eolf-seql
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<120> Anti-ROBO4 antibody

<130> U1999 PCT S3

<150> JP 2012-103929
<151> 2012-04-27

<150> JP 2013-011042
<151> 2013-01-24

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<170> PatentIn version 3.5

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Gln Ile Leu Val His Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro
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Ala Arg Met Ser Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg
    50                  55                  60

Trp Leu Leu Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His
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His Leu Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg
                85                  90                  95

Gly His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
            100                 105                 110

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly Ala
        115                 120                 125

Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln Pro Arg
    130                 135                 140

Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu Cys Gly Pro
145                 150                 155                 160

Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp Lys Asp Gly Lys
                165                 170                 175

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

Leu Met Ala Arg Ala Glu Lys Ser Asp Glu Gly Thr Tyr Met Cys Val
        195                 200                 205

Ala Thr Asn Ser Ala Gly His Arg Glu Ser Arg Ala Ala Arg Val Ser
    210                 215                 220

Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu Leu Ala Val
225                 230                 235                 240

Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp Pro Ala Glu
                245                 250                 255

Gly Pro Lys Pro Arg Pro Ala Val Trp Leu Ser Trp Lys Val Ser Gly
            260                 265                 270

Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr
        275                 280                 285
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Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu
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Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn
                325                 330                 335

Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln
            340                 345                 350

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp Val
        355                 360                 365

Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr Gln Val
    370                 375                 380

Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr Val Val
385                 390                 395                 400

Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met Pro Gly Ser Tyr
                405                 410                 415

Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser
            420                 425                 430

Arg Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala Thr Gln
        435                 440                 445

Glu Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr
    450                 455                 460

Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Ala Leu Trp Leu
465                 470                 475                 480

Leu Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg Arg Ala Arg
                485                 490                 495

Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile
            500                 505                 510

Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr
        515                 520                 525

Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu
    530                 535                 540

Ser Ser Arg Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg
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Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
            580                 585                 590

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu Pro
        595                 600                 605

Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp Ser Leu
    610                 615                 620

Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu Ala Pro Ala
625                 630                 635                 640

Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Ala Asn Ser
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Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu Leu Arg Ala Cys Glu
            660                 665                 670

Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly Ala Val
        675                 680                 685

Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu Leu Ser
    690                 695                 700

Ser Ser Asn Glu Leu Val Thr Arg His Leu Pro Pro Ala Pro Leu Phe
705                 710                 715                 720

Pro His Glu Thr Pro Pro Thr Gln Ser Gln Gln Thr Gln Pro Pro Val
                725                 730                 735

Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro
            740                 745                 750

Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser
        755                 760                 765

Gly Pro Ser Pro Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser
    770                 775                 780

Leu Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu
785                 790                 795                 800

Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser
                805                 810                 815

Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
            820                 825                 830
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Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly Gly
835 840 845

Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro Cys Leu
850 855 860

Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly Ser Ala
865 870 875 880

Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser Ser Ser
885 890 895

Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu Ala Val
900 905 910

Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala Asp Cys
915 920 925

Val Phe Ile Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Glu Ile Phe
930 935 940

Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp
945 950 955 960

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

Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser Cys Gln Ala Ser
50 55 60

Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu Asn Gly Gln Pro Leu
65 70 75 80

Ser Met Val Pro Pro Asp Pro His His Leu Leu Pro Asp Gly Thr Leu
85 90 95

Leu Leu Leu Gln Pro Pro Ala Arg Gly His Ala His Asp Gly Gln Ala
100 105 110

Leu Ser Thr Asp Leu Gly Val Tyr Thr Cys Glu Ala Ser Asn Arg Leu
115 120 125

Gly Thr Ala Val Ser Arg Gly Ala Arg Leu Ser Val Ala Val Leu Arg
130 135 140

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Gln Phe Thr Leu Glu Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr
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Val Ser Trp Trp Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg
            180                 185                 190

His Thr Val Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser
        195                 200                 205

Asp Glu Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg
    210                 215                 220

Glu Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr
225                 230                 235                 240

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val Thr
                245                 250                 255

Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro Ala Val
            260                 265                 270

Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala Gln Ser Tyr
        275                 280                 285

Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly Gln Gly Ala Pro
    290                 295                 300

Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser Ala Glu Leu Gly Gly
305                 310                 315                 320

Leu His Trp Gly Gln Asp Tyr Glu Phe Lys Val Arg Pro Ser Ser Gly
                325                 330                 335

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

Lys Val Pro Ser Ala Pro Pro Gln Glu Val Thr Leu Lys Pro Gly Asn
        355                 360                 365

Gly Thr Val Phe Val Ser Trp Val Pro Pro Pro Ala Glu Asn His Asn
    370                 375                 380

Gly Ile Ile Arg Gly Tyr Gln Val Trp Ser Leu Gly Asn Thr Ser Leu
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465                 470                 475                 480

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Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly Leu Tyr
            500                 505                 510

Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met Asp His Ser
        515                 520                 525

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Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu Leu Ser Trp Asp Ser Arg
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Ser Pro Gly Val Pro Leu Leu Pro Asp Thr Ser Thr Phe Tyr Gly Ser
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Leu Ile Ala Glu Leu Pro Ser Ser Thr Pro Ala Arg Pro Ser Pro Gln
        595                 600                 605

Val Pro Ala Val Arg Arg Leu Pro Pro Gln Leu Ala Gln Leu Ser Ser
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Pro Arg Leu Ser Leu Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys
                645                 650                 655

Gln Glu Leu Gln His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His
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Ser Leu Glu Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn
        675                 680                 685
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Leu Ser Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg
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Ala Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg
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His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr Gln
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Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser Ser Ile
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Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys Ser Pro Pro
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Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro Ala Ser Ser Arg
    770                 775                 780

Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu Asp Gln Asp Ser Val
785                 790                 795                 800

Leu Thr Pro Glu Glu Val Ala Leu Cys Leu Glu Leu Ser Glu Gly Glu
                805                 810                 815

Glu Thr Pro Arg Asn Ser Val Ser Pro Met Pro Arg Ala Pro Ser Pro
            820                 825                 830

Pro Thr Thr Tyr Gly Tyr Ile Ser Val Pro Thr Ala Ser Glu Phe Thr
        835                 840                 845

Asp Met Gly Arg Thr Gly Gly Gly Val Gly Pro Lys Gly Gly Val Leu
    850                 855                 860

Leu Cys Pro Pro Arg Pro Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser
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Leu Ala Asn Gly Trp Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala
                885                 890                 895

Arg Ala Ser Leu Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala
            900                 905                 910

His Phe Ala Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly
        915                 920                 925

Leu Glu Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro
    930                 935                 940

Pro Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro
945                 950                 955                 960
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Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser His
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Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp Ser Gln
980 985 990

Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro Lys Ala Gly
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Ala Ser Pro Val Asp Tyr Ser
1010 1015

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<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-46aa

<400> 6

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Leu Leu Leu Leu Leu Ile Met Gly Gly Met Ala Asp Tyr Lys Asp Asp
            20                  25                  30

Asp Asp Lys Pro Gly Pro Ala Arg Met Ser Cys Gln Ala Ser Gly Gln
        35                  40                  45

Pro Pro Pro Thr Ile Arg Trp Leu Leu Asn Gly Gln Pro Leu Ser Met
    50                  55                  60

Val Pro Pro Asp Pro His His Leu Leu Pro Asp Gly Thr Leu Leu Leu
65                  70                  75                  80

Leu Gln Pro Pro Ala Arg Gly His Ala His Asp Gly Gln Ala Leu Ser
                85                  90                  95

Thr Asp Leu Gly Val Tyr Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr
            100                 105                 110

Ala Val Ser Arg Gly Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp
        115                 120                 125

Phe Gln Ile Gln Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe
    130                 135                 140

Thr Leu Glu Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser
145                 150                 155                 160

Trp Trp Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr
                165                 170                 175

Val Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu
            180                 185                 190

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu Ser
        195                 200                 205

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

Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val Thr Leu Leu
225                 230                 235                 240

Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro Ala Val Trp Leu
                245                 250                 255

Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala
            260                 265                 270
```

```
Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly Gln Gly Ala Pro Trp Ala
        275                 280                 285

Glu Glu Leu Leu Ala Gly Trp Gln Ser Ala Glu Leu Gly Gly Leu His
    290                 295                 300

Trp Gly Gln Asp Tyr Glu Phe Lys Val Arg Pro Ser Ser Gly Arg Ala
305                 310                 315                 320

Arg Gly Pro Asp Ser Asn Val Leu Leu Leu Arg Leu Pro Glu Lys Val
                325                 330                 335

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

Val Phe Val Ser Trp Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile
        355                 360                 365

Ile Arg Gly Tyr Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro
    370                 375                 380

Ala Asn Trp Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr
385                 390                 395                 400

His Met Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala
                405                 410                 415

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

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr Leu
        435                 440                 445

Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala Thr Cys
    450                 455                 460

Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val Cys Ile His
465                 470                 475                 480

Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly Leu Tyr Arg Tyr
                485                 490                 495

Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met Asp His Ser Asp Ser
            500                 505                 510

Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu
        515                 520                 525

Ser Ser Ser Ser Ser Leu Ser Ser Arg Leu Gly Ala Asp Ala Arg Asp
    530                 535                 540
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Pro Leu Asp Cys Arg Arg Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro
545                 550                 555                 560

Gly Val Pro Leu Leu Pro Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile
                565                 570                 575

Ala Glu Leu Pro Ser Ser Thr Pro Ala Arg Pro Ser Pro Gln Val Pro
            580                 585                 590

Ala Val Arg Arg Leu Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys
        595                 600                 605

Ser Ser Ser Asp Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg
    610                 615                 620

Leu Ser Leu Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu
625                 630                 635                 640

Leu Gln His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu
                645                 650                 655

Glu Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser
            660                 665                 670

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala Leu
        675                 680                 685

Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg His Leu
    690                 695                 700

Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr Gln Ser Gln
705                 710                 715                 720

Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu
                725                 730                 735

Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro
            740                 745                 750

Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro Ala Ser Ser Arg Leu Ser
        755                 760                 765

Ser Ser Ser Leu Ser Ser Leu Gly Glu Asp Gln Asp Ser Val Leu Thr
    770                 775                 780

Pro Glu Glu Val Ala Leu Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr
785                 790                 795                 800

Pro Arg Asn Ser Val Ser Pro Met Pro Arg Ala Pro Ser Pro Pro Thr
                805                 810                 815
```

Thr Tyr Gly Tyr Ile Ser Val Pro Thr Ala Ser Glu Phe Thr Asp Met
820 825 830

Gly Arg Thr Gly Gly Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys
835 840 845

Pro Pro Arg Pro Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala
850 855 860

Asn Gly Trp Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala
865 870 875 880

Ser Leu Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe
885 890 895

Ala Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu
900 905 910

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro Ser
915 920 925

Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp
930 935 940

Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser His Thr Gln
945 950 955 960

Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp Ser Gln Ile Ser
965 970 975

Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro Lys Ala Gly Ala Ser
980 985 990

Pro Val Asp Tyr Ser Ala Ser
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<211> 2733
<212> DNA
<213> Artificial Sequence

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<223> FLAG-hROBO4-132na

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gaggatttcc agatccagcc tcgggacatg gtggctgtgg tgggtgagca gtttactctg 180

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<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-132aa

<400> 8

Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
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Leu Leu Leu Leu Leu Ile Met Gly Gly Met Ala Asp Tyr Lys Asp Asp
20 25 30

Asp Asp Lys Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln Pro Arg
35 40 45

Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu Cys Gly Pro
50 55 60

Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp Lys Asp Gly Lys
65 70 75 80

Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val Ser Gly Gly Ser Leu
85 90 95

Leu Met Ala Arg Ala Glu Lys Ser Asp Glu Gly Thr Tyr Met Cys Val
100 105 110

Ala Thr Asn Ser Ala Gly His Arg Glu Ser Arg Ala Ala Arg Val Ser
115 120 125

Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu Leu Ala Val
130 135 140

Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp Pro Ala Glu
145 150 155 160

Gly Pro Lys Pro Arg Pro Ala Val Trp Leu Ser Trp Lys Val Ser Gly
165 170 175

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Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr
            180                 185                 190

Ala Pro Gly Gly Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly
        195                 200                 205

Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu
    210                 215                 220

Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn
225                 230                 235                 240

Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln
                245                 250                 255

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp Val
            260                 265                 270

Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr Gln Val
        275                 280                 285

Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr Val Val
    290                 295                 300

Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met Pro Gly Ser Tyr
305                 310                 315                 320

Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser
                325                 330                 335

Arg Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala Thr Gln
            340                 345                 350

Glu Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr
        355                 360                 365

Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Ala Leu Trp Leu
    370                 375                 380

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

Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile
                405                 410                 415

Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr
            420                 425                 430

Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu
        435                 440                 445
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Ser Ser Arg Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg
    450                 455                 460

Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro
465                 470                 475                 480

Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
                485                 490                 495

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu Pro
            500                 505                 510

Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp Ser Leu
        515                 520                 525

Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu Ala Pro Ala
    530                 535                 540

Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Ala Asn Ser
545                 550                 555                 560

Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu Leu Arg Ala Cys Glu
                565                 570                 575

Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly Ala Val
            580                 585                 590

Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu Leu Ser
        595                 600                 605

Ser Ser Asn Glu Leu Val Thr Arg His Leu Pro Pro Ala Pro Leu Phe
    610                 615                 620

Pro His Glu Thr Pro Pro Thr Gln Ser Gln Gln Thr Gln Pro Pro Val
625                 630                 635                 640

Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro
                645                 650                 655

Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser
            660                 665                 670

Gly Pro Ser Pro Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser
        675                 680                 685

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

Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser
705                 710                 715                 720
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Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
                725                 730                 735

Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly Gly
            740                 745                 750

Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro Cys Leu
        755                 760                 765

Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly Ser Ala
    770                 775                 780

Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser Ser Ser
785                 790                 795                 800

Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu Ala Val
                805                 810                 815

Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala Asp Cys
            820                 825                 830

Val Phe Ile Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Glu Ile Phe
        835                 840                 845

Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp
    850                 855                 860

Leu Glu Asp Met Glu Val Ser His Thr Gln Arg Leu Gly Arg Gly Met
865                 870                 875                 880

Pro Pro Trp Pro Pro Asp Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu
                885                 890                 895

His Cys Arg Met Pro Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser
            900                 905                 910
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<211> 2505
<212> DNA
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-210na

<400> 9

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catagggaga gccgcgcagc ccgggtttcc atccaggagc cccaggacta cacggagcct      180

gtggagcttc tggctgtgcg aattcagctg gaaaatgtga cactgctgaa cccggatcct      240

gcagagggcc ccaagcctag accggcggtg tggctcagct ggaaggtcag tggccctgct      300

gcgcctgccc aatcttacac ggccttgttc aggacccaga ctgccccggg aggccaggga      360
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tcctccgatg gctccttcct cgctgatgct cactttgccc gggccctggc agtggctgtg 2220

gatagctttg gtttcggtct agagcccagg gaggcagact gcgtcttcat agatgcctca 2280

tcacctccct ccccacggga tgagatcttc ctgaccccca acctctccct gcccctgtgg 2340

gagtggaggc cagactggtt ggaagacatg gaggtcagcc acacccagcg gctgggaagg 2400

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<210> 10
<211> 835
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-210aa

<400> 10

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Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
1               5                  10                  15

Leu Leu Leu Leu Leu Ile Met Gly Gly Met Ala Asp Tyr Lys Asp Asp
            20                  25                  30

Asp Asp Lys Thr Asn Ser Ala Gly His Arg Glu Ser Arg Ala Ala Arg
        35                  40                  45

Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu Leu
    50                  55                  60

Ala Val Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp Pro
65                  70                  75                  80

Ala Glu Gly Pro Lys Pro Arg Pro Ala Val Trp Leu Ser Trp Lys Val
                85                  90                  95

Ser Gly Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg Thr
            100                 105                 110

Gln Thr Ala Pro Gly Gly Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu
        115                 120                 125

Ala Gly Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp
    130                 135                 140

Tyr Glu Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp
145                 150                 155                 160

Ser Asn Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro
                165                 170                 175

Pro Gln Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser
            180                 185                 190

Trp Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr
        195                 200                 205
```

```
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr
    210                 215                 220

Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met Pro Gly
225                 230                 235                 240

Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu
                245                 250                 255

Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala
            260                 265                 270

Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg
        275                 280                 285

Ala Thr Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Ala Leu
    290                 295                 300

Trp Leu Leu Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg Arg
305                 310                 315                 320

Ala Arg Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Glu Asp
                325                 330                 335

Ala Ile Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala
            340                 345                 350

Asp Thr Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser
        355                 360                 365

Ser Leu Ser Ser Arg Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys
    370                 375                 380

Arg Arg Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu
385                 390                 395                 400

Leu Pro Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro
                405                 410                 415

Ser Ser Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg
            420                 425                 430

Leu Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp
        435                 440                 445

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu Ala
    450                 455                 460

Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Ala
465                 470                 475                 480
```

```
Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu Leu Arg Ala
                485                 490                 495

Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly
            500                 505                 510

Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu
        515                 520                 525

Leu Ser Ser Ser Asn Glu Leu Val Thr Arg His Leu Pro Pro Ala Pro
    530                 535                 540

Leu Phe Pro His Glu Thr Pro Pro Thr Gln Ser Gln Gln Thr Gln Pro
545                 550                 555                 560

Pro Val Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Pro Ala Ala Pro
                565                 570                 575

Ile Pro Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser
            580                 585                 590

Leu Ser Gly Pro Ser Pro Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu
        595                 600                 605

Ser Ser Leu Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val
    610                 615                 620

Ala Leu Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser
625                 630                 635                 640

Val Ser Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr
                645                 650                 655

Ile Ser Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly
            660                 665                 670

Gly Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro
        675                 680                 685

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly
    690                 695                 700

Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser
705                 710                 715                 720

Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu
                725                 730                 735

Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala
            740                 745                 750
```

eolf-seql

Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Glu
755 760 765

Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro
770 775 780

Asp Trp Leu Glu Asp Met Glu Val Ser His Thr Gln Arg Leu Gly Arg
785 790 795 800

Gly Met Pro Pro Trp Pro Pro Asp Ser Gln Ile Ser Ser Gln Arg Ser
805 810 815

Gln Leu His Cys Arg Met Pro Lys Ala Gly Ala Ser Pro Val Asp Tyr
820 825 830

Ser Ala Ser
835

<210> 11
<211> 2454
<212> DNA
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-225na

<400> 11
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gactacacgg agcctgtgga gcttctggct gtgcgaattc agctggaaaa tgtgacactg 180

ctgaacccgg atcctgcaga gggccccaag cctagaccgg cggtgtggct cagctggaag 240

gtcagtggcc ctgctgcgcc tgcccaatct tacacggcct tgttcaggac ccagactgcc 300

ccgggaggcc agggagctcc gtgggcagag gagctgctgg ccggctggca gagcgcagag 360

cttggaggcc tccactgggg ccaagactac gagttcaaag tgagaccatc ctctggccgg 420

gctcgaggcc ctgacagcaa cgtgctgctc ctgaggctgc cggaaaaagt gcccagtgcc 480

ccacctcagg aagtgactct aaagcctggc aatggcactg tctttgtgag ctgggtccca 540

ccacctgctg aaaaccacaa tggcatcatc cgtggctacc aggtctggag cctgggcaac 600

acatcactgc caccagccaa ctggactgta gttggtgagc agacccagct ggaaatcgcc 660

acccatatgc caggctccta ctgcgtgcaa gtggctgcag tcactggtgc tggagctggg 720

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caccgccggc gccgagctag ggtgcacctg ggcccaggtc tgtacagata taccagtgag 960

gatgccatcc taaaacacag gatggatcac agtgactccc agtggttggc agacacttgg 1020

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gagctgcagc atgccaacag ttccccactg ctccggggca gccactcctt ggagctccgg 1440

gcctgtgagt taggaaatag aggttccaag aacctttccc aaagcccagg agctgtgccc 1500

caagctctgg ttgcctggcg ggccctggga ccgaaactcc tcagctcctc aaatgagctg 1560

gttactcgtc atctccctcc agcacccctc tttcctcatg aaactccccc aactcagagt 1620

caacagaccc agcctccggt ggcaccacag gctccctcct ccatcctgct gccagcagcc 1680

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gacagcgtgc tgacccctga ggaggtagcc ctgtgcttgg aactcagtga gggtgaggag 1860

actcccagga acagcgtctc tcccatgcca agggctcctt cacccccac cacctatggg 1920

tacatcagcg tcccaacagc ctcagagttc acggacatgg gcaggactgg aggaggggtg 1980

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cagcggctgg gaaaggggat gcctccctgg ccccctgact ctcagatctc ttcccagaga 2400

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<210> 12
<211> 818
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-225aa

<400> 12

Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
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Leu Leu Leu Leu Leu Ile Met Gly Gly Met Ala Asp Tyr Lys Asp Asp
20 25 30

Asp Asp Lys Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu
35 40 45

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Leu Ala Val Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp
    50                  55                  60

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

Val Ser Gly Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg
                85                  90                  95

Thr Gln Thr Ala Pro Gly Gly Gln Gly Ala Pro Trp Ala Glu Glu Leu
            100                 105                 110

Leu Ala Gly Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln
        115                 120                 125

Asp Tyr Glu Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro
    130                 135                 140

Asp Ser Asn Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala
145                 150                 155                 160

Pro Pro Gln Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val
                165                 170                 175

Ser Trp Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly
            180                 185                 190

Tyr Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp
        195                 200                 205

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met Pro
    210                 215                 220

Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly
225                 230                 235                 240

Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg
                245                 250                 255

Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu
            260                 265                 270

Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Ala
        275                 280                 285

Leu Trp Leu Leu Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg
    290                 295                 300

Arg Ala Arg Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Glu
305                 310                 315                 320
```

```
Asp Ala Ile Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu
                325                 330                 335

Ala Asp Thr Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser
            340                 345                 350

Ser Ser Leu Ser Ser Arg Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp
        355                 360                 365

Cys Arg Arg Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro
    370                 375                 380

Leu Leu Pro Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu
385                 390                 395                 400

Pro Ser Ser Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg
                405                 410                 415

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

Asp Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu
        435                 440                 445

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His
    450                 455                 460

Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu Leu Arg
465                 470                 475                 480

Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro
                485                 490                 495

Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys
            500                 505                 510

Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg His Leu Pro Pro Ala
        515                 520                 525

Pro Leu Phe Pro His Glu Thr Pro Pro Thr Gln Ser Gln Gln Thr Gln
    530                 535                 540

Pro Pro Val Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Pro Ala Ala
545                 550                 555                 560

Pro Ile Pro Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser
                565                 570                 575

Ser Leu Ser Gly Pro Ser Pro Ala Ser Ser Arg Leu Ser Ser Ser Ser
            580                 585                 590
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```
Leu Ser Ser Leu Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu
        595                 600                 605

Val Ala Leu Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn
    610                 615                 620

Ser Val Ser Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly
625                 630                 635                 640

Tyr Ile Ser Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr
                645                 650                 655

Gly Gly Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg
            660                 665                 670

Pro Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp
        675                 680                 685

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val
    690                 695                 700

Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala
705                 710                 715                 720

Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu
                725                 730                 735

Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp
            740                 745                 750

Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg
        755                 760                 765

Pro Asp Trp Leu Glu Asp Met Glu Val Ser His Thr Gln Arg Leu Gly
    770                 775                 780

Arg Gly Met Pro Pro Trp Pro Pro Asp Ser Gln Ile Ser Ser Gln Arg
785                 790                 795                 800

Ser Gln Leu His Cys Arg Met Pro Lys Ala Gly Ala Ser Pro Val Asp
                805                 810                 815

Tyr Ser
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<210> 13
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>

<223> FLAG-hROBO4-341na

<400> 13

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gtgcccagtg ccccacctca ggaagtgact ctaaagcctg gcaatggcac tgtctttgtg 180

agctgggtcc caccacctgc tgaaaaccac aatggcatca tccgtggcta ccaggtctgg 240

agcctgggca acacatcact gccaccagcc aactggactg tagttggtga gcagacccag 300

ctggaaatcg ccacccatat gccaggctcc tactgcgtgc aagtggctgc agtcactggt 360

gctggagctg gggagcccag tagacctgtc tgcctccttt tagagcaggc catggagcga 420

gccacccaag aacccagtga gcatggtccc tggaccctgg agcagctgag ggctaccttg 480

aagcggcctg aggtcattgc cacctgcggt gttgcactct ggctgctgct tctgggcacc 540

gccgtgtgta tccaccgccg gcgccgagct agggtgcacc tgggcccagg tctgtacaga 600

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gcagacactt ggcgttccac ctctggctct cgggacctga gcagcagcag cagcctcagc 720

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cgcctcccac cccagctggc ccagctctcc agcccctgtt ccagctcaga cagcctctgc 960

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ggggaggatc aagacagcgt gctgacccct gaggaggtag ccctgtgctt ggaactcagt 1500

gagggtgagg agactcccag gaacagcgtc tctcccatgc caagggctcc ttcacccccc 1560

accacctatg ggtacatcag cgtcccaaca gcctcagagt tcacggacat gggcaggact 1620

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gtcagccaca cccagcggct gggaaggggg atgcctccct ggccccctga ctctcagatc 2040

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tactcc 2106

<210> 14
<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG-hROBO4-341aa

<400> 14

Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
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Leu Leu Leu Leu Leu Ile Met Gly Gly Met Ala Asp Tyr Lys Asp Asp
20 25 30

Asp Asp Lys Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln Glu
35 40 45

Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp Val Pro
50 55 60

Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr Gln Val Trp
65 70 75 80

Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr Val Val Gly
85 90 95

Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met Pro Gly Ser Tyr Cys
100 105 110

Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser Arg
115 120 125

Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala Thr Gln Glu
130 135 140

Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr Leu
145 150 155 160

Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Ala Leu Trp Leu Leu
165 170 175

Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg Arg Ala Arg Val
180 185 190

His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu
195 200 205

```
Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp
    210                 215                 220

Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser
225                 230                 235                 240

Ser Arg Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser
                245                 250                 255

Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp
            260                 265                 270

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser Thr
        275                 280                 285

Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu Pro Pro
    290                 295                 300

Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp Ser Leu Cys
305                 310                 315                 320

Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu Ala Pro Ala Glu
                325                 330                 335

Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Ala Asn Ser Ser
            340                 345                 350

Pro Leu Leu Arg Gly Ser His Ser Leu Glu Leu Arg Ala Cys Glu Leu
        355                 360                 365

Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly Ala Val Pro
    370                 375                 380

Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu Leu Ser Ser
385                 390                 395                 400

Ser Asn Glu Leu Val Thr Arg His Leu Pro Pro Ala Pro Leu Phe Pro
                405                 410                 415

His Glu Thr Pro Pro Thr Gln Ser Gln Gln Thr Gln Pro Pro Val Ala
            420                 425                 430

Pro Gln Ala Pro Ser Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile
        435                 440                 445

Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly
    450                 455                 460

Pro Ser Pro Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu
465                 470                 475                 480
```

```
Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys
                485                 490                 495

Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro
            500                 505                 510

Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser Val
        515                 520                 525

Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly Gly Val
    530                 535                 540

Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro Cys Leu Thr
545                 550                 555                 560

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

Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser Ser Ser Asp
            580                 585                 590

Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu Ala Val Ala
        595                 600                 605

Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala Asp Cys Val
    610                 615                 620

Phe Ile Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Glu Ile Phe Leu
625                 630                 635                 640

Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp Leu
                645                 650                 655

Glu Asp Met Glu Val Ser His Thr Gln Arg Leu Gly Arg Gly Met Pro
            660                 665                 670

Pro Trp Pro Pro Asp Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His
        675                 680                 685

Cys Arg Met Pro Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser
    690                 695                 700
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<210> 15
<211> 3045
<212> DNA
<213> Mus musculus

<400> 15
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acggagtggc ctctgcctct gctgctgctt ttcatcatgg gaggtgaggc tctggattct 120

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atgaggtgca gatcatccgg ccaaccacct cccactatcc gctggctgct gaatgggcag      240
cccctcagca tggccacccc agacctacat tacctttgc cggatgggac cctcctgtta      300
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ggtgtctaca catgtgaggc cagcaaccgg ctgggcacag cagtgagccg gggtgctagg      420
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Met Gly Gly Glu Ala Leu Asp Ser Pro Pro Gln Ile Leu Val His Pro
35 40 45

Gln Asp Gln Leu Leu Gln Gly Ser Gly Pro Ala Lys Met Arg Cys Arg
50 55 60

Ser Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu Asn Gly Gln
65 70 75 80

Pro Leu Ser Met Ala Thr Pro Asp Leu His Tyr Leu Leu Pro Asp Gly
85 90 95

Thr Leu Leu Leu His Arg Pro Ser Val Gln Gly Arg Pro Gln Asp Asp
100 105 110

Gln Asn Ile Leu Ser Ala Ile Leu Gly Val Tyr Thr Cys Glu Ala Ser
115 120 125

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

Val Gly Glu Ser Leu Val Leu Glu Cys Gly Pro Pro Trp Gly Tyr Pro
                165                 170                 175

Lys Pro Ser Val Ser Trp Trp Lys Asp Gly Lys Pro Leu Val Leu Gln
            180                 185                 190

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

Glu Lys Asn Asp Ser Gly Thr Tyr Met Cys Met Ala Thr Asn Asn Ala
    210                 215                 220

Gly Gln Arg Glu Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Ser Gln
225                 230                 235                 240

Asp His Lys Glu His Leu Glu Leu Leu Ala Val Arg Ile Gln Leu Glu
                245                 250                 255

Asn Val Thr Leu Leu Asn Pro Glu Pro Val Lys Gly Pro Lys Pro Gly
            260                 265                 270

Pro Ser Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala
        275                 280                 285

Glu Ser Tyr Thr Ala Leu Phe Arg Thr Gln Arg Ser Pro Arg Asp Gln
    290                 295                 300

Gly Ser Pro Trp Thr Glu Val Leu Leu Arg Gly Leu Gln Ser Ala Lys
305                 310                 315                 320

Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys Val Arg Pro
                325                 330                 335

Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val Leu Leu Leu Arg
            340                 345                 350

Leu Pro Glu Gln Val Pro Ser Ala Pro Pro Gln Gly Val Thr Leu Arg
        355                 360                 365

Ser Gly Asn Gly Ser Val Phe Val Ser Trp Ala Pro Pro Pro Ala Glu
    370                 375                 380

Ser His Asn Gly Val Ile Arg Gly Tyr Gln Val Trp Ser Leu Gly Asn
385                 390                 395                 400
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Leu Glu Ile Ala Thr Arg Leu Pro Gly Ser Tyr Cys Val Gln Val Ala
            420                 425                 430

Ala Val Thr Gly Ala Gly Ala Gly Glu Leu Ser Thr Pro Val Cys Leu
        435                 440                 445

Leu Leu Glu Gln Ala Met Glu Gln Ser Ala Arg Asp Pro Arg Lys His
    450                 455                 460

Val Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr Leu Arg Arg Pro Glu
465                 470                 475                 480

Val Ile Ala Ser Ser Ala Val Leu Leu Trp Leu Leu Leu Leu Gly Ile
                485                 490                 495

Thr Val Cys Ile Tyr Arg Arg Arg Lys Ala Gly Val His Leu Gly Pro
            500                 505                 510

Gly Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met
        515                 520                 525

Asp His Ser Asp Ser Pro Trp Leu Ala Asp Thr Trp Arg Ser Thr Ser
    530                 535                 540

Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg Leu Gly
545                 550                 555                 560

Leu Asp Pro Arg Asp Pro Leu Glu Gly Arg Arg Ser Leu Ile Ser Trp
                565                 570                 575

Asp Pro Arg Ser Pro Gly Val Pro Leu Leu Pro Asp Thr Ser Thr Phe
            580                 585                 590

Tyr Gly Ser Leu Ile Ala Glu Gln Pro Ser Ser Pro Pro Val Arg Pro
        595                 600                 605

Ser Pro Lys Thr Pro Ala Ala Arg Arg Phe Pro Ser Lys Leu Ala Gly
    610                 615                 620

Thr Ser Ser Pro Trp Ala Ser Ser Asp Ser Leu Cys Ser Arg Arg Gly
625                 630                 635                 640

Leu Cys Ser Pro Arg Met Ser Leu Thr Pro Thr Glu Ala Trp Lys Ala
                645                 650                 655

Lys Lys Lys Gln Glu Leu His Gln Ala Asn Ser Ser Pro Leu Leu Arg
            660                 665                 670
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Gly Ser His Pro Met Glu Ile Trp Ala Trp Glu Leu Gly Ser Arg Ala
        675                 680                 685

Ser Lys Asn Leu Ser Gln Ser Pro Gly Glu Ala Pro Arg Ala Val Val
    690                 695                 700

Ser Trp Arg Ala Val Gly Pro Gln Leu His Arg Asn Ser Ser Glu Leu
705                 710                 715                 720

Ala Ser Arg Pro Leu Pro Pro Thr Pro Leu Ser Leu Arg Gly Ala Ser
                725                 730                 735

Ser His Asp Pro Gln Ser Gln Cys Val Glu Lys Leu Gln Ala Pro Ser
            740                 745                 750

Ser Asp Pro Leu Pro Ala Ala Pro Leu Ser Val Leu Asn Ser Ser Arg
        755                 760                 765

Pro Ser Ser Pro Gln Ala Ser Phe Leu Ser Cys Pro Ser Pro Ser Ser
    770                 775                 780

Ser Asn Leu Ser Ser Ser Ser Leu Ser Ser Leu Glu Glu Glu Glu Asp
785                 790                 795                 800

Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu Glu Leu
                805                 810                 815

Ser Asp Gly Glu Glu Thr Pro Thr Asn Ser Val Ser Pro Met Pro Arg
            820                 825                 830

Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser Ile Pro Thr Cys
        835                 840                 845

Ser Gly Leu Ala Asp Met Gly Arg Ala Gly Gly Gly Val Gly Ser Glu
    850                 855                 860

Val Gly Asn Leu Leu Tyr Pro Pro Arg Pro Cys Pro Thr Pro Thr Pro
865                 870                 875                 880

Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly Ser Ala Ser Glu Asp Asn
                885                 890                 895

Val Pro Ser Ala Arg Ala Ser Leu Val Ser Ser Ser Asp Gly Ser Phe
            900                 905                 910

Leu Ala Asp Thr His Phe Ala Arg Ala Leu Ala Val Ala Val Asp Ser
        915                 920                 925

Phe Gly Leu Ser Leu Asp Pro Arg Glu Ala Asp Cys Val Phe Thr Asp
    930                 935                 940
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Ala Ser Ser Pro Pro Ser Pro Arg Gly Asp Leu Ser Leu Thr Arg Ser
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Phe Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Ala
965 970 975

Glu Ile Ser His Thr Gln Arg Leu Gly Arg Gly Leu Pro Pro Trp Pro
980 985 990

Pro Asp Ser Arg Ala Ser Ser Gln Arg Ser Trp Leu Thr Gly Ala Val
995 1000 1005

Pro Lys Ala Gly Asp Ser Ser
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Met Gly Gly Lys Ala Leu Asp Ser Pro Pro Gln Ile Leu Val His Pro
        35                  40                  45

Gln Asp Gln Leu Leu Gln Gly Ser Gly Pro Ala Lys Met Ser Cys Arg
    50                  55                  60

Ala Ser Gly Gln Pro Leu Pro Thr Ile Arg Trp Leu Leu Asn Gly Gln
65                  70                  75                  80

Pro Leu Ser Met Ala Thr Pro Asp Leu His Tyr Leu Gln Ser Asp Gly
                85                  90                  95

Thr Leu Leu Leu His Arg Pro Pro Thr His Gly Arg Pro Gln Asp Asp
            100                 105                 110

Gln Asn Ile Leu Ser Ala Ile Leu Gly Val Tyr Thr Cys Glu Ala Ser
        115                 120                 125

Asn Arg Leu Gly Thr Ala Val Ser Arg Gly Ala Arg Leu Ser Val Ala
    130                 135                 140

Val Leu Gln Glu Asp Phe Arg Ile Gln Pro Arg Asp Thr Val Ala Val
145                 150                 155                 160

Val Gly Glu Ser Leu Val Leu Glu Cys Gly Pro Pro Trp Gly Tyr Pro
                165                 170                 175

Lys Pro Ser Val Ser Trp Trp Lys Asp Gly Lys Pro Leu Val Leu Gln
            180                 185                 190

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

Glu Lys Asn Asp Thr Gly Thr Tyr Met Cys Met Ala Thr Asn Asn Ala
    210                 215                 220

Gly Gln Arg Glu Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Ser Pro
225                 230                 235                 240

Asp His Lys Glu His Leu Glu Leu Leu Ala Val Arg Ile Gln Leu Glu
                245                 250                 255
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Asn Val Thr Leu Leu Asn Pro Glu Pro Val Lys Gly Pro Lys Pro Gly
            260                 265                 270

Pro Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala
        275                 280                 285

Gln Ser Tyr Thr Ala Leu Phe Arg Ala Gln Arg Asp Pro Arg Asp Gln
    290                 295                 300

Gly Ser Pro Trp Thr Glu Val Leu Leu Asp Gly Leu Leu Asn Ala Lys
305                 310                 315                 320

Leu Gly Gly Leu Arg Trp Gly Gln Asp Tyr Glu Phe Lys Val Arg Pro
                325                 330                 335

Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val Leu Leu Leu Arg
            340                 345                 350

Leu Pro Glu Gln Val Pro Ser Ala Pro Pro Gln Glu Val Thr Leu Arg
        355                 360                 365

Pro Gly Asn Gly Ser Val Phe Val Ser Trp Ala Pro Pro Pro Ala Glu
    370                 375                 380

Asn His Asn Gly Phe Ile Arg Gly Tyr Gln Val Trp Ser Leu Gly Asn
385                 390                 395                 400

Ala Ser Leu Pro Ala Ala Asn Trp Thr Val Val Gly Glu Gln Thr Gln
                405                 410                 415

Leu Glu Ile Ala Ala Arg Met Pro Gly Ser Tyr Cys Val Gln Val Ala
            420                 425                 430

Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser Ile Pro Val Cys Leu
        435                 440                 445

Leu Leu Glu Gln Ala Met Glu Gln Ser Ala Arg Asp Pro Ser Lys His
    450                 455                 460

Val Ser Trp Thr Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu
465                 470                 475                 480

Val Ile Ala Ser Gly Ala Val Leu Leu Trp Leu Leu Leu Leu Gly Ile
                485                 490                 495

Ala Val Cys Ile Tyr Arg Arg Arg Lys Ala Gly Val His Leu Gly Pro
            500                 505                 510

Gly Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met
        515                 520                 525
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Asp His Ser Asp Ser Pro Trp Leu Ala Asp Thr Trp Arg Ser Thr Ser
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Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg Leu Gly
545                 550                 555                 560

Val Asp Pro Arg Asp Pro Leu Asp Gly Arg Arg Ser Leu Ile Ser Trp
                565                 570                 575

Asp Pro Arg Ser Pro Gly Val Pro Leu Leu Pro Asp Thr Ser Thr Phe
            580                 585                 590

Tyr Gly Ser Leu Ile Ala Glu Gln Thr Ser Ser Pro Pro Val Arg Pro
        595                 600                 605

Ser Pro Gln Thr Pro Ala Ala Arg Arg Leu Pro Pro Lys Leu Thr Gly
    610                 615                 620

Thr Ser Ser Pro Trp Ala Ser Ser Asp Ser Leu Cys Ser Arg Arg Gly
625                 630                 635                 640

Leu Cys Ser Pro Arg Met Ser Leu Ala Pro Ala Glu Ala Trp Lys Ala
                645                 650                 655

Lys Lys Lys Gln Glu Leu His Gln Ala Asn Ser Ser Pro Leu Leu Gln
            660                 665                 670

Gly Ser His Pro Met Glu Ile Trp Ala Trp Glu Leu Gly Ser Arg Ala
        675                 680                 685

Ser Lys Asn Leu Ser Gln Ser Pro Gly Pro Asn Thr Cys Ser Pro Arg
    690                 695                 700

Glu Ala Pro Gly Ala Val Val Ala Trp Arg Ala Leu Gly Pro Gln Leu
705                 710                 715                 720

His Arg Asn Ser Ser Glu Leu Ala Ala Arg Pro Leu Pro Pro Thr Pro
                725                 730                 735

Leu Ser Leu Arg Gly Ala Pro Ser His Asp Pro Gln Ser Gln Cys Val
            740                 745                 750

Glu Lys Leu Gln Ala Pro Ser Ser Asp Pro Leu Pro Ala Ala Pro Leu
        755                 760                 765

Ser Val Leu Asn Ser Ser Arg Pro Ser Ser Pro Gln Ala Ser Phe Leu
    770                 775                 780

Ser Val Pro Ser Pro Gly Ser Ser Asn Leu Ser Ser Ser Ser Leu Ser
785                 790                 795                 800
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eolf-seql

Ser Leu Glu Glu Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val
805 810 815

Ala Leu Cys Leu Glu Leu Ser Asp Gly Glu Glu Thr Pro Thr Asn Ser
820 825 830

Val Ser Pro Met Pro Arg Ala Pro Ser Pro Pro Ala Thr Tyr Gly Tyr
835 840 845

Ile Ser Ile Pro Thr Ser Ser Gly Leu Ala Asp Met Gly Arg Ala Gly
850 855 860

Gly Gly Val Gly Ser Glu Val Gly Asn Leu Leu Cys Pro Pro Arg Leu
865 870 875 880

Cys Pro Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly
885 890 895

Ser Ala Ser Glu Asp Asn Val Pro Ser Ala Arg Ala Ser Leu Val Ser
900 905 910

Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu
915 920 925

Ala Val Ala Val Asp Ser Phe Gly Phe Ser Leu Glu Pro Arg Glu Ala
930 935 940

Asp Cys Val Phe Thr Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Asp
945 950 955 960

Leu Ser Leu Thr Arg Ser Phe Ser Leu Pro Leu Trp Glu Trp Arg Pro
965 970 975

Asp Trp Leu Glu Asp Ala Glu Ile Asn His Thr Gln Arg Leu Gly Arg
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Gly Leu Pro Pro Trp Pro Pro Asp Ser Arg Val Ser Ser Gln Arg Ser
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<213> Macaca fascicularis

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Gln Ile Leu Val His Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro
35 40 45

Ala Arg Met Ser Cys Arg Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg
50 55 60

Trp Leu Leu Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His
65 70 75 80

His Leu Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Trp
85 90 95

Gly His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
100 105 110

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly Ala
115 120 125

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Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln Pro Arg
    130                 135                 140

Asp Met Val Ala Val Val Gly Glu Gln Leu Thr Leu Glu Cys Gly Pro
145                 150                 155                 160

Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp Lys Asp Gly Lys
                165                 170                 175

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

Leu Met Ala Arg Ala Glu Lys Ser Asp Ala Gly Ala Tyr Met Cys Val
        195                 200                 205

Ala Ala Asn Ser Ala Gly His Arg Glu Ser His Ala Ala Arg Val Ser
    210                 215                 220

Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu Leu Ala Val
225                 230                 235                 240

Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp Pro Ala Lys
                245                 250                 255

Gly Pro Lys Pro Gly Pro Ala Val Trp Leu Ser Trp Lys Val Ser Gly
            260                 265                 270

Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr
        275                 280                 285

Ala Pro Gly Asp Gln Gly Ala Pro Trp Thr Glu Glu Leu Leu Ala Gly
    290                 295                 300

Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu
305                 310                 315                 320

Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn
                325                 330                 335

Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln
            340                 345                 350

Glu Val Thr Leu Lys Pro Gly Asn Gly Ser Val Leu Val Ser Trp Val
        355                 360                 365

Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr Gln Val
    370                 375                 380

Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr Val Val
385                 390                 395                 400
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Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr Arg Met Pro Gly Ser Tyr
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Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser
            420                 425                 430

Ser Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala Thr Arg
        435                 440                 445

Glu Pro Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr
    450                 455                 460

Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Val Leu Trp Leu
465                 470                 475                 480

Leu Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg Arg Ala Gly
                485                 490                 495

Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Lys Asp Ala Ile
            500                 505                 510

Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr
        515                 520                 525

Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu
    530                 535                 540

Ser Ser Arg Leu Gly Ala Asp Pro Arg Asp Pro Leu Asp Cys Arg Arg
545                 550                 555                 560

Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro
                565                 570                 575

Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
            580                 585                 590

Pro Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu Pro
        595                 600                 605

Pro Gln Leu Ala Arg Leu Ser Ser Pro Cys Ser Ser Ser Asp Ser Leu
    610                 615                 620

Cys Ser His Arg Gly Phe Ser Ser Pro Arg Leu Ser Leu Ala Pro Thr
625                 630                 635                 640

Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Val Asn Ser
                645                 650                 655

Ser Pro Leu Leu Arg Gly Ser Gln Pro Leu Glu Leu Arg Ala Cys Glu
            660                 665                 670
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Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly Ala Val
        675                 680                 685

Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu Leu Ser
    690                 695                 700

Ser Ser Asn Glu Leu Val Thr Arg Pro Leu Pro Pro Ala Pro Leu Phe
705                 710                 715                 720

Pro His Glu Thr Pro Gln Thr Gln Ser Gln Gln Thr Gln Pro Pro Val
                725                 730                 735

Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Ala Thr Ala Pro Ile Pro
            740                 745                 750

Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser
        755                 760                 765

Gly Pro Ser Pro Ala Ser Ser His Leu Ser Ser Ser Ser Leu Ser Ser
    770                 775                 780

Leu Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu
785                 790                 795                 800

Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser
                805                 810                 815

Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
            820                 825                 830

Thr Pro Thr Ala Ser Glu Phe Thr Gly Met Asp Arg Thr Gly Gly Gly
        835                 840                 845

Val Gly Ser Glu Gly Gly Val Leu Leu Cys Pro Pro Arg Pro Cys Leu
    850                 855                 860

Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly Ser Ala
865                 870                 875                 880

Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser Ser Ser
                885                 890                 895

Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu Ala Val
            900                 905                 910

Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala Asp Cys
        915                 920                 925

Val Phe Thr Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Asp Ile Phe
    930                 935                 940
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eolf-seql

Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp
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Leu Glu Asp Met Glu Val Asn His Thr Gln Leu Leu Gly Arg Gly Met
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Pro Pro Trp Ser Pro Asp Ser Arg Ile Ser Ser Gln Arg Ser Gln Leu
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His Cys Pro Val Pro Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser
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<400> 21
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Gln Ile Leu Val His Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro
        35                  40                  45

Ala Arg Met Ser Cys Arg Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg
    50                  55                  60

Trp Leu Leu Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His
65                  70                  75                  80

His Leu Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg
                85                  90                  95

Gly His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
            100                 105                 110

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly Ala
        115                 120                 125

Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln Pro Arg
    130                 135                 140

Asp Met Val Ala Val Val Gly Glu Gln Leu Thr Leu Glu Cys Gly Pro
145                 150                 155                 160

Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp Lys Asp Gly Lys
                165                 170                 175

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

Leu Met Ala Arg Ala Glu Lys Ser Asp Thr Gly Ala Tyr Met Cys Val
        195                 200                 205

Ala Ala Asn Ser Ala Gly His Arg Glu Ser Arg Ala Ala Arg Val Ser
    210                 215                 220

Ile Gln Glu Pro Gln Asp Tyr Thr Glu Pro Val Glu Leu Leu Ala Val
225                 230                 235                 240

Arg Ile Gln Leu Glu Asn Val Thr Leu Leu Asn Pro Asp Pro Ala Lys
                245                 250                 255

Gly Pro Lys Pro Gly Pro Ala Val Trp Leu Ser Trp Lys Val Ser Gly
            260                 265                 270

Pro Ala Ala Pro Ala Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr
        275                 280                 285
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Ala Pro Gly Asp Gln Gly Ala Pro Trp Thr Glu Glu Leu Leu Ala Gly
    290                 295                 300

Trp Gln Ser Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu
305                 310                 315                 320

Phe Lys Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn
                325                 330                 335

Val Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln
            340                 345                 350

Glu Val Thr Leu Lys Pro Gly Asn Gly Ser Val Leu Val Ser Trp Val
        355                 360                 365

Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr Gln Val
    370                 375                 380

Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp Thr Val Val
385                 390                 395                 400

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

Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly Ala Gly Glu Pro Ser
            420                 425                 430

Ser Pro Val Cys Leu Leu Leu Glu Gln Ala Met Glu Arg Ala Thr Arg
        435                 440                 445

Glu Leu Ser Glu His Gly Pro Trp Thr Leu Glu Gln Leu Arg Ala Thr
    450                 455                 460

Leu Lys Arg Pro Glu Val Ile Ala Thr Cys Gly Val Val Leu Trp Leu
465                 470                 475                 480

Leu Leu Leu Gly Thr Ala Val Cys Ile His Arg Arg Arg Arg Ala Gly
                485                 490                 495

Val His Leu Gly Pro Gly Leu Tyr Arg Tyr Thr Ser Lys Asp Ala Ile
            500                 505                 510

Leu Lys His Arg Met Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr
        515                 520                 525

Trp Arg Ser Thr Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu
    530                 535                 540

Ser Ser Arg Leu Gly Ala Asp Pro Arg Asp Pro Leu Asp Cys Arg Arg
545                 550                 555                 560
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Ser Leu Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Leu
                565                 570                 575

Asp Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
            580                 585                 590

Pro Leu Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu Pro
        595                 600                 605

Pro Gln Leu Ala Arg Leu Ser Ser Pro Cys Ser Ser Ser Asp Ser Leu
    610                 615                 620

Cys Ser His Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu Ala Pro Thr
625                 630                 635                 640

Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln His Val Asn Ser
                645                 650                 655

Ser Pro Leu Leu Arg Gly Ser Gln Pro Leu Glu Leu Arg Ala Cys Glu
            660                 665                 670

Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser Gln Ser Pro Gly Ala Val
        675                 680                 685

Pro Gln Ala Leu Val Ala Trp Arg Ala Leu Gly Pro Lys Leu Leu Ser
    690                 695                 700

Ser Ser Asn Glu Leu Val Thr Arg Pro Leu Pro Pro Ala Pro Leu Phe
705                 710                 715                 720

Pro His Glu Thr Pro Gln Thr Gln Ser Gln Gln Thr Gln Pro Pro Val
                725                 730                 735

Ala Pro Gln Ala Pro Ser Ser Ile Leu Leu Ala Thr Ala Pro Ile Pro
            740                 745                 750

Ile Leu Ser Pro Cys Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser
        755                 760                 765

Gly Pro Ser Pro Ala Ser Ser His Leu Ser Ser Ser Ser Leu Ser Ser
    770                 775                 780

Leu Gly Glu Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu
785                 790                 795                 800

Cys Leu Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser
                805                 810                 815

Pro Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
            820                 825                 830
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Thr Pro Thr Ala Ser Glu Phe Thr Gly Met Asp Arg Thr Gly Gly Gly
        835                 840                 845

Val Gly Ser Glu Gly Gly Val Leu Leu Cys Pro Pro Arg Pro Cys Leu
    850                 855                 860

Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp Gly Ser Ala
865                 870                 875                 880

Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu Val Ser Ser Ser
                885                 890                 895

Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala Arg Ala Leu Ala Val
            900                 905                 910

Ala Val Asp Ser Phe Gly Phe Gly Leu Glu Pro Arg Glu Ala Asp Cys
        915                 920                 925

Val Phe Thr Asp Ala Ser Ser Pro Pro Ser Pro Arg Asp Asp Ile Phe
    930                 935                 940

Leu Thr Pro Asn Leu Ser Leu Pro Leu Trp Glu Trp Arg Pro Asp Trp
945                 950                 955                 960

Leu Glu Asp Met Glu Val Asn His Thr Gln Leu Leu Gly Arg Gly Met
                965                 970                 975

Pro Pro Trp Ser Pro Asp Ser Arg Ile Ser Ser Gln Arg Ser Gln Leu
            980                 985                 990

His Cys Pro Val Pro Lys Ala Gly  Ala Ser Pro Val Asp  Tyr Ser
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Ser Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro
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Thr Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp
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Phe Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly
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Gln Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp
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Gly Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly
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Lys Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val
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Leu Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu
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Ala Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly
                245                 250                 255

Asp Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro
            260                 265                 270

Lys Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys
        275                 280                 285

Val Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met
    290                 295                 300

Val Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Val Gly Ser
305                 310                 315                 320

Glu Pro Pro His Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu
                325                 330                 335

Gly Arg Thr Val Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro
            340                 345                 350

Ala Ile Phe Trp Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr
        355                 360                 365

Gln Pro Pro Gln Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp
    370                 375                 380

Leu Thr Ile Thr Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys
385                 390                 395                 400

Gln Thr Leu Asn Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu
                405                 410                 415

Val Thr Asp Val Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly
            420                 425                 430

Pro Val Asn Gln Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys
        435                 440                 445

Val Ala Thr Gly Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly
    450                 455                 460

Val Leu Val Ser Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly
465                 470                 475                 480
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Val Leu Gln Ile Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr
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Cys Ile Ala Ser Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile
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Glu Val Gln Glu Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp
        515                 520                 525

Pro Asn Leu Ile Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val
    530                 535                 540

Ser Arg Asn Thr Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly
545                 550                 555                 560

Ala Thr Pro Thr Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly
                565                 570                 575

Ser Ser Trp Gln Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala
            580                 585                 590

Ile Lys Gly Leu Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala
        595                 600                 605

Ala Asn Ala Tyr Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val
    610                 615                 620

Lys Thr Gln Asp Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln
625                 630                 635                 640

Val Gln Arg Glu Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr
                645                 650                 655

Val Leu Ser Ser Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln
            660                 665                 670

Ser Gln Tyr Ile Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala
        675                 680                 685

Asn His Gly Glu Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala
    690                 695                 700

Lys Asn Ser Val Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu
705                 710                 715                 720

Ile Lys Ala Arg Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu
                725                 730                 735

Ile Lys Phe Ala Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln
            740                 745                 750
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Gly Val Thr Val Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val
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Ser Trp Gln Pro Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu
    770                 775                 780

Tyr Lys Val Trp Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys
785                 790                 795                 800

Thr Val Asp Gly Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro
                805                 810                 815

Gly Ile Arg Tyr Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser
            820                 825                 830

Gly Val Lys Ser Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn
        835                 840                 845

Pro Val Ser Pro Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp
    850                 855                 860

Val Val Lys Gln Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp
865                 870                 875                 880

Ile Ile Leu Met Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys
                885                 890                 895

Arg Asn Gly Leu Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Thr Tyr
            900                 905                 910

Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly Arg Pro Gly Leu Leu
        915                 920                 925

Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu Ala Asp Thr Trp Pro
    930                 935                 940

Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile Ser Cys Cys Thr Ala
945                 950                 955                 960

Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr Tyr Ser Arg Pro Ala
                965                 970                 975

Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp Asn Lys Gln Thr Asn
            980                 985                 990

Leu Met Leu Pro Glu Ser Thr Val  Tyr Gly Asp Val Asp  Leu Ser Asn
        995                 1000                1005

Lys Ile  Asn Glu Met Lys Thr  Phe Asn Ser Pro Asn  Leu Lys Asp
    1010                1015                1020
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Gly Arg  Phe Val Asn Pro Ser  Gly Gln Pro Thr Pro  Tyr Ala Thr
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Thr Gln  Leu Ile Gln Ser Asn  Leu Ser Asn Asn Met  Asn Asn Gly
    1040                1045                1050

Ser Gly  Asp Ser Gly Glu Lys  His Trp Lys Pro Leu  Gly Gln Gln
    1055                1060                1065

Lys Gln  Glu Val Ala Pro Val  Gln Tyr Asn Ile Val  Glu Gln Asn
    1070                1075                1080

Lys Leu  Asn Lys Asp Tyr Arg  Ala Asn Asp Thr Val  Pro Pro Thr
    1085                1090                1095

Ile Pro  Tyr Asn Gln Ser Tyr  Asp Gln Asn Thr Gly  Gly Ser Tyr
    1100                1105                1110

Asn Ser  Ser Asp Arg Gly Ser  Ser Thr Ser Gly Ser  Gln Gly His
    1115                1120                1125

Lys Lys  Gly Ala Arg Thr Pro  Lys Val Pro Lys Gln  Gly Gly Met
    1130                1135                1140

Asn Trp  Ala Asp Leu Leu Pro  Pro Pro Pro Ala His  Pro Pro Pro
    1145                1150                1155

His Ser  Asn Ser Glu Glu Tyr  Asn Ile Ser Val Asp  Glu Ser Tyr
    1160                1165                1170

Asp Gln  Glu Met Pro Cys Pro  Val Pro Pro Ala Arg  Met Tyr Leu
    1175                1180                1185

Gln Gln  Asp Glu Leu Glu Glu  Glu Glu Asp Glu Arg  Gly Pro Thr
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Pro Pro  Val Arg Gly Ala Ala  Ser Ser Pro Ala Ala  Val Ser Tyr
    1205                1210                1215

Ser His  Gln Ser Thr Ala Thr  Leu Thr Pro Ser Pro  Gln Glu Glu
    1220                1225                1230

Leu Gln  Pro Met Leu Gln Asp  Cys Pro Glu Glu Thr  Gly His Met
    1235                1240                1245

Gln His  Gln Pro Asp Arg Arg  Arg Gln Pro Val Ser  Pro Pro Pro
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Pro Pro  Arg Pro Ile Ser Pro  Pro His Thr Tyr Gly  Tyr Ile Ser
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Gly Pro  Leu Val Ser Asp Met  Asp Thr Asp Ala Pro  Glu Glu Glu
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Glu Asp  Glu Ala Asp Met Glu  Val Ala Lys Met Gln  Thr Arg Arg
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Leu Leu  Leu Arg Gly Leu Glu  Gln Thr Pro Ala Ser  Ser Val Gly
    1310                1315                1320

Asp Leu  Glu Ser Ser Val Thr  Gly Ser Met Ile Asn  Gly Trp Gly
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Ser Ala  Ser Glu Glu Asp Asn  Ile Ser Ser Gly Arg  Ser Ser Val
    1340                1345                1350

Ser Ser  Ser Asp Gly Ser Phe  Phe Thr Asp Ala Asp  Phe Ala Gln
    1355                1360                1365

Ala Val  Ala Ala Ala Ala Glu  Tyr Ala Gly Leu Lys  Val Ala Arg
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Arg Gln  Met Gln Asp Ala Ala  Gly Arg Arg His Phe  His Ala Ser
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Gln Cys  Pro Arg Pro Thr Ser  Pro Val Ser Thr Asp  Ser Asn Met
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Ser Ala  Ala Val Met Gln Lys  Thr Arg Pro Ala Lys  Lys Leu Lys
    1415                1420                1425

His Gln  Pro Gly His Leu Arg  Arg Glu Thr Tyr Thr  Asp Asp Leu
    1430                1435                1440

Pro Pro  Pro Pro Val Pro Pro  Pro Ala Ile Lys Ser  Pro Thr Ala
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Gln Ser  Lys Thr Gln Leu Glu  Val Arg Pro Val Val  Val Pro Lys
    1460                1465                1470

Leu Pro  Ser Met Asp Ala Arg  Thr Asp Arg Ser Ser  Asp Arg Lys
    1475                1480                1485

Gly Ser  Ser Tyr Lys Gly Arg  Glu Val Leu Asp Gly  Arg Gln Val
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Val Asp  Met Arg Thr Asn Pro  Gly Asp Pro Arg Glu  Ala Gln Glu
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Gln Gln  Asn Asp Gly Lys Gly  Arg Gly Asn Lys Ala  Ala Lys Arg
    1520                1525                1530
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Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile Leu
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Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp
1550 1555 1560

Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg
1565 1570 1575

Gln Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met
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35 40 45

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Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser
65                  70                  75                  80

His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val
                85                  90                  95

His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala
            100                 105                 110

Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val
        115                 120                 125

Ala Leu Leu Arg Asp Asp Phe Arg Gln Asn Pro Thr Asp Val Val Val
    130                 135                 140

Ala Ala Gly Glu Pro Ala Ile Leu Glu Cys Gln Pro Pro Arg Gly His
145                 150                 155                 160

Pro Glu Pro Thr Ile Tyr Trp Lys Lys Asp Lys Val Arg Ile Asp Asp
                165                 170                 175

Lys Glu Glu Arg Ile Ser Ile Arg Gly Gly Lys Leu Met Ile Ser Asn
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Thr Arg Lys Ser Asp Ala Gly Met Tyr Thr Cys Val Gly Thr Asn Met
        195                 200                 205

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

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            260                 265                 270

Lys Asp Asp Tyr Thr Leu Arg Ile Lys Lys Thr Met Ser Thr Asp Glu
        275                 280                 285

Gly Thr Tyr Met Cys Ile Ala Glu Asn Arg Val Gly Lys Met Glu Ala
    290                 295                 300

Ser Ala Thr Leu Thr Val Arg Ala Arg Pro Val Ala Pro Pro Gln Phe
305                 310                 315                 320
```

```
Val Val Arg Pro Arg Asp Gln Ile Val Ala Gln Gly Arg Thr Val Thr
                325                 330                 335

Phe Pro Cys Glu Thr Lys Gly Asn Pro Gln Pro Ala Val Phe Trp Gln
            340                 345                 350

Lys Glu Gly Ser Gln Asn Leu Leu Phe Pro Asn Gln Pro Gln Gln Pro
        355                 360                 365

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

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

Ala Gly Ser Ile Leu Ala Lys Ala Gln Leu Glu Val Thr Asp Val Leu
                405                 410                 415

Thr Asp Arg Pro Pro Pro Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr
            420                 425                 430

Leu Ala Val Asp Gly Thr Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp
        435                 440                 445

Pro Leu Pro Val Ile Ser Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly
    450                 455                 460

Arg Asp Pro Arg Ala Thr Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys
465                 470                 475                 480

Asn Leu Arg Ile Ser Asp Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser
                485                 490                 495

Ser Ser Gly Glu Thr Ser Trp Ser Ala Val Leu Asp Val Thr Glu Ser
            500                 505                 510

Gly Ala Thr Ile Ser Lys Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro
        515                 520                 525

Pro Ser Lys Pro Gln Val Thr Asp Val Thr Lys Asn Ser Val Thr Leu
    530                 535                 540

Ser Trp Gln Pro Gly Thr Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile
545                 550                 555                 560

Ile Glu Ala Phe Ser Gln Ser Val Ser Asn Ser Trp Gln Thr Val Ala
                565                 570                 575

Asn His Val Lys Thr Thr Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn
            580                 585                 590
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Thr Ile Tyr Leu Phe Met Val Arg Ala Ile Asn Pro Gln Gly Leu Ser
        595                 600                 605

Asp Pro Ser Pro Met Ser Asp Pro Val Arg Thr Gln Asp Ile Ser Pro
    610                 615                 620

Pro Ala Gln Gly Val Asp His Arg Gln Val Gln Lys Glu Leu Gly Asp
625                 630                 635                 640

Val Leu Val Arg Leu His Asn Pro Val Val Leu Thr Pro Thr Thr Val
                645                 650                 655

Gln Val Thr Trp Thr Val Asp Arg Gln Pro Gln Phe Ile Gln Gly Tyr
            660                 665                 670

Arg Val Met Tyr Arg Gln Thr Ser Gly Leu Gln Ala Thr Ser Ser Trp
        675                 680                 685

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

Asn Leu Lys Lys Gly Val Thr Tyr Glu Ile Lys Val Arg Pro Tyr Phe
705                 710                 715                 720

Asn Glu Phe Gln Gly Met Asp Ser Glu Ser Lys Thr Val Arg Thr Thr
                725                 730                 735

Glu Glu Ala Pro Ser Ala Pro Pro Gln Ser Val Thr Val Leu Thr Val
            740                 745                 750

Gly Ser Tyr Asn Ser Thr Ser Ile Ser Val Ser Trp Asp Pro Pro Pro
        755                 760                 765

Pro Asp His Gln Asn Gly Ile Ile Gln Glu Tyr Lys Ile Trp Cys Leu
    770                 775                 780

Gly Asn Glu Thr Arg Phe His Ile Asn Lys Thr Val Asp Ala Ala Ile
785                 790                 795                 800

Arg Ser Val Ile Ile Gly Gly Leu Phe Pro Gly Ile Gln Tyr Arg Val
                805                 810                 815

Glu Val Ala Ala Ser Thr Ser Ala Gly Val Gly Val Lys Ser Glu Pro
            820                 825                 830

Gln Pro Ile Ile Ile Gly Arg Arg Asn Glu Val Val Ile Thr Glu Asn
        835                 840                 845

Asn Asn Ser Ile Thr Glu Gln Ile Thr Asp Val Val Lys Gln Pro Ala
    850                 855                 860
```

```
Phe Ile Ala Gly Ile Gly Gly Ala Cys Trp Val Ile Leu Met Gly Phe
865                 870                 875                 880

Ser Ile Trp Leu Tyr Trp Arg Arg Lys Lys Arg Lys Gly Leu Ser Asn
                885                 890                 895

Tyr Ala Val Thr Phe Gln Arg Gly Asp Gly Gly Leu Met Ser Asn Gly
            900                 905                 910

Ser Arg Pro Gly Leu Leu Asn Ala Gly Asp Pro Ser Tyr Pro Trp Leu
        915                 920                 925

Ala Asp Ser Trp Pro Ala Thr Ser Leu Pro Val Asn Asn Ser Asn Ser
    930                 935                 940

Gly Pro Asn Glu Ile Gly Asn Phe Gly Arg Gly Asp Val Leu Pro Pro
945                 950                 955                 960

Val Pro Gly Gln Gly Asp Lys Thr Ala Thr Met Leu Ser Asp Gly Ala
                965                 970                 975

Ile Tyr Ser Ser Ile Asp Phe Thr Thr Lys Thr Ser Tyr Asn Ser Ser
            980                 985                 990

Ser Gln Ile Thr Gln Ala Thr Pro  Tyr Ala Thr Thr Gln  Ile Leu His
        995                 1000                1005

Ser Asn  Ser Ile His Glu Leu  Ala Val Asp Leu Pro  Asp Pro Gln
    1010                1015                1020

Trp Lys  Ser Ser Ile Gln Gln  Lys Thr Asp Leu Met  Gly Phe Gly
    1025                1030                1035

Tyr Ser  Leu Pro Asp Gln Asn  Lys Gly Asn Asn Gly  Gly Lys Gly
    1040                1045                1050

Gly Lys  Lys Lys Lys Asn Lys  Asn Ser Ser Lys Pro  Gln Lys Asn
    1055                1060                1065

Asn Gly  Ser Thr Trp Ala Asn  Val Pro Leu Pro Pro  Pro Pro Val
    1070                1075                1080

Gln Pro  Leu Pro Gly Thr Glu  Leu Glu His Tyr Ala  Val Glu Gln
    1085                1090                1095

Gln Glu  Asn Gly Tyr Asp Ser  Asp Ser Trp Cys Pro  Pro Leu Pro
    1100                1105                1110

Val Gln  Thr Tyr Leu His Gln  Gly Leu Glu Asp Glu  Leu Glu Glu
    1115                1120                1125
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Asp Asp  Asp Arg Val Pro Thr  Pro Pro Val Arg Gly  Val Ala Ser
    1130                1135                1140

Ser Pro  Ala Ile Ser Phe Gly  Gln Gln Ser Thr Ala  Thr Leu Thr
    1145                1150                1155

Pro Ser  Pro Arg Glu Glu Met  Gln Pro Met Leu Gln  Ala His Leu
    1160                1165                1170

Asp Glu  Leu Thr Arg Ala Tyr  Gln Phe Asp Ile Ala  Lys Gln Thr
    1175                1180                1185

Trp His  Ile Gln Ser Asn Asn  Gln Pro Pro Gln Pro  Pro Val Pro
    1190                1195                1200

Pro Leu  Gly Tyr Val Ser Gly  Ala Leu Ile Ser Asp  Leu Glu Thr
    1205                1210                1215

Asp Val  Ala Asp Asp Asp Ala  Asp Asp Glu Glu Glu  Ala Leu Glu
    1220                1225                1230

Ile Pro  Arg Pro Leu Arg Ala  Leu Asp Gln Thr Pro  Gly Ser Ser
    1235                1240                1245

Met Asp  Asn Leu Asp Ser Ser  Val Thr Gly Ser Met  Val Asn Gly
    1250                1255                1260

Trp Gly  Ser Ala Ser Asp Glu  Asp Arg Asn Phe Ser  Ser His Arg
    1265                1270                1275

Ser Ser  Val Gly Ser Ser Ser  Asp Gly Ser Ile Phe  Ala Ser Gly
    1280                1285                1290

Ser Phe  Ala Gln Ala Leu Val  Ala Ala Ala Asp Lys  Ala Gly Phe
    1295                1300                1305

Arg Leu  Asp Gly Thr Ser Leu  Thr Arg Thr Gly Lys  Ala Phe Thr
    1310                1315                1320

Ser Ser  Gln Arg Pro Arg Pro  Thr Ser Pro Phe Ser  Thr Asp Ser
    1325                1330                1335

Asn Thr  Ser Ala Ala Leu Ser  Gln Ser Gln Arg Pro  Arg Pro Thr
    1340                1345                1350

Lys Lys  His Lys Gly Gly Arg  Met Asp Gln Gln Pro  Ala Leu Pro
    1355                1360                1365

His Arg  Arg Glu Gly Met Thr  Asp Asp Leu Pro Pro  Pro Pro Asp
    1370                1375                1380
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Pro Pro Pro Gly Gln Gly Leu Arg Gln Gln Ile Gly Pro Ser Gln
1385 1390 1395

Gln Ala Gly Asn Val Glu Asn Ser Ala Glu Arg Lys Gly Ser Ser
1400 1405 1410

Leu Glu Arg Gln His Ala Ser Ser Leu Glu Asp Thr Lys Ser Ser
1415 1420 1425

Leu Asp Cys Pro Ala Arg Thr Ser Leu Glu Trp Gln Arg Gln Thr
1430 1435 1440

Gln Glu Trp Ile Ser Ser Thr Glu Arg Gln Glu Asp Ile Arg Lys
1445 1450 1455

Ala Pro His Lys Gln Gly Val Gly Ser Glu Glu Ala Leu Val Pro
1460 1465 1470

Tyr Ser Lys Pro Ser Phe Pro Ser Pro Gly Gly His Ser Ser Ser
1475 1480 1485

Gly Thr Ala Ser Ser Lys Gly Ser Thr Gly Pro Arg Lys Thr Glu
1490 1495 1500

Val Leu Arg Ala Gly His Gln Arg Asn Ala Ser Asp Leu Leu Asp
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Ile Gly Tyr Met Gly Ser Asn Ser Gln Gly Gln Phe Thr Gly Glu
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aaccacaccc tgctgcctcc cggcgatccc tctctcaacg ggtcaagggt aggaccggag 180

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<212> PRT
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<400> 28

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Asp Ser Leu Ala Gly Asp Ile Ser Asn Ser Ser Glu Leu Leu Leu Gly
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```
Phe Asn Ser Ser Leu Ala Ala Leu Asn His Thr Leu Leu Pro Pro Gly
        35                  40                  45

Asp Pro Ser Leu Asn Gly Ser Arg Val Gly Pro Glu Asp Ala Met Pro
    50                  55                  60

Arg Ile Val Glu Gln Pro Pro Asp Leu Leu Val Ser Arg Gly Glu Pro
65                  70                  75                  80

Ala Thr Leu Pro Cys Arg Ala Glu Gly Arg Pro Arg Pro Asn Ile Glu
                85                  90                  95

Trp Tyr Lys Asn Gly Ala Arg Val Ala Thr Val Arg Glu Asp Pro Arg
            100                 105                 110

Ala His Arg Leu Leu Leu Pro Ser Gly Ala Leu Phe Phe Pro Arg Ile
        115                 120                 125

Val His Gly Arg Arg Ala Arg Pro Asp Glu Gly Val Tyr Thr Cys Val
    130                 135                 140

Ala Arg Asn Tyr Leu Gly Ala Ala Ala Ser Arg Asn Ala Ser Leu Glu
145                 150                 155                 160

Val Ala Val Leu Arg Asp Asp Phe Arg Gln Ser Pro Gly Asn Val Val
                165                 170                 175

Val Ala Val Gly Glu Pro Ala Val Leu Glu Cys Val Pro Pro Arg Gly
            180                 185                 190

His Pro Glu Pro Ser Val Ser Trp Arg Lys Asp Gly Ala Arg Leu Lys
        195                 200                 205

Glu Glu Glu Gly Arg Ile Thr Ile Arg Gly Gly Lys Leu Met Met Ser
    210                 215                 220

His Thr Leu Lys Ser Asp Ala Gly Met Tyr Val Cys Val Ala Ser Asn
225                 230                 235                 240

Met Ala Gly Glu Arg Glu Ser Ala Ala Ala Glu Val Met Val Leu Glu
                245                 250                 255

Arg Pro Ser Phe Leu Arg Arg Pro Val Asn Gln Val Val Leu Ala Asp
            260                 265                 270

Ala Pro Val Thr Phe Leu Cys Glu Val Lys Gly Asp Pro Pro Pro Arg
        275                 280                 285

Leu Arg Trp Arg Lys Glu Asp Gly Glu Leu Pro Thr Gly Arg Tyr Glu
    290                 295                 300
```

```
Ile Arg Ser Asp His Ser Leu Trp Ile Gly His Val Ser Ala Glu Asp
305                 310                 315                 320

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

Ala Ser Gly Ser Leu Ser Val His Val Pro Pro Gln Leu Val Thr Gln
            340                 345                 350

Pro Gln Asp Gln Met Ala Ala Pro Gly Glu Ser Val Ala Phe Gln Cys
        355                 360                 365

Glu Thr Lys Gly Asn Pro Pro Pro Ala Ile Phe Trp Gln Lys Glu Gly
    370                 375                 380

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

Phe Ser Val Ser Pro Arg Gly Gln Leu Asn Ile Thr Ala Val Gln Arg
                405                 410                 415

Gly Asp Ala Gly Tyr Tyr Val Cys Gln Ala Val Ser Val Ala Gly Ser
            420                 425                 430

Ile Leu Ala Lys Ala Leu Leu Glu Ile Lys Gly Ala Ser Leu Asp Gly
        435                 440                 445

Leu Pro Pro Val Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Val Leu
    450                 455                 460

Gly Ser Ser Val Trp Leu Pro Cys Arg Val Thr Gly Asn Pro Gln Pro
465                 470                 475                 480

Ser Val Arg Trp Lys Lys Asp Gly Gln Trp Leu Gln Gly Asp Asp Leu
                485                 490                 495

Gln Phe Lys Thr Met Ala Asn Gly Thr Leu Tyr Ile Ala Asn Val Gln
            500                 505                 510

Glu Met Asp Met Gly Phe Tyr Ser Cys Val Ala Lys Ser Ser Thr Gly
        515                 520                 525

Glu Ala Thr Trp Ser Gly Trp Leu Lys Met Arg Glu Asp Trp Gly Val
    530                 535                 540

Ser Pro Asp Pro Pro Thr Glu Pro Ser Ser Pro Pro Gly Ala Pro Ser
545                 550                 555                 560

Gln Pro Val Val Thr Glu Ile Thr Lys Asn Ser Ile Thr Leu Thr Trp
                565                 570                 575
```

```
Lys Pro Asn Pro Gln Thr Gly Ala Ala Val Thr Ser Tyr Val Ile Glu
            580                 585                 590

Ala Phe Ser Pro Ala Ala Gly Asn Thr Trp Arg Thr Val Ala Asp Gly
        595                 600                 605

Val Gln Leu Glu Thr His Thr Val Ser Gly Leu Gln Pro Asn Thr Ile
    610                 615                 620

Tyr Leu Phe Leu Val Arg Ala Val Gly Ala Trp Gly Leu Ser Glu Pro
625                 630                 635                 640

Ser Pro Val Ser Glu Pro Val Arg Thr Gln Asp Ser Ser Pro Ser Arg
                645                 650                 655

Pro Val Glu Asp Pro Trp Arg Gly Gln Gln Gly Leu Ala Glu Val Ala
            660                 665                 670

Val Arg Leu Gln Glu Pro Ile Val Leu Gly Pro Arg Thr Leu Gln Val
        675                 680                 685

Ser Trp Thr Val Asp Gly Pro Val Gln Leu Val Gln Gly Phe Arg Val
    690                 695                 700

Ser Trp Arg Val Ala Gly Pro Glu Gly Gly Ser Trp Thr Met Leu Asp
705                 710                 715                 720

Leu Gln Ser Pro Ser Gln Gln Ser Thr Val Leu Arg Gly Leu Pro Pro
                725                 730                 735

Gly Thr Gln Ile Gln Ile Lys Val Gln Ala Gln Gly Gln Glu Gly Leu
            740                 745                 750

Gly Ala Glu Ser Leu Ser Val Thr Arg Ser Ile Pro Glu Glu Ala Pro
        755                 760                 765

Ser Gly Pro Pro Gln Gly Val Ala Val Ala Leu Gly Gly Asp Gly Asn
    770                 775                 780

Ser Ser Ile Thr Val Ser Trp Glu Pro Pro Leu Pro Ser Gln Gln Asn
785                 790                 795                 800

Gly Val Ile Thr Glu Tyr Gln Ile Trp Cys Leu Gly Asn Glu Ser Arg
                805                 810                 815

Phe His Leu Asn Arg Ser Ala Ala Gly Trp Ala Arg Ser Ala Met Leu
            820                 825                 830

Arg Gly Leu Val Pro Gly Leu Leu Tyr Arg Thr Leu Val Ala Ala Ala
        835                 840                 845
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Thr Ser Ala Gly Val Gly Val Pro Ser Ala Pro Val Leu Val Gln Leu
    850                 855                 860

Pro Ser Pro Pro Asp Leu Glu Pro Gly Leu Glu Val Gly Ala Gly Leu
865                 870                 875                 880

Ala Val Arg Leu Ala Arg Val Leu Arg Glu Pro Ala Phe Leu Ala Gly
                885                 890                 895

Ser Gly Ala Ala Cys Gly Ala Leu Leu Leu Gly Leu Cys Ala Ala Leu
            900                 905                 910

Tyr Trp Arg Arg Lys Gln Arg Lys Glu Leu Ser His Tyr Thr Ala Ser
        915                 920                 925

Phe Ala Tyr Thr Pro Ala Val Ser Phe Pro His Ser Glu Gly Leu Ser
    930                 935                 940

Gly Ala Ser Ser Arg Pro Pro Met Gly Leu Gly Pro Ala Pro Tyr Ser
945                 950                 955                 960

Trp Leu Ala Asp Ser Trp Pro His Pro Ser Arg Ser Pro Ser Ala Gln
                965                 970                 975

Glu Pro Arg Gly Ser Cys Cys Pro Ser Asn Pro Asp Pro Asp Asp Arg
            980                 985                 990

Tyr Tyr Asn Glu Ala Gly Ile Ser  Leu Tyr Leu Ala Gln  Thr Ala Arg
        995                 1000                1005

Gly Thr  Ala Ala Pro Gly Glu  Gly Pro Val Tyr Ser  Thr Ile Asp
    1010                1015                1020

Pro Ala  Gly Glu Glu Leu Gln  Thr Phe His Gly Gly  Phe Pro Gln
    1025                1030                1035

His Pro  Ser Gly Asp Leu Gly  Pro Trp Ser Gln Tyr  Ala Pro Pro
    1040                1045                1050

Glu Trp  Ser Gln Gly Asp Ser  Gly Ala Lys Gly Gly  Lys Val Lys
    1055                1060                1065

Leu Leu  Gly Lys Pro Val Gln  Met Pro Ser Leu Asn  Trp Pro Glu
    1070                1075                1080

Ala Leu  Pro Pro Pro Pro Pro  Ser Cys Glu Leu Ser  Cys Leu Glu
    1085                1090                1095

Gly Pro  Glu Glu Glu Leu Glu  Gly Ser Ser Glu Pro  Glu Glu Trp
    1100                1105                1110
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Cys Pro  Pro Met Pro Glu Arg  Ser His Leu Thr Glu  Pro Ser Ser
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Ser Gly  Gly Cys Leu Val Thr  Pro Ser Arg Arg Glu  Thr Pro Ser
    1130                1135                1140

Pro Thr  Pro Ser Tyr Gly Gln  Gln Ser Thr Ala Thr  Leu Thr Pro
    1145                1150                1155

Ser Pro  Pro Asp Pro Pro Gln  Pro Pro Thr Asp Met  Pro His Leu
    1160                1165                1170

His Gln  Met Pro Arg Arg Val  Pro Leu Gly Pro Ser  Ser Pro Leu
    1175                1180                1185

Ser Val  Ser Gln Pro Met Leu  Gly Ile Arg Glu Ala  Arg Pro Ala
    1190                1195                1200

Gly Leu  Gly Ala Gly Pro Ala  Ala Ser Pro His Leu  Ser Pro Ser
    1205                1210                1215

Pro Ala  Pro Ser Thr Ala Ser  Ser Ala Pro Gly Arg  Thr Trp Gln
    1220                1225                1230

Gly Asn  Gly Glu Met Thr Pro  Pro Leu Gln Gly Pro  Arg Ala Arg
    1235                1240                1245

Phe Arg  Lys Lys Pro Lys Ala  Leu Pro Tyr Arg Arg  Glu Asn Ser
    1250                1255                1260

Pro Gly  Asp Leu Pro Pro Pro  Pro Leu Pro Pro Pro  Glu Glu Glu
    1265                1270                1275

Ala Ser  Trp Ala Leu Glu Leu  Arg Ala Ala Gly Ser  Met Ser Ser
    1280                1285                1290

Leu Glu  Arg Glu Arg Ser Gly  Glu Arg Lys Ala Val  Gln Ala Val
    1295                1300                1305

Pro Leu  Ala Ala Gln Arg Val  Leu His Pro Asp Glu  Glu Ala Trp
    1310                1315                1320

Leu Pro  Tyr Ser Arg Pro Ser  Phe Leu Ser Arg Gly  Gln Gly Thr
    1325                1330                1335

Ser Thr  Cys Ser Thr Ala Gly  Ser Asn Ser Ser Arg  Gly Ser Ser
    1340                1345                1350

Ser Ser  Arg Gly Ser Arg Gly  Pro Gly Arg Ser Arg  Ser Arg Ser
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Glu Pro Arg
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tagggtgatg atataaaaag ccaccggagc actccataag gcacaaactt tcagagacag 180

cagagcacac aagct 195

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<211> 354
<212> DNA
<213> Mus musculus

<400> 30
gaagtgcagc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt acctatgcca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtaatg gtggtactta cacctactat 180

ccagacagtg tgaagggtcg attcaccatc tccagagaca atgccgagaa caccctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt atttctgtgc aagactaatc 300

tactatgatt accttgacta ctggggccac ggcaccactc tcacagtctc ctca 354

<210> 31
<211> 118
<212> PRT
<213> Mus musculus

<400> 31

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

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

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

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

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

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

Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly His Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 32
<211> 342
<212> DNA
<213> Mus musculus

<400> 32
gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 120

tacttccaga aaccaggcca gtctccacag ctcctgatct acagggtttc caaccgattt 180

tctggggtcc tagacaggtt cagtggtagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgaaga tttcggagtt tatttctgcc tccaagttac tcatgtcccg 300

tggacgttcg gtggaggcac caagctggaa atcaaacggg ct 342

<210> 33
<211> 114
<212> PRT
<213> Mus musculus

<400> 33

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Glu Asn Ser
20 25 30

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

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

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

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

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Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Ala

<210> 34
<211> 449
<212> DNA
<213> Homo sapiens

<400> 34
gcctccggac tctagagcca ccatggtgct gcagacccag gtgttcatct ccctgctgct 60

gtggatctcc ggcgcgtacg gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120

cgtgttcatc ttcccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg 180

cctgctgaat aacttctacc ccagagaggc caaggtgcag tggaaggtgg acaacgccct 240

gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300

cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360

cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420

ttaggggccc gtttaaacgg gggaggcta 449

<210> 35
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> human H-chain signal and IgG1 constant DNA

<400> 35
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120

ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 240

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 540

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 780

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 840

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1080

tccctgtctc ccggcaaatg agatatcggg cccgtttaaa cgggggaggc ta 1132

<210> 36
<211> 1118
<212> DNA
<213> Homo sapiens

<400> 36
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc cagcaccaag 120

ggcccttccg tgttccctct ggcccccttgt agccgttcca ccagcgagtc caccgccgcc 180

cttggctgtc tggtgaagga ctacttccct gagcctgtga ccgtgagctg gaactccgga 240

gcccttacca gcggcgtgca caccttccct gccgtgctgc agtccagcgg cctttactcc 300

ctgagctccg tggtgaccgt gcctagctcc aacttcggca cccaaaccta cacctgtaac 360

gtggaccaca agcctagcaa caccaaggtg gacaagaccg tggagcgtaa gtgttgtgtg 420

gagtgtcctc cttgtcctgc ccctcctgtg gccggacctt ccgtgttcct tttccctcct 480

aagcctaagg acaccctgat gatcagccgt acccctgagg tgacctgtgt ggtggtggac 540

gtgtcccacg aggaccctga ggtgcagttc aactggtacg tggacggcgt ggaggtgcac 600

aacgccaaga ccaagcctcg tgaggagcaa ttcaacagca ccttccgtgt ggtgtccgtg 660

cttaccgtgg tgcaccaaga ctggctgaac ggcaaggagt acaagtgtaa ggtgagcaac 720

aagggacttc ctgcccctat cgagaagacc atctccaaga ccaagggcca acctcgtgag 780

cctcaagtgt acacccttcc tcctagccgt gaggagatga ccaagaacca agtgtccctt 840

acctgtctgg tgaagggctt ctaccctagc gacatcgccg tggagtggga gtccaacgga 900

caacctgaga acaactacaa gaccacccct cctatgcttg acagcgacgg ctccttcttc 960

ctgtacagca agctgaccgt ggacaagtcc cgttggcaac aaggcaacgt gttcagctgt 1020

tccgtgatgc acgaggccct gcacaaccac tacacccaaa agagcctttc cctgagccct 1080

ggaaagtgat atcgggcccg tttaaacggg ggaggcta 1118

<210> 37
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> cMAb1 L chain na

<400> 37
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 120

atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 180

tacttccaga aaccaggcca gtctccacag ctcctgatct acagggtttc caaccgattt 240

tctggggtcc tagacaggtt cagtggtagt ggatcaggga cagatttcac actgaaaatc 300

agcagagtgg aggctgaaga tttcggagtt tatttctgcc tccaagttac tcatgtcccg 360

tggacgttcg gtggaggcac caagctggaa atcaaacggg ctgtggccgc cccctccgtg 420

ttcatcttcc ccccctccga cgagcagctg aagtccggca ccgcctccgt ggtgtgcctg 480

ctgaataact tctaccccag agaggccaag gtgcagtgga aggtggacaa cgccctgcag 540

tccgggaact cccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 600

agcagcaccc tgaccctgag caaagccgac tacgagaagc acaaggtgta cgcctgcgag 660

gtgacccacc agggcctgag ctcccccgtc accaagagct tcaacagggg ggagtgt 717

<210> 38
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> cMAb1 L chain aa

<400> 38

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ala Val Met Thr Gln Thr Pro Leu Ser Leu Pro
20 25 30

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

Leu Glu Asn Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Phe Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Leu Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

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

Cys Leu Gln Val Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys
115 120 125

Leu Glu Ile Lys Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

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Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 39
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> cMAb1-1 H chain na

<400> 39
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgaa 60

gtgcagctgg tggagtctgg gggaggctta gtgaagcctg gagggtccct gaaactctcc 120

tgtgcagcct ctggattcac tttcagtacc tatgccatgt cttgggttcg ccagactccg 180

gagaagaggc tggagtgggt cgcaaccatt agtaatggtg gtacttacac ctactatcca 240

gacagtgtga agggtcgatt caccatctcc agagacaatg ccgagaacac cctgtacctg 300

caaatgagca gtctgaggtc tgaggacacg gccatgtatt tctgtgcaag actaatctac 360

tatgattacc ttgactactg gggccacggc accactctca cagtcagctc agcctccacc 420

aagggcccaa gcgtcttccc cctggcaccc tcctccaaga gcacctctgg cggcacagcc 480

gccctgggct gcctggtcaa ggactacttc cccgaacccg tgaccgtgag ctggaactca 540

ggcgccctga ccagcggcgt gcacaccttc cccgctgtcc tgcagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660

aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt 720

gacaaaactc acacatgccc accctgccca gcacctgaac tcctgggggg accctcagtc 780

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 900

ggcgtggagg tgcataatgc caagacaaag ccccgggagg agcagtacaa cagcacgtac 960

cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080

ggccagcccc gggaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1140

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200

tgggagagca atggccagcc cgagaacaac tacaagacca cccctcccgt gctggactcc 1260

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggc 1320

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac ccagaagagc 1380

ctctccctgt ctcccggcaa a 1401

<210> 40
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> cMAb1-1 H chain aa

<400> 40

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Phe Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
115 120 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

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

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 41
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> cMAb1-2 H chain na

<400> 41
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgaa 60

gtgcagctgg tggagtctgg gggaggctta gtgaagcctg gagggtccct gaaactctcc 120

tgtgcagcct ctggattcac tttcagtacc tatgccatgt cttgggttcg ccagactccg 180

gagaagaggc tggagtgggt cgcaaccatt agtaatggtg gtacttacac ctactatcca 240

gacagtgtga agggtcgatt caccatctcc agagacaatg ccgagaacac cctgtacctg 300

caaatgagca gtctgaggtc tgaggacacg gccatgtatt tctgtgcaag actaatctac 360

tatgattacc ttgactactg gggccacggc accactctca cagtcagctc agccagcacc 420

aagggccctt ccgtgttccc tctggccct tgtagccgtt ccaccagcga gtccaccgcc 480

gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540

ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600

tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660

aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720

gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtaccctg aggtgacctg tgtggtggtg 840

gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggaggtg 900

cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960

gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc 1020

aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080

gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140

cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200

ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260

ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320

tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380

cctggaaag 1389

<210> 42
<211> 463

<212> PRT
<213> Artificial Sequence

<220>
<223> cMAb1-2 H chain aa

<400> 42

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
    50                  55                  60

Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Thr Tyr Thr Tyr Tyr Pro
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
            100                 105                 110

Tyr Phe Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
        115                 120                 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
225                 230                 235                 240
```

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Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

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

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
                405                 410                 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460


<210>  43
<211>  15
<212>  DNA
<213>  Mus musculus

<400>  43
acctatgcca tgtct                                                    15


<210>  44
<211>  5
<212>  PRT
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<213> Mus musculus

<400> 44

Thr Tyr Ala Met Ser
1 5

<210> 45
<211> 51
<212> DNA
<213> Mus musculus

<400> 45
accattagta atggtggtac ttacacctac tatccagaca gtgtgaaggg t 51

<210> 46
<211> 17
<212> PRT
<213> Mus musculus

<400> 46

Thr Ile Ser Asn Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 47
<211> 27
<212> DNA
<213> Mus musculus

<400> 47
ctaatctact atgattacct tgactac 27

<210> 48
<211> 9
<212> PRT
<213> Mus musculus

<400> 48

Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr
1 5

<210> 49
<211> 48
<212> DNA
<213> Mus musculus

<400> 49
aggtctagtc agagccttga aaacagtaat ggaaacacct atttgaac 48

<210> 50
<211> 16
<212> PRT
<213> Mus musculus

<400> 50

Arg Ser Ser Gln Ser Leu Glu Asn Ser Asn Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 51
<211> 21
<212> DNA
<213> Mus musculus

<400> 51
agggtttcca accgattttc t 21

<210> 52
<211> 7
<212> PRT
<213> Mus musculus

<400> 52

Arg Val Ser Asn Arg Phe Ser
1 5

<210> 53
<211> 27
<212> DNA
<213> Mus musculus

<400> 53
ctccaagtta ctcatgtccc gtggacg 27

<210> 54
<211> 9
<212> PRT
<213> Mus musculus

<400> 54

Leu Gln Val Thr His Val Pro Trp Thr
1 5

<210> 55
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T1H

<400> 55
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gtgcagctgg tggaaagcgg cggaggcctg gtgcagcctg gcggctctct gagactgagc 120

tgtgccgcca gcggcttcac cttcagcacc tacgccatga gctgggtccg acaggccct 180

ggcaagggac tggaatgggt ggcaaccatc agcaacggcg gcacctacac ctactacccc 240

gacagcgtga agggccggtt caccatcagc cgggacaacg ccaagaacac cctgtacctg 300

cagatgaaca gcctgcgggc cgaggacacc gccgtgtact actgcgccag actgatctac 360

tacgactacc tggactactg gggccagggc accctggtca ccgtcagctc agccagcacc 420

aagggccctt ccgtgttccc tctggccct tgtagccgtt ccaccagcga gtccaccgcc 480

gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540

ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600

tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660

aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720

gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtaccccctg aggtgacctg tgtggtggtg 840

gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggaggtg 900

cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960

gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc 1020

aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080

gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140

cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200

ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260

ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320

tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380

cctggaaag 1389

<210> 56
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> hMAb1-T1H aa

<400> 56

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

```
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
        115                 120                 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

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

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350

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

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Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 57
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T2H na

<400> 57
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60

gtgcagctgg tggaaagcgg cggaggcctg gtgcagcctg gcggctctct gagactgagc 120

tgtgccgcca gcggcttcac cttcagcacc tacgccatga gctgggtccg acaggcccct 180

ggcaagggac tggaatgggt ggcaaccatc agccaaggcg gcacctacac ctactacccc 240

gacagcgtga agggccggtt caccatcagc cgggacaacg ccaagaacac cctgtacctg 300

cagatgaaca gcctgcgggc cgaggacacc gccgtgtact actgcgccag actgatctac 360

tacgactacc tggactactg gggccagggc accctggtca ccgtcagctc agccagcacc 420

aagggccctt ccgtgttccc tctggccccc tgtagccgtt ccaccagcga gtccaccgcc 480

gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540

ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600

tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660

aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720

gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtacccctg aggtgacctg tgtggtggtg 840

gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggaggtg 900

cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960

gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc 1020

aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080

gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140

cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200

ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260

ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320

tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380

cctggaaag 1389

<210> 58
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> hMAb1-T2H aa

<400> 58

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Gln Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
115 120 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

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

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
                405                 410                 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
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His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 59
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T3H na

<400> 59
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60

gtgcagctgg tggaaagcgg cggaggcctg gtgcagcctg gcggctctct gagactgagc 120

tgtgccgcca gcggcttcac cttcagcacc tacgccatga gctgggtccg acaggcccct 180

ggcaagcggc tggaatgggt ggcaaccatc agcaacggcg gcacctacac ctactacccc 240

gacagcgtga agggccggtt caccatcagc cgggacaacg ccaagaacac cctgtacctg 300

cagatgaaca gcctgcgggc cgaggacacc gccgtgtact actgcgccag actgatctac 360

tacgactacc tggactactg gggccagggc accctggtca ccgtcagctc agccagcacc 420

aagggccctt ccgtgttccc tctggccccc tgtagccgtt ccaccagcga gtccaccgcc 480

gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540

ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600

tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660

aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720

gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtacccctg aggtgacctg tgtggtggtg 840

gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggaggtg 900

cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960

gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc 1020

aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080

gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140

cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200

ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260

ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320

tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380

cctggaaag 1389

<210> 60
<211> 463
<212> PRT
<213> Artificial Sequence

<220>

<223> hMAb1-T3H aa

<400> 60

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu
    50                  55                  60

Glu Trp Val Ala Thr Ile Ser Asn Gly Gly Thr Tyr Thr Tyr Tyr Pro
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
        115                 120                 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

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

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 61
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T4H na

<400> 61
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gtgcagctgg tggaaagcgg cggaggcctg gtgcagcctg gcggctctct gagactgagc 120

tgtgccgcca gcggcttcac cttcagcacc tacgccatga gctgggtccg acaggcccct 180

ggcaagcggc tggaatgggt ggcaaccatc agccaaggcg gcacctacac ctactacccc 240

gacagcgtga agggccggtt caccatcagc cgggacaacg ccaagaacac cctgtacctg 300

cagatgaaca gcctgcgggc cgaggacacc gccgtgtact actgcgccag actgatctac 360

tacgactacc tggactactg gggccagggc accctggtca ccgtcagctc agccagcacc 420

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gcccttggct gtctggtgaa ggactacttc cctgagcctg tgaccgtgag ctggaactcc 540

ggagccctta ccagcggcgt gcacaccttc cctgccgtgc tgcagtccag cggcctttac 600

tccctgagct ccgtggtgac cgtgcctagc tccaacttcg gcacccaaac ctacacctgt 660

aacgtggacc acaagcctag caacaccaag gtggacaaga ccgtggagcg taagtgttgt 720

gtggagtgtc ctccttgtcc tgcccctcct gtggccggac cttccgtgtt ccttttccct 780

cctaagccta aggacaccct gatgatcagc cgtacccctg aggtgacctg tgtggtggtg 840

gacgtgtccc acgaggaccc tgaggtgcag ttcaactggt acgtggacgg cgtggaggtg 900

cacaacgcca agaccaagcc tcgtgaggag caattcaaca gcaccttccg tgtggtgtcc 960

gtgcttaccg tggtgcacca agactggctg aacggcaagg agtacaagtg taaggtgagc 1020

aacaagggac ttcctgcccc tatcgagaag accatctcca agaccaaggg ccaacctcgt 1080

gagcctcaag tgtacaccct tcctcctagc cgtgaggaga tgaccaagaa ccaagtgtcc 1140

cttacctgtc tggtgaaggg cttctaccct agcgacatcg ccgtggagtg ggagtccaac 1200

ggacaacctg agaacaacta caagaccacc cctcctatgc ttgacagcga cggctccttc 1260

ttcctgtaca gcaagctgac cgtggacaag tcccgttggc aacaaggcaa cgtgttcagc 1320

tgttccgtga tgcacgaggc cctgcacaac cactacaccc aaaagagcct ttccctgagc 1380

cctggaaag 1389

<210> 62
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> hMAb1-T4H aa

<400> 62

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu
50 55 60

```
Glu Trp Val Ala Thr Ile Ser Gln Gly Gly Thr Tyr Thr Tyr Tyr Pro
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Leu Ile Tyr Tyr Asp Tyr Leu Asp Tyr Trp Gly
        115                 120                 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

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

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
```

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Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 63
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T1L na

<400> 63
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gacatcgtga tgacccagag ccccctgagc ctgcccgtga cactgggcga gcctgccagc 120

atcagctgca gaagcagcca gagcctggaa aacagcaacg gcaacaccta cctgaactgg 180

tatctgcaga agcccggcca gtcccccccag ctgctgatct accgggtgtc caaccggttc 240

agcggcgtgc ccgacagatt cagcggcagc ggctccggca ccgacttcac cctgaagatc 300

agccgggtgg aagccgagga cgtgggcgtg tactactgtc tgcaggtcac acacgtgccc 360

tggaccttcg gccctggcac caaggtggac atcaagcgta cggtggccgc cccctccgtg 420

ttcatcttcc ccccctccga cgagcagctg aagtccggca ccgcctccgt ggtgtgcctg 480

ctgaataact tctaccccag agaggccaag gtgcagtgga aggtggacaa cgccctgcag 540

tccgggaact cccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 600

agcagcaccc tgaccctgag caaagccgac tacgagaagc acaaggtgta cgcctgcgag 660

gtgacccacc agggcctgag ctcccccgtc accaagagct tcaacagggg ggagtgt 717

<210> 64
<211> 239

<212> PRT
<213> Artificial Sequence

<220>
<223> hMAb1-T1L aa

<400> 64

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30

Val Thr Leu Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

Leu Glu Asn Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys
    50                  55                  60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe
65                  70                  75                  80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

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

Cys Leu Gln Val Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 65
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> hMAb1-T2L na

<400> 65
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gacatcgtga tgacccagag ccccctgagc ctgcccgtga cactgggcga gcctgccagc 120

atcagctgca gaagcagcca gagcctggaa aacgagaaca agaacctgta cctgaactgg 180

tatctgcaga agcccggcca gtcccccag ctgctgatct accgggtgtc caaccggttc 240

agcggcgtgc ccgacagatt cagcggcagc ggctccggca ccgacttcac cctgaagatc 300

agccgggtgg aagccgagga cgtgggcgtg tactactgtc tgcaggtcac acacgtgccc 360

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Val Thr Leu Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

Leu Glu Asn Glu Asn Lys Asn Leu Tyr Leu Asn Trp Tyr Leu Gln Lys
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Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

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

Cys Leu Gln Val Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
115 120 125

Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
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Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
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Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
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