ser Leu Ser Ser Asn
20 25 30

Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Thr Ser Ile Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Lys Tyr Gly Ser Trp Pro
85 90 95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Val
100 105

<210> 1614
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-1G5

<400> 1614

Gln Ser Leu Ser Ser Asn Ser
1 5

<210> 1615
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-1G5

<400> 1615

Asp Thr Ser
1

<210> 1616
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-1G5

<400> 1616

His Lys Tyr Gly Ser Trp Pro Arg Thr
1 5

<210> 1617
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-4C10

<400> 1617

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Ser Ser Ser Trp Tyr Gly Leu Gly Ala Phe Asp Ile

100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 1618
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-4C10

<400> 1618

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 1619
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-4C10

<400> 1619

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 1620
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-4C10

<400> 1620

Ala Arg Glu Tyr Ser Ser Ser Trp Tyr Gly Leu Gly Ala Phe Asp Ile
1 5 10 15

<210> 1621
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-4C10

<400> 1621

Asp Ile Arg Leu 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 Asn Ile His Tyr Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Ser Leu Leu Val
        35   40   45

Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Phe Lys Ser Pro Ala
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 1622
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-4C10

<400> 1622

Gln Asn Ile His Tyr Tyr
1   5

<210> 1623
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-4C10

<400> 1623

Gly Ala Ser
1

<210> 1624
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-4C10

<400> 1624

Gln Gln Ser Phe Lys Ser Pro Ala Thr
1 5

<210> 1625
<211> 117
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-4E12

<400> 1625

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 Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Ser Gly Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 1626
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-4E12

<400> 1626

Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 1627
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-4E12

<400> 1627

Ile Asn Pro Ser Gly Gly Ser Thr
1 5

<210> 1628
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-4E12

<400> 1628

Ala Arg Asp Leu Ser Gly Gly Leu Asp Tyr
1 5 10

<210> 1629
<211> 107
<212> PRT

<213> artificial sequence

<220>
<223> VL STE72-4E12

<400> 1629

Glu Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ala Cys Arg Ala Gly Gln Thr Ile Ser Ser Lys
20 25 30

Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Ser Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Asp Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1630
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-4E12

<400> 1630

Gln Thr Ile Ser Ser Lys
1 5

<210> 1631
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-4E12

<400> 1631

Asp Ala Ser
1

<210> 1632
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-4E12

<400> 1632

Gln Gln Tyr Ser Asp Trp Pro Pro Thr
1   5

<210> 1633
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-8A2

<400> 1633

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 Ser Tyr
            20   25   30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50   55   60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1634
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-8A2

<400> 1634

Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 1635
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-8A2

<400> 1635

Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 1636
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-8A2

<400> 1636

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr
1 5 10

<210> 1637

<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-8A2

<400> 1637

Asp Ile Arg Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1638
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-8A2

<400> 1638

Gln Asp Ile Ser Asn Tyr
1 5

<210> 1639
<211> 3
<212> PRT

<213> artificial sequence

<220>
<223> CDR2 VL STE72-8A2

<400> 1639

Asp Ala Ser
1

<210> 1640
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-8A2

<400> 1640

Gln Gln Tyr Asp Asn Leu Pro Arg Thr
1 5

<210> 1641
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-8A6

<400> 1641

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 Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1642
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-8A6

<400> 1642

Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 1643
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-8A6

<400> 1643

Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 1644
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-8A6

<400> 1644

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr
1 5 10

<210> 1645
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-8A6

<400> 1645

Asp Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asn Ile Gly Thr Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Ser Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Tyr Leu Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Arg
100 105

<210> 1646
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-8A6

<400> 1646

Gln Asn Ile Gly Thr Trp
1 5

<210> 1647

<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-8A6

<400> 1647

Lys Ala Ser
1

<210> 1648
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-8A6

<400> 1648

Gln Gln Tyr Asp Ser Tyr Leu Phe Thr
1   5

<210> 1649
<211> 122
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-8E1

<400> 1649

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Gln Pro Ser Glu
1   5   10   15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20   25   30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35   40   45

Trp Ile Gly Arg Ile Tyr Pro Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50   55   60

Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Glu Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Gly Pro Lys Arg Ser Gly Ser Pro Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 1650
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-8E1

<400> 1650

Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 1651
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-8E1

<400> 1651

Ile Tyr Pro Ser Gly Ser Thr
1 5

<210> 1652
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-8E1

<400> 1652

Ala Arg Gly Gly Pro Lys Arg Ser Gly Ser Pro Phe Asp Val

1 5 10

<210> 1653
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-8E1

<400> 1653

Glu Val Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Phe Gly Pro Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Met Ala Ser Glu Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Ser Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Phe Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1654
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-8E1

<400> 1654

Gln Thr Phe Gly Pro Trp
1 5

<210> 1655
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-8E1

<400> 1655

Met Ala Ser
1

<210> 1656
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-8E1

<400> 1656

Gln Gln Tyr Asn Thr Phe Ser Pro Trp Thr
1   5   10

<210> 1657
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> VH STE72-2G4

<400> 1657

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 Ser Tyr
            20   25   30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50   55   60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1658
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE72-2G4

<400> 1658

Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 1659
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE72-2G4

<400> 1659

Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 1660
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE72-2G4

<400> 1660

Ala Arg Phe Phe Tyr Asp Ser Ser Gly Tyr Ser Thr Asp Tyr
1 5 10

<210> 1661
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> VL STE72-2G4

<400> 1661

Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Asp Ser His
20 25 30

Leu Ala Trp Tyr His Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Ser
65 70 75 80

Glu Asp Leu Gly Val Tyr Tyr Cys Gln Gln Tyr Ala Ser Trp Pro Pro
85 90 95

Gly Tyr Asn Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1662
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE72-2G4

<400> 1662

Gln Ser Val Asp Ser His

1 5

<210> 1663
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE72-2G4

<400> 1663

Gly Ala Ser
1

<210> 1664
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE72-2G4

<400> 1664

Gln Gln Tyr Ala Ser Trp Pro Pro Gly Tyr Asn
1 5 10

<210> 1665
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-2B2

<400> 1665

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 Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Ser Gly Trp Tyr Phe Gly Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 1666
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE73-2B2

<400> 1666

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 1667
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE73-2B2

<400> 1667

Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 1668
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-2B2

<400> 1668

Ala Arg Val Ser Gly Trp Tyr Phe Gly Ala Phe Asp Ile
1 5 10

<210> 1669
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-2B2

<400> 1669

Leu Pro Val Leu Thr Gln Pro His Ser Leu Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Asn Ile Ser Cys Thr Gly Ser Ser Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Ser His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Ser Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
85 90 95

Ser Asn Asn Gln Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1670
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-2B2

<400> 1670

Ser Gly Ser Ile Ala Ser Asn Tyr
1 5

<210> 1671
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-2B2

<400> 1671

Glu Asp Ser
1

<210> 1672
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-2B2

<400> 1672

Gln Ser Tyr Asp Ser Ser Asn Asn Gln Trp Val
1 5 10

<210> 1673
<211> 115
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-2C2

<400> 1673

Gln 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 Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
                85   90   95

Arg Gly His Asp Asn Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ser
        115

<210> 1674
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE73-2C2

<400> 1674

Gly Ile Thr Val Ser Ser Asn Tyr
1   5

<210> 1675
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE73-2C2

<400> 1675

Ile Tyr Ser Gly Gly Ser Thr
1   5

<210> 1676
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-2C2

<400> 1676

Ala Arg Gly His Asp Asn Leu Asp Tyr
1   5

<210> 1677
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-2C2

<400> 1677

Leu Pro Val Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Ile Ile Ser Cys Thr Gly Ser Ser Asp Ser Ile Ala Ser Asn
            20   25   30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
        35   40   45

Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Thr Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

Leu Lys Thr Glu Asp Glu Ala Glu Tyr Tyr Cys Gln Ser Tyr Asp Ser
                85   90   95

Asn Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105   110

<210> 1678
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-2C2

<400> 1678

Ser Asp Ser Ile Ala Ser Asn Tyr
1 5

<210> 1679
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-2C2

<400> 1679

Glu Asp Asn
1

<210> 1680
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-2C2

<400> 1680

Gln Ser Tyr Asp Ser Asn Asn His Trp Val
1 5 10

<210> 1681
<211> 114
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-2E9

<400> 1681

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 Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

```
        35                  40                  45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 1682
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE73-2E9

<400> 1682

```
Gly Tyr Thr Phe Thr Ser Tyr Gly
1               5
```

<210> 1683
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE73-2E9

<400> 1683

```
Ile Ser Ala Tyr Asn Gly Asn Thr
1               5
```

<210> 1684
<211> 7
<212> PRT

<213> artificial sequence

<220>
<223> CDR3 VH STE73-2E9

<400> 1684

Ala Arg Gly Lys Phe Asp Tyr
1 5

<210> 1685
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-2E9

<400> 1685

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Ser Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Val Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Gly Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1686
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-2E9

<400> 1686

Ser Ser Asn Ile Gly Asn Asn Ala
1   5

<210> 1687
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-2E9

<400> 1687

Tyr Asp Asp
1

<210> 1688
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-2E9

<400> 1688

Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val
1   5   10

<210> 1689
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-2G8

<400> 1689

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Val Ser Ser Asn
            20   25   30

```
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ile Leu Tyr Ser Gly Gly Thr Thr Phe Tyr Thr Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu His Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Trp Ser Gly Thr Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  1690
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE73-2G8

<400>  1690

Gly Ile Thr Val Ser Ser Asn Tyr
1               5


<210>  1691
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE73-2G8

<400>  1691

Leu Tyr Ser Gly Gly Thr Thr
1               5


<210>  1692
```

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-2G8

<400> 1692

Ala Arg Trp Ser Gly Thr Tyr Tyr Asp Tyr
1 5 10

<210> 1693
<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-2G8

<400> 1693

Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Thr Asn Asp Pro
85 90 95

Val Leu Phe Gly Ala Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1694
<211> 6
<212> PRT

<213> artificial sequence

<220>
<223> CDR1 VL STE73-2G8

<400> 1694

Ser Leu Arg Ser Tyr Tyr
1 5

<210> 1695
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-2G8

<400> 1695

Gly Lys Asn
1

<210> 1696
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-2G8

<400> 1696

Asn Ser Arg Asp Ser Thr Asn Asp Pro Val Leu
1 5 10

<210> 1697
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-6B10

<400> 1697

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 Ser Tyr

```
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Leu Arg Tyr Gly Asp Ser Gly Ser Tyr Tyr Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  1698
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE73-6B10

<400>  1698

Gly Tyr Thr Phe Thr Ser Tyr Gly
1               5


<210>  1699
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE73-6B10

<400>  1699

Ile Asn Pro Asn Ser Gly Gly Thr
1               5
```

<210> 1700
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-6B10

<400> 1700

Ala Arg Asp Arg Leu Arg Tyr Gly Asp Ser Gly Ser Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 1701
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-6B10

<400> 1701

Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Leu Ile Ser Glu Val Thr Arg Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65 70 75 80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Ser Tyr Ala Gly Ser
85 90 95

Asn Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 1702
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-6B10

<400> 1702

Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1 5

<210> 1703
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-6B10

<400> 1703

Glu Val Thr
1

<210> 1704
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-6B10

<400> 1704

Gly Ser Tyr Ala Gly Ser Asn Thr Trp Val
1 5 10

<210> 1705
<211> 117
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-6C1

<400> 1705

```
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 Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Tyr Val Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  1706
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR1 VH STE73-6C1

<400>  1706

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  1707
<211>  8
<212>  PRT
<213>  artificial sequence

<220>
<223>  CDR2 VH STE73-6C1
```

<400> 1707

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 1708
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-6C1

<400> 1708

Ala Arg Ser Tyr Val Gly Gly Met Asp Val
1 5 10

<210> 1709
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-6C1

<400> 1709

Gln Leu Val Leu Thr Gln Ser Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Asp Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Lys Leu
35 40 45

Ile Ile Ser Tyr Thr Asp Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Asp Arg Thr
85 90 95

Leu Val Gly Ser Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 1710
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-6C1

<400> 1710

Asp Ser Asn Ile Gly Ala Gly Tyr Asn
1 5

<210> 1711
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-6C1

<400> 1711

Tyr Thr Asp
1

<210> 1712
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-6C1

<400> 1712

Gln Ser Ser Asp Arg Thr Leu Val Gly Ser Leu
1 5 10

<210> 1713
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-6C8

<400> 1713

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Ala Leu Asn Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 1714
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE73-6C8

<400> 1714

Gly Gly Thr Phe Ser Ser Tyr Ala
1 5

<210> 1715
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VH STE73-6C8

<400> 1715

Ile Ile Pro Ile Leu Gly Ile Ala
1   5

<210> 1716
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-6C8

<400> 1716

Ala Arg Ser Ile Ala Ala Leu Asn Trp Phe Asp Pro
1   5   10

<210> 1717
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-6C8

<400> 1717

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Pro Cys Thr Gly Ser Arg Gly Ser Ile Ala Asn Asn
            20   25   30

Tyr Val Gln Trp Tyr Arg Gln Arg Pro Gly Arg Ala Pro Thr Thr Val
        35   40   45

Ile Phe Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Ile Asp Arg Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65   70   75   80

Leu Glu Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly

85 90 95

Ser Asn Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 1718
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-6C8

<400> 1718

Arg Gly Ser Ile Ala Asn Asn Tyr
1 5

<210> 1719
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-6C8

<400> 1719

Glu Asp Asn
1

<210> 1720
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-6C8

<400> 1720

Gln Ser Tyr Asp Gly Ser Asn Val Ile
1 5

<210> 1721
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> VH STE73-9G3

<400> 1721

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Leu Val Leu Gly Ser Gly Ser Ser Asn Asp Trp Gly Arg
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 1722
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VH STE73-9G3

<400> 1722

Gly Phe Thr Phe Ser Ser Tyr Ala
1   5

<210> 1723
<211> 8
<212> PRT

<213> artificial sequence

<220>
<223> CDR2 VH STE73-9G3

<400> 1723

Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 1724
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VH STE73-9G3

<400> 1724

Ala Arg Asp Leu Val Leu Gly Ser Gly Ser Ser Asn Asp
1 5 10

<210> 1725
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> VL STE73-9G3

<400> 1725

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Asp Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Lys Leu
35 40 45

Ile Ile Ser Tyr Thr Asp Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Asp Arg Thr
85 90 95

Leu Val Gly Ser Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 1726
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> CDR1 VL STE73-9G3

<400> 1726

Asp Ser Asn Ile Gly Ala Gly Tyr Asn
1 5

<210> 1727
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> CDR2 VL STE73-9G3

<400> 1727

Tyr Thr Asp
1

<210> 1728
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> CDR3 VL STE73-9G3

<400> 1728

Gln Ser Ser Asp Arg Thr Leu Val Gly Ser Leu
1 5 10

<210> 1729
<211> 669
<212> DNA

<213> artificial sequence

<220>
<223> SARS-CoV-2 RBD 7PM Mutant

<400> 1729
cgggtgcagc ccaccgaatc catcgtgcgg ttccccaata tcaccaatct gtgccccttc 60

ggcgaggtgt tcaatgccac cagattcgcc tctgtgtacg cctggaaccg gaagcggatc 120

agcaattgcg tggccgacta ctccttcctg tacaactccg ccagcttcag caccttcaag 180

tgctacggcg tgtcccctac caagctgaac gacctgtgct tcacaaacgt gtacgccgac 240

agcttcgtga tccggggaga tgaagtgcgg cagattgccc ctggacagac aggcaagatc 300

gccgactaca actacaagct gcccgacgac ttcaccggct gtgtgattgc ctggaacagc 360

aagaacctgg actccaaagt cggcggcaac tacaattacc tgtaccggct gttccggaag 420

tccaatctga agcccttcga gcgggacatc tccaccgaga tctatcaggc cagcagcacc 480

ccttgtaacg gcgcgaaacg cgtcaactgc tacttcccac tgcagtccta cggctttcag 540

cccacaaatg gcgtgggcta ccagccttac agagtggtgg tgctgagctt cgagctgctg 600

catgctcctg ccacagtgtg cggccctaag aaaagcacca atctcgtgaa gaacaaatgc 660

gtgaacttc 669

<210> 1730
<211> 223
<212> PRT
<213> artificial sequence

<220>
<223> SARS-CoV-2 RBD 7PM Mutant

<400> 1730

Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
1 5 10 15

Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
20 25 30

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
35 40 45

Phe Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val

50 55 60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65 70 75 80

Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
85 90 95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
100 105 110

Gly Cys Val Ile Ala Trp Asn Ser Lys Asn Leu Asp Ser Lys Val Gly
115 120 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
130 135 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Ser Ser Thr
145 150 155 160

Pro Cys Asn Gly Ala Lys Arg Val Asn Cys Tyr Phe Pro Leu Gln Ser
165 170 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
180 185 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
195 200 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe
210 215 220

<210> 1731
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR1 DNA

<400> 1731
gactactaca tgagc 15

<210> 1732
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR1 PRT

<400> 1732
Asp Tyr Tyr Met Ser
1 5

<210> 1733
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR2 DNA

<400> 1733
tacattactt atagtggtag taccatatac tacgcagact ctgtgaaggg c 51

<210> 1734
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR2 PRT

<400> 1734
Tyr Ile Thr Tyr Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1735
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR3 DNA

<400> 1735
gatcgcggta caactatggt ccccttgac tac 33

<210> 1736
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 HCDR3 PRT

<400> 1736
Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr
1 5 10

<210> 1737
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR1 DNA

<400> 1737
caggcgagtc aggacattac caactattta aat 33

<210> 1738
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR1 PRT

<400> 1738
Gln Ala Ser Gln Asp Ile Thr Asn Tyr Leu Asn
1 5 10

<210> 1739
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR2 DNA

<400> 1739
gctgcatcca atttggaaac a 21

<210> 1740

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR2 PRT

<400> 1740
Ala Ala Ser Asn Leu Glu Thr
1 5

<210> 1741
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR3 DNA

<400> 1741
caacagtatg ataatctccc tctcact 27

<210> 1742
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 LCDR3 PRT

<400> 1742
Gln Gln Tyr Asp Asn Leu Pro Leu Thr
1 5

<210> 1743
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 VL DNA

<400> 1743
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1744
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 VL PRT

<400> 1744
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 Gln Ala Ser Gln Asp Ile Thr Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1745
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 VH DNA

<400> 1745
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc 300

ggtacaacta tggtcccctt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

360

<210> 1746
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 VH PRT

<400> 1746
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Thr Tyr Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1747
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 VH complete DNA

<400> 1747
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc 300

ggtacaacta tggtcccctt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 1748
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10933 VH complete PRT

<400> 1748
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Thr Tyr Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
```

```
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1749
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10933 VL complete DNA

<400> 1749

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca      180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct      240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga      300

gggaccaagg tggagatcaa acgtacggtg gctgcaccat ctgtgttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag      480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642
```

<210> 1750
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> REGN10933 VL complete PRT

<400> 1750

```
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 Gln Ala Ser Gln Asp Ile Thr Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
                85                  90                  95


Thr Phe Gly Gly 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> 1751
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR1 DNA

<400> 1751
aactatgcta tgtac   15

<210> 1752
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR1 PRT

<400> 1752
Asn Tyr Ala Met Tyr
1   5

<210> 1753
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR2 DNA

<400> 1753
gttatatcat atgatggaag taataaatac tatgcagact ccgtgaaggg c   51

<210> 1754
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR2 PRT

<400> 1754
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 1755
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR3 DNA

<400> 1755
ggctccgact acggtgacta cttattggtt tac 33

<210> 1756
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 HCDR3 PRT

<400> 1756
Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr
1 5 10

<210> 1757
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR1 DNA

<400> 1757
actggaacca gcagtgacgt tggtggttat aactatgtct cc 42

<210> 1758
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR1 PRT

<400> 1758
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 1759
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR2 DNA

<400> 1759
gatgtcagta agcggccctc a 21

<210> 1760
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR2 PRT

<400> 1760
Asp Val Ser Lys Arg Pro Ser
1 5

<210> 1761
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR3 DNA

<400> 1761
aactctttga caagcatcag cacttgggtg 30

<210> 1762
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 LCDR3 PRT

<400> 1762
Asn Ser Leu Thr Ser Ile Ser Thr Trp Val

1 5 10

<210> 1763
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 VL DNA

<400> 1763
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 1764
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 VL PRT

<400> 1764
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

```
Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
                85                  90                  95


Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  1765
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  REGN10987 VH DNA

<400>  1765
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc      300

gactacggtg actacttatt ggtttactgg ggccagggaa ccctggtcac cgtgtcctca      360

                                                                       360



<210>  1766
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  REGN10987 VH PRT

<400>  1766
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 1767
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> REGN10987 VH complete DNA

<400> 1767

```
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc      300

gactacggtg actacttatt ggtttactgg ggccagggaa ccctggtcac cgtgtcctca      360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc      600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctccagt ggccggaccg      720
```

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtggg cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaacagctc ccatccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aaaagcctct ccctgtcccc gggt 1344

<210> 1768
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 VH complete PRT

<400> 1768
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys

```
                85                  90                  95

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val 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 Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
```

```
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320


Tyr Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys
                325                 330                 335


Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350


Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365


Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380


Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400


Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415


Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430


Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445


<210>  1769
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  REGN10987 VL complete DNA

<400>  1769
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa      120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtt      180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc      240
```

cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcacc aagtgtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 1770
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> REGN10987 VL complete PRT

<400> 1770
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
85 90 95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu

115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1771
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 HCDR1 DNA

<400> 1771
agtaattata tgtca 15

<210> 1772
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 HCDR1 PRT

<400> 1772
Ser Asn Tyr Met Ser
1 5

<210> 1773

<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 HCDR2 DNA

<400> 1773
gtgatctaca gcggtgggag cacattttat gcggatagtg ttaagggt 48

<210> 1774
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 HCDR2 PRT

<400> 1774
Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 1775
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 HCDR3 DNA

<400> 1775
gttcttccaa tgtatggcga ttacttggat tat 33

<210> 1776
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 HCDR3 PRT

<400> 1776
Val Leu Pro Met Tyr Gly Asp Tyr Leu Asp Tyr
1 5 10

<210> 1777
<211> 33
<212> DNA

<213> Artificial Sequence

<220>
<223> CB6 LCDR1 DNA

<400> 1777
cgcgcatccc aaagcatctc tcggtatctt aat 33

<210> 1778
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 LCDR1 PRT

<400> 1778
Arg Ala Ser Gln Ser Ile Ser Arg Tyr Leu Asn
1 5 10

<210> 1779
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 LCDR2 DNA

<400> 1779
gcagctagtt cacttcagtc a 21

<210> 1780
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 LCDR2 PRT

<400> 1780
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 1781
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 LCDR3 DNA

<400> 1781
caacagtcat atagcacacc gcccgagtac act   33

<210> 1782
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 LCDR3 PRT

<400> 1782
Gln Gln Ser Tyr Ser Thr Pro Pro Glu Tyr Thr
1   5   10

<210> 1783
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 VL DNA

<400> 1783
gatatagtaa tgacacagtc cccctccagt cttagtgcct ccgtgggcga ccgagttacg   60

attacctgcc gcgcatccca aagcatctct cggtatctta attggtacca acaaaagcct   120

ggaaaggcgc ccaaattgtt gatatacgca gctagttcac ttcagtcagg ggtgccgagt   180

cggttcagcg ggtccggtag cggcaccgat ttcacactca caatttctag cctgcaaccc   240

gaagactttg ctacctatta ctgtcaacag tcatatagca caccgcccga gtacactttc   300

gggcagggga ccaagctgga gatcaaa   327

<210> 1784
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 VL PRT

<400> 1784
Asp Ile Val 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 Ser Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Glu Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1785
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 VH DNA

<400> 1785
gaagttcagt tggtggagtc agggggaggt cttgtccagc caggtggctc cctgagattg 60

agttgcgctg cttctggatt cactgtgagc agtaattata tgtcatgggt gcgccaggcg 120

cctgggaagg ggcttgagtg ggtgtccgtg atctacagcg gtgggagcac attttatgcg 180

gatagtgtta agggtaggtt tacgatatct cgagataatt ccatgaacac attgttcttg 240

caaatgaaca gccttcgggc tgaagacact gccgtctatt actgtgctag agttcttcca 300

atgtatggcg attacttgga ttattggggg caagggacac tcgtgactgt ttcctca 357

<210> 1786
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 VH PRT

<400> 1786
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 Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Phe Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Val Leu Pro Met Tyr Gly Asp Tyr Leu Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 1787
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 VH complete DNA

<400> 1787
gaagttcagt tggtggagtc agggggaggt cttgtccagc caggtggctc cctgagattg   60

agttgcgctg cttctggatt cactgtgagc agtaattata tgtcatgggt gcgccaggcg   120

cctgggaagg ggcttgagtg ggtgtccgtg atctacagcg gtgggagcac attttatgcg   180

gatagtgtta agggtaggtt tacgatatct cgagataatt ccatgaacac attgttcttg   240

caaatgaaca gccttcgggc tgaagacact gccgtctatt actgtgctag agttcttcca 300

atgtatggcg attacttgga ttattggggg caagggacac tcgtgactgt ttcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctccagtggc cggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtgggcgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgggtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa acagctccca tcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaaa 1320

agcctctccc tgtccccggg t 1341

<210> 1788
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 VH complete PRT

<400> 1788
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 Thr Val Ser Ser Asn

```
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Phe Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Val Leu Pro Met Tyr Gly Asp Tyr Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240
```

```
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1789

<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> CB6 VL complete DNA

<400> 1789
gatatagtaa tgacacagtc cccctccagt cttagtgcct ccgtgggcga ccgagttacg 60

attacctgcc gcgcatccca aagcatctct cggtatctta attggtacca acaaaagcct 120

ggaaaggcgc ccaaattgtt gatatacgca gctagttcac ttcagtcagg ggtgccgagt 180

cggttcagcg ggtccggtag cggcaccgat ttcacactca caatttctag cctgcaaccc 240

gaagactttg ctacctatta ctgtcaacag tcatatagca caccgcccga gtacactttc 300

gggcagggga ccaagctgga gatcaaacgt acggtggctg caccatctgt gttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 648

<210> 1790
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> CB6 VL complete PRT

<400> 1790
Asp Ile Val 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 Ser Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Glu Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 1791
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 HCDR1 DNA

<400> 1791
acgtactgga ttggc 15

<210> 1792
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 HCDR1 PRT

<400> 1792
Thr Tyr Trp Ile Gly
1 5

<210> 1793
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 HCDR2 DNA

<400> 1793
ataatttacc ctggcgattc agagactcgg tattctccat cctttcaggg c 51

<210> 1794
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 HCDR2 PRT

<400> 1794
Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

<210> 1795
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 HCDR3 DNA

<400> 1795
ggatcaggaa tcagcacgcc catggacgta 30

<210> 1796
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 HCDR3 PRT

<400> 1796
Gly Ser Gly Ile Ser Thr Pro Met Asp Val
1 5 10

<210> 1797
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 LCDR1 DNA

<400> 1797
aaatctagcc agtctgttct gtactcatct ataaataaga actatcttgc g 51

<210> 1798
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 LCDR1 PRT

<400> 1798
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Ile Asn Lys Asn Tyr Leu
1 5 10 15

<210> 1799
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 LCDR2 DNA

<400> 1799
tgggcttcca cgagagaaag c 21

<210> 1800
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 LCDR2 PRT

<400> 1800
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 1801
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 LCDR3 DNA

<400> 1801
cagcaatact attccacacc ctacaca 27

<210> 1802
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 LCDR3 PRT

<400> 1802
Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
1 5

<210> 1803
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 VL DNA

<400> 1803
gatattcagc tcacccagtc tccagactct ctggcggtct cactcggtga gagagcgaca 60

ataaactgta aatctagcca gtctgttctg tactcatcta taaataagaa ctatcttgcg 120

tggtaccagc agaaaccagg tcagcctcct aagctcttga tttactgggc ttccacgaga 180

gaaagcggcg tgcccgaccg gttcagcggc tcagggagcg gcactgattt cactctgacg 240

atcagcagtc tgcaggccga ggatgtagcc gtatattatt gtcagcaata ctattccaca 300

ccctacacat tcgggcaggg aactaaagtt gagataaag 339

<210> 1804
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 VL PRT

<400> 1804
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Ile Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

<210> 1805
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 VH DNA

<400> 1805
caaatgcagt tggtacagag tggtaccgag gtcaaaaaac ctggcgagag tctcaaaatc 60

tcatgcaaag ggtccggcta tggattcatt acgtactgga ttggctgggt taggcagatg 120

ccggggaaag ggcttgagtg gatgggaata atttaccctg gcgattcaga gactcggtat 180

tctccatcct ttcagggcca agtcacaatt tcagcagata agtccatcaa caccgcgtac 240

ctccagtggt ctagtttgaa agcaagcgac acagccatat attattgcgc cggtggatca 300

ggaatcagca cgcccatgga cgtatgggga cagggcacta cagtcacagt ttcaagt 357

<210> 1806
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 VH PRT

<400> 1806
Gln Met Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile Thr Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 1807
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 VH complete DNA

<400> 1807
caaatgcagt tggtacagag tggtaccgag gtcaaaaaac ctggcgagag tctcaaaatc 60

tcatgcaaag ggtccggcta tggattcatt acgtactgga ttggctgggt taggcagatg 120

ccggggaaag ggcttgagtg gatgggaata atttaccctg gcgattcaga gactcggtat 180

tctccatcct ttcagggcca agtcacaatt tcagcagata agtccatcaa caccgcgtac 240

ctccagtggt ctagtttgaa agcaagcgac acagccatat attattgcgc cggtggatca 300

ggaatcagca cgcccatgga cgtatgggga cagggcacta cagtcacagt ttcaagtgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctccagtggc cggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtgggcgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgggtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa acagctccca tcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaaa 1320

agcctctccc tgtccccggg t 1341

<210> 1808
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 VH complete PRT

<400> 1808
Gln Met Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Gly Phe Ile Thr Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Gly Gly Ser Gly Ile Ser Thr Pro Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

```
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Gly Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gln Leu Pro Ser Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
```

```
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 1809
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> CR3022 VL complete DNA

<400> 1809

```
gatattcagc tcacccagtc tccagactct ctggcggtct cactcggtga gagagcgaca       60

ataaactgta aatctagcca gtctgttctg tactcatcta taaataagaa ctatcttgcg      120

tggtaccagc agaaaccagg tcagcctcct aagctcttga tttactgggc ttccacgaga      180

gaaagcggcg tgcccgaccg gttcagcggc tcagggagcg gcactgattt cactctgacg      240

atcagcagtc tgcaggccga ggatgtagcc gtatattatt gtcagcaata ctattccaca      300

ccctacacat tcgggcaggg aactaaagtt gagataaagc gtacggtggc tgcaccatct      360

gtgttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc      480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660
```

<210> 1810
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> CR3022 VL complete PRT

<400> 1810
Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20   25   30

Ser Ile Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85   90   95

Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100   105   110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115   120   125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130   135   140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145   150   155   160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165   170   175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180   185   190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 1811
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 437 to 463)

<400> 1811
Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu
1 5 10 15

Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
20 25

<210> 1812
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 445 to 451)

<400> 1812
Val Gly Gly Asn Tyr Asn Tyr
1 5

<210> 1813
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 445 to 455)

<400> 1813
Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu
1 5 10

<210> 1814
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 445 to 459)

<400> 1814

Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser
1 5 10 15

<210> 1815
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 449 to 459)

<400> 1815
Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser
1 5 10

<210> 1816
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 342 to 351)

<400> 1816
Val Phe Asn Thr Arg Phe Ala Ser Val Tyr
1 5 10

<210> 1817
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 349 to 359)

<400> 1817
Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser
1 5 10

<210> 1818
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 485 to 491)

<400> 1818
Gly Phe Asn Cys Tyr Phe Pro
1 5

<210> 1819
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 497 to 502)

<400> 1819
Phe Gln Pro Thr Asn Val
1 5

<210> 1820
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 400 to 422)

<400> 1820
Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gln Thr Gly
1 5 10 15

Lys Ile Ala Asp Asp Tyr Asn
20

<210> 1821
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 165 to 180)

<400> 1821
Ala Lys Arg Val Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln
1 5 10 15

<210> 1822
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 365 to 369)

<400> 1822
Tyr Ser Phe Leu Tyr
1 5

<210> 1823
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Epitope within RBD (amino acids 436 to 443)

<400> 1823
Trp Asn Ser Lys Asn Leu Asp
1   5

<210> 1824
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 474 to 489)

<400> 1824
Gln Ala Ser Ser Thr Pro Cys Asn Gly Ala Lys Arg Val Asn Cys Tyr
1   5   10   15

<210> 1825
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 483 to 490)

<400> 1825
Val Glu Gly Phe Asn Cys Tyr Phe
1   5

<210> 1826
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 400 to 422)

<400> 1826
Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gln Thr Gly
1   5   10   15

Lys Ile Ala Asp Tyr Asn
            20

<210> 1827
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 470 to 480)

<400> 1827
Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
1 5 10

<210> 1828
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope within RBD (amino acids 483 to 505)

<400> 1828
Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln
1 5 10 15

Pro Thr Asn Gly Val
20

<210> 1829
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> partial S1-Domain (7PM)

<400> 1829
Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
1 5 10 15

Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
20 25 30

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
35 40 45

Phe Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
50 55 60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65 70 75 80

Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
85 90 95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
100 105 110

Gly Cys Val Ile Ala Trp Asn Ser Lys Asn Leu Asp Ser Lys Val Gly
115 120 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
130 135 140

```
Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Ser Ser Thr
145                 150                 155                 160

Pro Cys Asn Gly Ala Lys Arg Val Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
        195                 200                 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn
    210                 215                 220

<210>  1830
<211>  224
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  partial S1-Domain (wild-type)

<400>  1830
Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
1               5                   10                  15

Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
            20                  25                  30

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
        35                  40                  45

Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
    50                  55                  60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65                  70                  75                  80

Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
                85                  90                  95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
            100                 105                 110

Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly
        115                 120                 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
    130                 135                 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
145                 150                 155                 160
```

```
Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
        195                 200                 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn
    210                 215                 220
```

<210> 1831
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" light chain CDR1

<400> 1831

```
Arg Ala Ser Gln Gly Ile Ser Ser Tyr Leu Ala
1               5                   10
```

<210> 1832
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" light chain CDR2

<400> 1832

```
Ala Ala Ser Thr Leu Gln Ser
1               5
```

<210> 1833
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" light chain CDR3

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa is proline or can be deleted

<220>
<221> VARIANT

<222> (9)..(9)
<223> Xaa is phenylalanine or isoleucine

<400> 1833

Gln Gln Leu Asn Ser Tyr Pro Xaa Xaa Thr
1   5   10

<210> 1834
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" heavy chain CDR1

<400> 1834

Ser Asn Tyr Met Ser
1   5

<210> 1835
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" heavy chain CDR2

<400> 1835

Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1   5   10   15

<210> 1836
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> "archetype" heavy chain CDR3

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is valine or leucine

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa is alanine or valine

<220>
<221> VARIANT

<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa is alanine or glycine

<220>
<221> VARIANT
<222> (7)..(7)
<223> Xaa is phenylalanine or leucine

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa is isoleucine or valine

<400> 1836

Asp Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
1 5

<210> 1837
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR1

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is alanine or glycine

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is glycine or serine

<220>
<221> VARIANT
<222> (5)..(5)

<223> Xaa is serine or glycine

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa is asparagine or serine

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa is asparagine or serine

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa is leucine or valine

<220>
<221> VARIANT
<222> (13)..(13)
<223> Xaa is alanine or serine

<400> 1837

Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa
1 5 10

<210> 1838
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR1

<220>
<221> VARIANT
<222> (1)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (4)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (12)..(13)
<223> Xaa can be any naturally occurring amino acid

<400> 1838

Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa
1 5 10

<210> 1839
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR2

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is threonine or alanine

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa is asparagine or serine

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is lysine or threonine

<220>
<221> VARIANT
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 1839

Xaa Xaa Xaa Xaa Xaa Xaa Ser
1 5

<210> 1840
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR2

<220>
<221> VARIANT
<222> (1)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 1840

Xaa Xaa Xaa Xaa Xaa Xaa Ser
1   5

<210> 1841
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR3

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is asparagine or aspartic acid

<220>
<221> VARIANT
<222> (4)..(10)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is valine or threonine

<400> 1841

Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10

<210> 1842
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" light chain CDR3

<220>
<221> VARIANT
<222> (1)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (8)..(9)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (10)..(11)
<223> Xaa can be any naturally occurring amino acid

<400> 1842

Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 1843
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" heavy chain CDR3

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa is glycine or aspartic acid

<220>
<221> VARIANT
<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (4)..(6)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT
<222> (8)..(8)
<223> Xaa is alanine or glycine

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa is methionine, phenylalanine or leucine

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is isoleucine or valine

<400> 1843

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
1 5 10

<210> 1844
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "generalized" heavy chain CDR3

<220>
<221> VARIANT
<222> (1)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (4)..(6)
<223> Xaa can be deleted or any naturally occurring amino acid

<220>
<221> VARIANT
<222> (7)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be any naturally occurring amino acid

<400> 1844

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
1 5 10