SEQUENCE LISTING

<110> BIOGEN IDEC MA INC.
Arnett, et al.

<120> ONCOSTATIN M RECEPTOR ANTIGEN BINDING PROTEINS

<130> 01017/47340

<160> 46

<170> PatentIn version 3.5

<210> 1
<211> 979
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<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human OSMR

<400> 1

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Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
            20                  25                  30

Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Thr Arg Gln Ser Leu
        35                  40                  45

His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
    50                  55                  60

Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Ile
65                  70                  75                  80

Trp Val Gly Asn Tyr Ser Thr Thr Val Lys Trp Asn Gln Val Leu His
                85                  90                  95

Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
            100                 105                 110

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

Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Ser Thr
    130                 135                 140

Gly Gln Asp Ile Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145                 150                 155                 160

Gly Thr Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn
                165                 170                 175
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Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
180 185 190

Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
195 200 205

Lys Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Glu
210 215 220

Gly Met Lys Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225 230 235 240

Lys Asp Phe Ser Cys Glu Thr Glu Asp Phe Lys Thr Leu His Cys Thr
245 250 255

Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
260 265 270

Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
275 280 285

Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
290 295 300

Thr Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305 310 315 320

Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
325 330 335

Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
340 345 350

Trp Lys Val His Ser Ile Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
355 360 365

Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asn Val Ser Ile Lys
370 375 380

Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385 390 395 400

Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Ser
405 410 415

Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
420 425 430

Ala Pro Asp Val Trp Arg Ile Val Ser Leu Glu Pro Gly Asn His Thr
435 440 445

Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys

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     450                 455                 460

Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Ser
465                 470                 475                 480

Ser Glu Leu His Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
                485                 490                 495

Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Ile Ala Asn Asn Ser Val
            500                 505                 510

Gly Ala Ser Pro Ala Ser Val Ile Val Ile Ser Ala Asp Pro Glu Asn
        515                 520                 525

Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
    530                 535                 540

Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545                 550                 555                 560

Trp Cys Asp His Thr Gln Asp Val Leu Gly Asp Phe Gln Trp Lys Asn
                565                 570                 575

Val Gly Pro Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg
            580                 585                 590

Pro Gly Val Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg
        595                 600                 605

Ile Ala Cys Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala
    610                 615                 620

Pro Ser Asp Asn Pro His Val Leu Val Asp Thr Leu Thr Ser His Ser
625                 630                 635                 640

Phe Thr Leu Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe
                645                 650                 655

Ile Gln Gly Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His
            660                 665                 670

Pro Arg Phe Glu Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Lys
        675                 680                 685

Tyr Lys Ile Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu
    690                 695                 700

Lys Pro Glu Ser Phe Tyr Glu Phe Phe Ile Thr Pro Phe Thr Ser Ala
705                 710                 715                 720

Gly Glu Gly Pro Ser Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu
                725                 730                 735
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His Ser Ser Met Leu Ile His Ile Leu Leu Pro Met Val Phe Cys Val
            740                 745                 750

Leu Leu Ile Met Val Met Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu
        755                 760                 765

Thr Cys Tyr Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser
    770                 775                 780

Leu Ile Lys Phe Lys Glu Asn Pro His Leu Ile Ile Met Asn Val Ser
785                 790                 795                 800

Asp Cys Ile Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr
                805                 810                 815

Lys Ile Gln Phe Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu
            820                 825                 830

Thr Lys Pro Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser
        835                 840                 845

Gly Pro Gly Pro Cys Ile Cys Phe Glu Asn Leu Thr Tyr Asn Gln Ala
    850                 855                 860

Ala Ser Asp Ser Gly Ser Cys Gly His Val Pro Val Ser Pro Lys Ala
865                 870                 875                 880

Pro Ser Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala
                885                 890                 895

Leu Glu Lys Asn Tyr Met Asn Ser Leu Gly Glu Ile Pro Ala Gly Glu
            900                 905                 910

Thr Ser Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Phe Gly Asp
        915                 920                 925

Lys Asp Ser Leu Pro Thr Asn Pro Val Glu Ala Pro His Cys Ser Glu
    930                 935                 940

Tyr Lys Met Gln Met Ala Val Ser Leu Arg Leu Ala Leu Pro Pro Pro
945                 950                 955                 960

Thr Glu Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu
                965                 970                 975

His Tyr Cys
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<210> 2
<211> 977
<212> PRT

<213> Macaca fascicularis

<220>
<221> MISC_FEATURE
<223> Cynomolgus monkey OSMR

<400> 2

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Met Ala Leu Phe Val Val Phe Gln Thr Thr Phe Phe Leu Ile Leu Leu
1               5                  10                  15

Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
            20                  25                  30

Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Ile His Gln Ser Leu
        35                  40                  45

His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
    50                  55                  60

Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Val
65                  70                  75                  80

Trp Val Gly Asn Tyr Ser Thr Pro Val Lys Trp Asn Gln Val Leu His
                85                  90                  95

Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
            100                 105                 110

Arg Ile Lys Ser Val Ile Asp Asp Ala Ser Phe Pro Glu Pro Asn Phe
        115                 120                 125

Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Tyr Leu
    130                 135                 140

Gly Arg Gly Thr Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145                 150                 155                 160

Gly Ser Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn
                165                 170                 175

Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
            180                 185                 190

Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
        195                 200                 205

Arg Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Lys
    210                 215                 220

Gly Ile Glu Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225                 230                 235                 240
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Lys Asp Phe Ser Cys Glu Ser Gln Asp Phe Lys Thr Leu His Cys Thr
                245                 250                 255

Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
            260                 265                 270

Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
        275                 280                 285

Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
    290                 295                 300

Met Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305                 310                 315                 320

Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
                325                 330                 335

Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
            340                 345                 350

Trp Lys Val His Ser Met Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
        355                 360                 365

Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asp Val Ser Ile Asn
    370                 375                 380

Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385                 390                 395                 400

Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Thr
                405                 410                 415

Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
            420                 425                 430

Ala Pro Asp Val Trp Arg Ser Val Asn Ser Glu Pro Gly Asn His Thr
        435                 440                 445

Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys
    450                 455                 460

Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Arg
465                 470                 475                 480

Ser Glu Leu Arg Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
                485                 490                 495

Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Thr Ala Asn Asn Ser Val
            500                 505                 510

Gly Ala Ser Pro Ala Ser Ile Ile Val Ile Ser Ala Asp Pro Glu Asn
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515 520 525

Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
530 535 540

Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545 550 555 560

Trp Cys Asp His Pro Gln Asp Val Leu Gln Trp Lys Asn Val Gly Pro
565 570 575

Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg Pro Gly Val
580 585 590

Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg Ile Ala Cys
595 600 605

Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp
610 615 620

Asn Pro His Val Leu Val Asp Met Leu Thr Ser His Ser Phe Thr Leu
625 630 635 640

Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly
645 650 655

Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His Pro Arg Phe
660 665 670

Gln Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Arg Tyr Lys Ile
675 680 685

Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu Lys Pro Glu
690 695 700

Ser Phe Tyr Glu Phe Phe Val Thr Pro Phe Thr Ser Ala Gly Glu Gly
705 710 715 720

Pro Asn Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu His Ser Ser
725 730 735

Met Leu Ile Arg Ile Leu Leu Pro Met Val Phe Cys Val Leu Leu Ile
740 745 750

Met Ile Val Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu Thr Cys Tyr
755 760 765

Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser Leu Ile Lys
770 775 780

Phe Lys Glu Asn Pro His Leu Thr Ile Met Asn Val Ser Asp Cys Ile
785 790 795 800

Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr Lys Ile Gln
805 810 815

Leu Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu Thr Lys Pro
820 825 830

Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser Gly Pro Gly
835 840 845

Pro Cys Ile Cys Phe Glu Asn Phe Thr Tyr Asn Gln Ala Ala Ser Asp
850 855 860

Ala Gly Ser Cys Gly His Val Pro Val Pro Pro Lys Ala Pro Pro Ser
865 870 875 880

Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala Leu Glu
885 890 895

Lys Asn Tyr Met Asn Ser Leu Gly Glu Val Pro Ala Gly Glu Thr Ser
900 905 910

Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Ser Gly Asp Lys Asp
915 920 925

Ser Leu Pro Thr Asn Pro Val Glu Pro Pro His Cys Ser Glu Tyr Lys
930 935 940

Met Gln Met Ala Val Pro Leu Arg Leu Ala Leu Pro Pro Pro Thr Glu
945 950 955 960

Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu His Tyr
965 970 975

Arg

<210> 3
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab1 Heavy chain

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actggacagg ggcttgagtg gatgggatgg atgaacccta atagtggtaa cacagactat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca tttccataag cacggcctac 240

attgagctga gcagcctgag atctgaggac acggccgttt attactgtgc gagagatatg 300

gtggctgcga atacggatta ctacttctac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

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tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 4
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab2 Heavy chain

<400> 4
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tcctgcaagg cttctggata caccttcacc agttatgaaa tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtggtta cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggaaatga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatata 300

gtggctgcga atacggatta ctacttctat tatggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

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gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

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<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab3 Heavy chain

<400> 5
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tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ctcagcactt acagtggtaa cacaaactat 180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240

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agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 600

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tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 900

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag 1020

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gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

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tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

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ctgtctccgg gtaaa 1335

<210> 6
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Heavy chain

<400> 6

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

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

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

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
        195                 200                 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 7
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Heavy chain

<400> 7

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

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

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
195 200 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
    450
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<210> 8
<211> 445
<212> PRT

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Heavy chain

<400> 8

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

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

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

Gly Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

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

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

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

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

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140

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

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

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

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225                 230                 235                 240
```

```
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

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

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300

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

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

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


<210>  9
<211>  126
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Ab1 Heavy chain variable region

<400>  9

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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```
            20                  25                  30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

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

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
            100                 105                 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  10
<211>  126
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Ab2 Heavy chain variable region

<400>  10

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

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

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

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

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

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

Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
            100                 105                 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
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<210> 11
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Heavy chain variable region

<400> 11

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

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

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

Gly Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

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

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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 12
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Heavy chain CDR1

<400> 12

Ser Tyr Asp Ile Asn
1 5

<210> 13
<211> 5
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<223> Ab2 Heavy chain CDR1

<400> 13

Ser Tyr Glu Ile Asn
1 5

<210> 14
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Heavy chain CDR1

<400> 14

Ser Tyr Gly Ile Ser
1 5

<210> 15
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Heavy chain CDR2

<400> 15

Trp Met Asn Pro Asn Ser Gly Asn Thr Asp Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 16
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Heavy chain CDR2

<400> 16

Trp Met Gly Trp Met Asn Pro Asn Ser Gly Tyr Thr Gly Tyr Ala Gln
1 5 10 15

Lys Phe Gln Gly
20

<210> 17
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Heavy chain CDR2

<400> 17

Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 18
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Heavy chain CD3

<400> 18

Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 19
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Heavy chain CDR3

<400> 19

Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 20
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Heavy chain CDR3

<400> 20

Gly Asn Phe Tyr Tyr Tyr Gly Met Asp Val

1 5 10

<210> 21
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab1 Light chain

<400> 21
cagtctgtgc tgactcagcc accctcagca tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacgtcgga agtaatactg taagctggta ccaacagctc 120

ccaggaacgg cccccaaact cctcatctat actaataatc ggcggccctc cggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta tttctgtgca gcgttagatg acagtctgaa tggtgtggta 300

ttcggcggag ggaccaaact gaccgtccta ggccaaccga aagcggcgcc ctcggtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 22
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab2 Light chain

<400> 22
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcaactc caacatcgga agtaatactg tcaactggta ccaccagctc 120

ccaggaacgg cccccaaact cctcatctat aatattaata agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggctcc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgttca acatgggatg acagcctgga tggtgtggta 300

ttcggcggag ggaccaagct gaccgtccta ggccaaccga aagcggcgcc ctcggtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 23
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ab3 Light chain

<400> 23
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatcttt ggtgcttcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcgcctcc gatcaccttc 300

ggccaaggga cacgactgga gattaaacgt acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 648

<210> 24
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Light chain

<400> 24

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

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

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

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

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

Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ala Ala Leu Asp Asp Ser Leu

```
                85                  90                  95

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

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  25
<211>  216
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Ab2 Light chain

<400>  25

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

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

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

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

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

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

```
Asp Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  26
<211>  216
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Ab3 light chain

<400>  26

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

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

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

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

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 27
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Light chain variable

<400> 27

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

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

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

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

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

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

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

<210> 28
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Light chain variable

<400> 28

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

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

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

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

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

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

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

<210> 29
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Light chain variable

<400> 29

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

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

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

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

<210> 30
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Light chain CDR1

<400> 30

Ser Gly Ser Ser Ser Asn Val Gly Ser Asn Thr Val Ser
1 5 10

<210> 31
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Light chain CDR1

<400> 31

Ser Gly Ser Asn Ser Asn Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 32
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Light chain CDR1

<400> 32

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 33
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Light chain CDR2

<400> 33

Thr Asn Asn Arg Arg Pro Ser
1 5

<210> 34
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Light chain CDR2

<400> 34

Asn Ile Asn Lys Arg Pro Ser
1 5

<210> 35
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Light chain CDR2

<400> 35

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 36
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab1 Light chain CDR3

<400> 36

Ala Ala Leu Asp Asp Ser Leu Asn Gly Val Val
1 5 10

<210> 37
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab2 Light chain CDR3

<400> 37

Ser Thr Trp Asp Asp Ser Leu Asp Gly Val Val
1 5 10

<210> 38
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Ab3 Light chain CDR3

<400> 38

Gln Gln Tyr Gly Ser Ser Pro Pro Ile Thr
1 5 10

<210> 39
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human OSM

<400> 39

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

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Ala Ile Gly Ser Cys Ser
20 25 30

Lys Glu Tyr Arg Val Leu Leu Gly Gln Leu Gln Lys Gln Thr Asp Leu
35 40 45

Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile Arg Ile Gln Gly
50 55 60

Leu Asp Val Pro Lys Leu Arg Glu His Cys Arg Glu Arg Pro Gly Ala
65 70 75 80

Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg Arg Gly Phe Leu
85 90 95

Gln Thr Leu Asn Ala Thr Leu Gly Cys Val Leu His Arg Leu Ala Asp
100 105 110

Leu Glu Gln Arg Leu Pro Lys Ala Gln Asp Leu Glu Arg Ser Gly Leu
115 120 125

Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg Pro Asn Ile Leu
130 135 140

```
Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu Leu Asp Asn Ser
145                 150                 155                 160

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

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

Arg Phe Leu His Gly Tyr His Arg Phe Met His Ser Val Gly Arg Val
        195                 200                 205

Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro
    210                 215                 220

His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg Pro Ser Arg Lys
225                 230                 235                 240

Gly Lys Arg Leu Met Thr Arg Gly Gln Leu Pro Arg
                245                 250
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<210> 40
<211> 196
<212> PRT
<213> Macaca fascicularis

<220>
<221> MISC_FEATURE
<223> Cynomolgus monkey OSM protein

<400> 40

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Ala Ala Met Gly Ser Cys Ser Lys Glu Tyr Arg Met Leu Leu Gly Gln
1               5                   10                  15

Leu Gln Lys Gln Thr Asp Leu Met Gln Asp Thr Ser Arg Leu Leu Asp
            20                  25                  30

Pro Tyr Ile Arg Ile Gln Gly Leu Asp Ile Pro Lys Leu Arg Glu His
        35                  40                  45

Cys Arg Glu Ser Pro Gly Ala Phe Pro Ser Glu Glu Thr Leu Arg Gly
    50                  55                  60

Leu Gly Arg Arg Gly Phe Leu Gln Thr Leu Asn Ala Thr Leu Gly Arg
65                  70                  75                  80

Ile Leu His Arg Leu Ala Asp Leu Glu Gln His Leu Pro Lys Ala Gln
                85                  90                  95

Asp Leu Glu Arg Ser Gly Leu Asn Ile Glu Asp Leu Glu Lys Leu Gln
            100                 105                 110

Met Ala Arg Pro Asn Val Leu Gly Leu Arg Asn Asn Val Tyr Cys Met
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115 120 125

Ala Gln Leu Leu Asp Asn Ser Asp Met Thr Glu Pro Thr Lys Ala Gly
130 135 140

Arg Gly Thr Pro Gln Pro Pro Thr Pro Thr Pro Thr Ser Asp Val Phe
145 150 155 160

Gln Arg Lys Leu Glu Gly Cys Ser Phe Leu Arg Gly Tyr His Arg Phe
165 170 175

Met His Ser Val Gly Arg Val Phe Ser Lys Trp Gly Glu Ser Pro Asn
180 185 190

Arg Ser Arg Arg
195

<210> 41
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human IL-31

<400> 41

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

Cys Leu Gly Gly Trp Leu Ala Ser His Thr Leu Pro Val Arg Leu Leu
20 25 30

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

Ser Lys Met Leu Leu Lys Asp Val Glu Glu Glu Lys Gly Val Leu Val
50 55 60

Ser Gln Asn Tyr Thr Leu Pro Cys Leu Ser Pro Asp Ala Gln Pro Pro
65 70 75 80

Asn Asn Ile His Ser Pro Ala Ile Arg Ala Tyr Leu Lys Thr Ile Arg
85 90 95

Gln Leu Asp Asn Lys Ser Val Ile Asp Glu Ile Ile Glu His Leu Asp
100 105 110

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

Asp Thr His Glu Cys Lys Arg Phe Ile Leu Thr Ile Ser Gln Gln Phe
130 135 140

Ser Glu Cys Met Asp Leu Ala Leu Lys Ser Leu Thr Ser Gly Ala Gln
145 150 155 160

Gln Ala Thr Thr

<210> 42
<211> 138
<212> PRT
<213> Macaca fascicularis

<220>
<221> MISC_FEATURE
<223> Cynomolgus monkey IL-31

<400> 42

Thr Leu Pro Val His Phe Leu Gln Pro Ser Asp Ile Gln Lys Ile Val
1 5 10 15

Glu Glu Leu Gln Ser Leu Ser Lys Met Leu Leu Lys Asp Val Lys Glu
20 25 30

Asp Lys Gly Val Leu Val Ser Gln Asn Tyr Thr Leu Pro Cys Leu Thr
35 40 45

Pro Asp Ala Gln Pro Pro Asn Ile Ile His Ser Pro Ala Ile Arg Ala
50 55 60

Tyr Leu Lys Thr Ile Arg Gln Leu Asp Asn Lys Ser Val Ile Asp Glu
65 70 75 80

Ile Ile Glu His Leu Asp Lys Leu Ile Phe Gln Asp Ala Pro Glu Thr
85 90 95

Asn Ile Ser Val Pro Thr Asp Thr His Glu Cys Lys Arg Phe Ile Leu
100 105 110

Thr Ile Ser Gln Gln Phe Ser Glu Cys Met Asp Leu Ala Leu Lys Ser
115 120 125

Leu Thr Ser Gly Ala Gln Gln Ala Thr Thr
130 135

<210> 43
<211> 662
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human IL-31RA

<400> 43

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Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
1               5                  10                  15

Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
            20                  25                  30

Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45

Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60

Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80

Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95

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

Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125

Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140

Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160

Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175

Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190

Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205

Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220

Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
225                 230                 235                 240

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

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

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

Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
    290                 295                 300

His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
305                 310                 315                 320

Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
                325                 330                 335

Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
            340                 345                 350

Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
        355                 360                 365

Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
    370                 375                 380

Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
385                 390                 395                 400

Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
                405                 410                 415

Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
            420                 425                 430

Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
        435                 440                 445

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

Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
465                 470                 475                 480

Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
                485                 490                 495

Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser
            500                 505                 510

Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
        515                 520                 525

Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
    530                 535                 540

Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
```

545 550 555 560

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

Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
580 585 590

Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
595 600 605

Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
610 615 620

Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
625 630 635 640

Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser
645 650 655

Ser Cys Pro Thr Ser Ile
660

<210> 44
<211> 649
<212> PRT
<213> Macaca fascicularis

<220>
<221> misc_feature
<223> Cynomolgus monkey IL-21RA

<400> 44

Met Met Trp Thr Trp Ala Leu Trp Met Phe Pro Leu Leu Cys Lys Phe
1 5 10 15

Gly Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
20 25 30

Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
35 40 45

Ser Tyr Thr Gln Tyr Thr Ala Lys Arg Thr Tyr Ala Phe Gly Lys Lys
50 55 60

His Asp Asn Cys Thr Thr Ser Ser Ser Thr Ser Glu Asn Arg Ala Ser
65 70 75 80

Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
85 90 95

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser Asp Met Thr
100 105 110

```
Cys Trp Arg Leu Glu Asp Ile Ala Lys Thr Glu Pro Pro Glu Ile Phe
        115                 120                 125

Ser Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Arg Ile Glu Trp
    130                 135                 140

Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Ala Leu
145                 150                 155                 160

Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
                165                 170                 175

Lys Asn Arg Lys Asp Thr Asn Gln Thr Tyr Asn Leu Met Gly Leu Gln
            180                 185                 190

Ala Phe Thr Glu Tyr Val Val Ala Leu Arg Cys Ala Val Lys Glu Ser
        195                 200                 205

Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
    210                 215                 220

Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Thr Glu
225                 230                 235                 240

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

Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Phe Pro
            260                 265                 270

Glu Asn Asn Thr Asn Leu Thr Glu Thr Val Asn Thr Thr Asn Gln Gln
        275                 280                 285

Leu Glu Leu His Leu Gly Gly Glu Ser Tyr Trp Val Ser Met Ile Ser
    290                 295                 300

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

Ile Gln Glu Lys Ser Phe Arg Cys Ile Glu Val Met Gln Ala Cys Leu
                325                 330                 335

Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
            340                 345                 350

Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Met Asp Ser Glu His Pro
        355                 360                 365

Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
    370                 375                 380
```

```
Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
385                 390                 395                 400

Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
                405                 410                 415

Lys Glu Gly Ile Pro Ser Lys Gly Pro Glu Thr Lys Val Glu Asn Ile
            420                 425                 430

Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
        435                 440                 445

Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
    450                 455                 460

Gly Thr Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
465                 470                 475                 480

Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Thr Val Arg Val Met Ala
                485                 490                 495

Ser Thr Ser Ala Gly Gly Ile Asn Gly Thr Ser Ile Asn Phe Lys Thr
            500                 505                 510

Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
        515                 520                 525

Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
    530                 535                 540

Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Ser Val Pro Asn Pro
545                 550                 555                 560

Ala Glu Ser Ser Ile Ala Thr Trp Arg Gly Asp Asp Phe Lys Asp Lys
                565                 570                 575

Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
            580                 585                 590

Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Ser
        595                 600                 605

Val Val Asn Phe Gly Asn Val Leu Gln Glu Met Phe Thr Asp Glu Ala
    610                 615                 620

Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Glu Asn Arg
625                 630                 635                 640

Ile Leu Ser Ser Cys Pro Thr Ser Ile
                645
```

<210> 45
<211> 918
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human gp130

<400> 45

Met Leu Thr Leu Gln Thr Trp Leu Val Gln Ala Leu Phe Ile Phe Leu
1 5 10 15

Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
20 25 30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
85 90 95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100 105 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115 120 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
130 135 140

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145 150 155 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
165 170 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
180 185 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
195 200 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
210 215 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu

```
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335

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

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400

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

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460

Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480

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

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510
```

```
Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
    610                 615                 620

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625                 630                 635                 640

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
                645                 650                 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
            660                 665                 670

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Ser Asn Phe
        675                 680                 685

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

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705                 710                 715                 720

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
                725                 730                 735

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
            740                 745                 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
        755                 760                 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
    770                 775                 780
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Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785 790 795 800

His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys
805 810 815

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
865 870 875 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala
885 890 895

Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
900 905 910

Gly Gly Tyr Met Pro Gln
915

<210> 46
<211> 918
<212> PRT
<213> Macaca fascicularis

<220>
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<223> Cynomolgus monkey gp130

<400> 46

Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
1 5 10 15

Thr Thr Glu Ser Ile Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
20 25 30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80

```
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ser Ser
                85                  90                  95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
            100                 105                 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140

Glu Trp Asn Arg Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Arg Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Cys Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Asn Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335

Asp Pro Ser His Ala Gln Gly Tyr Arg Thr Val Gln Leu Met Trp Lys
            340                 345                 350

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
```

```
        355                 360                 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Asp
    370                 375                 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Val Ala Thr Leu
385                 390                 395                 400

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

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460

Pro Cys Ile Ala Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480

His Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
                485                 490                 495

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
    610                 615                 620

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625                 630                 635                 640
```

```
Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
                645                 650                 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
            660                 665                 670

Arg His Asn Phe Ser Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
        675                 680                 685

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

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705                 710                 715                 720

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
                725                 730                 735

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
            740                 745                 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
        755                 760                 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
    770                 775                 780

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785                 790                 795                 800

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

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
            820                 825                 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
        835                 840                 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Glu
    850                 855                 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Pro Phe Gly Pro Gly
865                 870                 875                 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Ile Gly Met Glu Ala Ala
                885                 890                 895

Ile Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
            900                 905                 910
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Gly Gly Tyr Met Pro Gln
915

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<140> PCT/US2014/040360
<141> 2014-05-30

<150> 61/829,082
<151> 2013-05-30

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<213> Homo sapiens

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Met Ala Leu Phe Ala Val Phe Gln Thr Thr Phe Phe Leu Thr Leu Leu
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Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
20 25 30

Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Thr Arg Gln Ser Leu
35 40 45

His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
50 55 60

Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Ile
65 70 75 80

Trp Val Gly Asn Tyr Ser Thr Thr Val Lys Trp Asn Gln Val Leu His
85 90 95

Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
100 105 110

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

Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Ser Thr
130 135 140

Gly Gln Asp Ile Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145 150 155 160

Gly Thr Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn

165 170 175

Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
180 185 190

Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
195 200 205

Lys Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Glu
210 215 220

Gly Met Lys Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225 230 235 240

Lys Asp Phe Ser Cys Glu Thr Glu Asp Phe Lys Thr Leu His Cys Thr
245 250 255

Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
260 265 270

Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
275 280 285

Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
290 295 300

Thr Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305 310 315 320

Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
325 330 335

Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
340 345 350

Trp Lys Val His Ser Ile Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
355 360 365

Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asn Val Ser Ile Lys
370 375 380

Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385 390 395 400

Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Ser
405 410 415

Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
420 425 430

Ala Pro Asp Val Trp Arg Ile Val Ser Leu Glu Pro Gly Asn His Thr
435 440 445

```
Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys
    450                 455                 460

Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Ser
465                 470                 475                 480

Ser Glu Leu His Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
                485                 490                 495

Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Ile Ala Asn Asn Ser Val
            500                 505                 510

Gly Ala Ser Pro Ala Ser Val Ile Val Ile Ser Ala Asp Pro Glu Asn
        515                 520                 525

Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
    530                 535                 540

Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545                 550                 555                 560

Trp Cys Asp His Thr Gln Asp Val Leu Gly Asp Phe Gln Trp Lys Asn
                565                 570                 575

Val Gly Pro Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg
            580                 585                 590

Pro Gly Val Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg
        595                 600                 605

Ile Ala Cys Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala
    610                 615                 620

Pro Ser Asp Asn Pro His Val Leu Val Asp Thr Leu Thr Ser His Ser
625                 630                 635                 640

Phe Thr Leu Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe
                645                 650                 655

Ile Gln Gly Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His
            660                 665                 670

Pro Arg Phe Glu Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Lys
        675                 680                 685

Tyr Lys Ile Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu
    690                 695                 700

Lys Pro Glu Ser Phe Tyr Glu Phe Phe Ile Thr Pro Phe Thr Ser Ala
705                 710                 715                 720
```

```
Gly Glu Gly Pro Ser Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu
                725                 730                 735

His Ser Ser Met Leu Ile His Ile Leu Leu Pro Met Val Phe Cys Val
            740                 745                 750

Leu Leu Ile Met Val Met Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu
        755                 760                 765

Thr Cys Tyr Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser
    770                 775                 780

Leu Ile Lys Phe Lys Glu Asn Pro His Leu Ile Ile Met Asn Val Ser
785                 790                 795                 800

Asp Cys Ile Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr
                805                 810                 815

Lys Ile Gln Phe Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu
            820                 825                 830

Thr Lys Pro Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser
        835                 840                 845

Gly Pro Gly Pro Cys Ile Cys Phe Glu Asn Leu Thr Tyr Asn Gln Ala
    850                 855                 860

Ala Ser Asp Ser Gly Ser Cys Gly His Val Pro Val Ser Pro Lys Ala
865                 870                 875                 880

Pro Ser Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala
                885                 890                 895

Leu Glu Lys Asn Tyr Met Asn Ser Leu Gly Glu Ile Pro Ala Gly Glu
            900                 905                 910

Thr Ser Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Phe Gly Asp
        915                 920                 925

Lys Asp Ser Leu Pro Thr Asn Pro Val Glu Ala Pro His Cys Ser Glu
    930                 935                 940

Tyr Lys Met Gln Met Ala Val Ser Leu Arg Leu Ala Leu Pro Pro Pro
945                 950                 955                 960

Thr Glu Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu
                965                 970                 975

His Tyr Cys
```

<210> 2
<211> 977
<212> PRT
<213> Macaca fascicularis

<220>
<221> source
<223> /note="Cynomolgus monkey OSMR"

<400> 2
Met Ala Leu Phe Val Val Phe Gln Thr Thr Phe Phe Leu Ile Leu Leu
1 5 10 15

Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
20 25 30

Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Ile His Gln Ser Leu
35 40 45

His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
50 55 60

Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Val
65 70 75 80

Trp Val Gly Asn Tyr Ser Thr Pro Val Lys Trp Asn Gln Val Leu His
85 90 95

Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
100 105 110

Arg Ile Lys Ser Val Ile Asp Asp Ala Ser Phe Pro Glu Pro Asn Phe
115 120 125

Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Tyr Leu
130 135 140

Gly Arg Gly Thr Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145 150 155 160

Gly Ser Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn
165 170 175

Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
180 185 190

Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
195 200 205

Arg Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Lys
210 215 220

Gly Ile Glu Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225 230 235 240

```
Lys Asp Phe Ser Cys Glu Ser Gln Asp Phe Lys Thr Leu His Cys Thr
                245                 250                 255

Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
            260                 265                 270

Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
        275                 280                 285

Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
    290                 295                 300

Met Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305                 310                 315                 320

Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
                325                 330                 335

Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
            340                 345                 350

Trp Lys Val His Ser Met Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
        355                 360                 365

Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asp Val Ser Ile Asn
    370                 375                 380

Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385                 390                 395                 400

Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Thr
                405                 410                 415

Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
            420                 425                 430

Ala Pro Asp Val Trp Arg Ser Val Asn Ser Glu Pro Gly Asn His Thr
        435                 440                 445

Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys
    450                 455                 460

Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Arg
465                 470                 475                 480

Ser Glu Leu Arg Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
                485                 490                 495

Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Thr Ala Asn Asn Ser Val
            500                 505                 510
```

Gly Ala Ser Pro Ala Ser Ile Ile Val Ile Ser Ala Asp Pro Glu Asn
515 520 525

Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
530 535 540

Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545 550 555 560

Trp Cys Asp His Pro Gln Asp Val Leu Gln Trp Lys Asn Val Gly Pro
565 570 575

Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg Pro Gly Val
580 585 590

Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg Ile Ala Cys
595 600 605

Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp
610 615 620

Asn Pro His Val Leu Val Asp Met Leu Thr Ser His Ser Phe Thr Leu
625 630 635 640

Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly
645 650 655

Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His Pro Arg Phe
660 665 670

Gln Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Arg Tyr Lys Ile
675 680 685

Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu Lys Pro Glu
690 695 700

Ser Phe Tyr Glu Phe Phe Val Thr Pro Phe Thr Ser Ala Gly Glu Gly
705 710 715 720

Pro Asn Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu His Ser Ser
725 730 735

Met Leu Ile Arg Ile Leu Leu Pro Met Val Phe Cys Val Leu Leu Ile
740 745 750

Met Ile Val Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu Thr Cys Tyr
755 760 765

Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser Leu Ile Lys
770 775 780

Phe Lys Glu Asn Pro His Leu Thr Ile Met Asn Val Ser Asp Cys Ile

785 790 795 800

Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr Lys Ile Gln
805 810 815

Leu Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu Thr Lys Pro
820 825 830

Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser Gly Pro Gly
835 840 845

Pro Cys Ile Cys Phe Glu Asn Phe Thr Tyr Asn Gln Ala Ala Ser Asp
850 855 860

Ala Gly Ser Cys Gly His Val Pro Val Pro Pro Lys Ala Pro Pro Ser
865 870 875 880

Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala Leu Glu
885 890 895

Lys Asn Tyr Met Asn Ser Leu Gly Glu Val Pro Ala Gly Glu Thr Ser
900 905 910

Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Ser Gly Asp Lys Asp
915 920 925

Ser Leu Pro Thr Asn Pro Val Glu Pro Pro His Cys Ser Glu Tyr Lys
930 935 940

Met Gln Met Ala Val Pro Leu Arg Leu Ala Leu Pro Pro Pro Thr Glu
945 950 955 960

Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu His Tyr
965 970 975

Arg

<210> 3
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain"

<400> 3
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcaactgggt gcgacaggcc 120

actggacagg ggcttgagtg gatgggatgg atgaacccta atagtggtaa cacagactat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca tttccataag cacggcctac 240

attgagctga gcagcctgag atctgaggac acggccgttt attactgtgc gagagatatg 300

gtggctgcga atacggatta ctacttctac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 4
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain"

<400> 4
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgaaa tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtggtta cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggaaatga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatata 300

gtggctgcga atacggatta ctacttctat tatggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 5
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain"

<400> 5
caggttcatc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ctcagcactt acagtggtaa cacaaactat 180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagggaac 300

ttctactact acggtatgga cgtctggggc caggggacca cggtcaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa 660

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 900

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtaaa 1335

<210> 6
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain"

<400> 6
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

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

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
        195                 200                 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
```

450

<210> 7
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain"

<400> 7
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

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

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
195 200 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 8
<211> 445
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain"

<400> 8
Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

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

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

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

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

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

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

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

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

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

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

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225 230 235 240

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

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

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300

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

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

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


<210> 9
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain variable region"

<400> 9
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Asp Tyr Ala Gln Lys Phe
    50                  55                  60
```

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 10
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain variable region"

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

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

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

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

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

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

Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 11
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain variable region"

<400> 11

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

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

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

Gly Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

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

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

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

Thr Thr Val Thr Val Ser Ser
        115


<210> 12
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain CDR1"

<400> 12
Ser Tyr Asp Ile Asn
1               5


<210> 13
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain CDR1"

<400> 13
Ser Tyr Glu Ile Asn
1               5


<210> 14
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain CDR1"
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<400> 14
Ser Tyr Gly Ile Ser
1 5

<210> 15
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain CDR2"

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

Gly

<210> 16
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain CDR2"

<400> 16
Trp Met Gly Trp Met Asn Pro Asn Ser Gly Tyr Thr Gly Tyr Ala Gln
1 5 10 15

Lys Phe Gln Gly
20

<210> 17
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain CDR2"

<400> 17
Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 18
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Heavy chain CDR3"

<400> 18

Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 19
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Heavy chain CDR3"

<400> 19
Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 20
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Heavy chain CDR3"

<400> 20
Gly Asn Phe Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 21
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain"

<400> 21
cagtctgtgc tgactcagcc accctcagca tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacgtcgga agtaatactg taagctggta ccaacagctc 120

ccaggaacgg cccccaaact cctcatctat actaataatc ggcggccctc cggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta tttctgtgca gcgttagatg acagtctgaa tggtgtggta 300

ttcggcggag ggaccaaact gaccgtccta ggccaaccga aagcggcgcc ctcggtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 22
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain"

<400> 22
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcaactc caacatcgga agtaatactg tcaactggta ccaccagctc 120

ccaggaacgg cccccaaact cctcatctat aatattaata agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggctcc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgttca acatgggatg acagcctgga tggtgtggta 300

ttcggcggag ggaccaagct gaccgtccta ggccaaccga aagcggcgcc ctcggtcact 360

ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420

agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480

gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540

tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600

catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttca 648

<210> 23
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Light chain"

<400> 23
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatcttt ggtgcttcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcgcctcc gatcaccttc 300

ggccaaggga cacgactgga gattaaacgt acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 648

<210> 24
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain"

<400> 24
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 25
<211> 216

<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain"

<400> 25
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 26
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 light chain"

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

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

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 27
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain variable"

<400> 27
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

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

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

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

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

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

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

<210> 28
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain variable"

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

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

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

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

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

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

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

<210> 29

<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Light chain variable"

<400> 29
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

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

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

<210> 30
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain CDR1"

<400> 30
Ser Gly Ser Ser Ser Asn Val Gly Ser Asn Thr Val Ser
1 5 10

<210> 31
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain CDR1"

<400> 31
Ser Gly Ser Asn Ser Asn Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 32
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Light chain CDR1"

<400> 32
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1   5   10

<210> 33
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain CDR2"

<400> 33
Thr Asn Asn Arg Arg Pro Ser
1   5

<210> 34
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain CDR2"

<400> 34
Asn Ile Asn Lys Arg Pro Ser
1   5

<210> 35
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Light chain CDR2"

<400> 35
Gly Ala Ser Ser Arg Ala Thr
1   5

<210> 36
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab1 Light chain CDR3"

<400> 36
Ala Ala Leu Asp Asp Ser Leu Asn Gly Val Val
1   5   10

<210> 37
<211> 11
<212> PRT

<213> Homo sapiens

<220>
<221> source
<223> /note="Ab2 Light chain CDR3"

<400> 37
Ser Thr Trp Asp Asp Ser Leu Asp Gly Val Val
1 5 10

<210> 38
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Ab3 Light chain CDR3"

<400> 38
Gln Gln Tyr Gly Ser Ser Pro Pro Ile Thr
1 5 10

<210> 39
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Human OSM"

<400> 39
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Ala Ile Gly Ser Cys Ser
20 25 30

Lys Glu Tyr Arg Val Leu Leu Gly Gln Leu Gln Lys Gln Thr Asp Leu
35 40 45

Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile Arg Ile Gln Gly
50 55 60

Leu Asp Val Pro Lys Leu Arg Glu His Cys Arg Glu Arg Pro Gly Ala
65 70 75 80

Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg Arg Gly Phe Leu
85 90 95

Gln Thr Leu Asn Ala Thr Leu Gly Cys Val Leu His Arg Leu Ala Asp
100 105 110

Leu Glu Gln Arg Leu Pro Lys Ala Gln Asp Leu Glu Arg Ser Gly Leu
115 120 125

Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg Pro Asn Ile Leu
130 135 140

```
Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu Leu Asp Asn Ser
145                 150                 155                 160

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

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

Arg Phe Leu His Gly Tyr His Arg Phe Met His Ser Val Gly Arg Val
        195                 200                 205

Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro
    210                 215                 220

His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg Pro Ser Arg Lys
225                 230                 235                 240

Gly Lys Arg Leu Met Thr Arg Gly Gln Leu Pro Arg
                245                 250
```

<210> 40
<211> 196
<212> PRT
<213> Macaca fascicularis

<220>
<221> source
<223> /note="Cynomolgus monkey OSM protein"

<400> 40

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Ala Ala Met Gly Ser Cys Ser Lys Glu Tyr Arg Met Leu Leu Gly Gln
1               5                   10                  15

Leu Gln Lys Gln Thr Asp Leu Met Gln Asp Thr Ser Arg Leu Leu Asp
            20                  25                  30

Pro Tyr Ile Arg Ile Gln Gly Leu Asp Ile Pro Lys Leu Arg Glu His
        35                  40                  45

Cys Arg Glu Ser Pro Gly Ala Phe Pro Ser Glu Glu Thr Leu Arg Gly
    50                  55                  60

Leu Gly Arg Arg Gly Phe Leu Gln Thr Leu Asn Ala Thr Leu Gly Arg
65                  70                  75                  80

Ile Leu His Arg Leu Ala Asp Leu Glu Gln His Leu Pro Lys Ala Gln
                85                  90                  95

Asp Leu Glu Arg Ser Gly Leu Asn Ile Glu Asp Leu Glu Lys Leu Gln
            100                 105                 110

Met Ala Arg Pro Asn Val Leu Gly Leu Arg Asn Asn Val Tyr Cys Met
```

115 120 125

Ala Gln Leu Leu Asp Asn Ser Asp Met Thr Glu Pro Thr Lys Ala Gly
130 135 140

Arg Gly Thr Pro Gln Pro Pro Thr Pro Thr Pro Thr Ser Asp Val Phe
145 150 155 160

Gln Arg Lys Leu Glu Gly Cys Ser Phe Leu Arg Gly Tyr His Arg Phe
165 170 175

Met His Ser Val Gly Arg Val Phe Ser Lys Trp Gly Glu Ser Pro Asn
180 185 190

Arg Ser Arg Arg
195

<210> 41
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Human IL-31"

<400> 41
Met Ala Ser His Ser Gly Pro Ser Thr Ser Val Leu Phe Leu Phe Cys
1 5 10 15

Cys Leu Gly Gly Trp Leu Ala Ser His Thr Leu Pro Val Arg Leu Leu
20 25 30

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

Ser Lys Met Leu Leu Lys Asp Val Glu Glu Glu Lys Gly Val Leu Val
50 55 60

Ser Gln Asn Tyr Thr Leu Pro Cys Leu Ser Pro Asp Ala Gln Pro Pro
65 70 75 80

Asn Asn Ile His Ser Pro Ala Ile Arg Ala Tyr Leu Lys Thr Ile Arg
85 90 95

Gln Leu Asp Asn Lys Ser Val Ile Asp Glu Ile Ile Glu His Leu Asp
100 105 110

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

Asp Thr His Glu Cys Lys Arg Phe Ile Leu Thr Ile Ser Gln Gln Phe
130 135 140

Ser Glu Cys Met Asp Leu Ala Leu Lys Ser Leu Thr Ser Gly Ala Gln
145 150 155 160

Gln Ala Thr Thr

<210> 42
<211> 138
<212> PRT
<213> Macaca fascicularis

<220>
<221> source
<223> /note="Cynomolgus monkey IL-31"

<400> 42
Thr Leu Pro Val His Phe Leu Gln Pro Ser Asp Ile Gln Lys Ile Val
1 5 10 15

Glu Glu Leu Gln Ser Leu Ser Lys Met Leu Leu Lys Asp Val Lys Glu
20 25 30

Asp Lys Gly Val Leu Val Ser Gln Asn Tyr Thr Leu Pro Cys Leu Thr
35 40 45

Pro Asp Ala Gln Pro Pro Asn Ile Ile His Ser Pro Ala Ile Arg Ala
50 55 60

Tyr Leu Lys Thr Ile Arg Gln Leu Asp Asn Lys Ser Val Ile Asp Glu
65 70 75 80

Ile Ile Glu His Leu Asp Lys Leu Ile Phe Gln Asp Ala Pro Glu Thr
85 90 95

Asn Ile Ser Val Pro Thr Asp Thr His Glu Cys Lys Arg Phe Ile Leu
100 105 110

Thr Ile Ser Gln Gln Phe Ser Glu Cys Met Asp Leu Ala Leu Lys Ser
115 120 125

Leu Thr Ser Gly Ala Gln Gln Ala Thr Thr
130 135

<210> 43
<211> 662
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Human IL-31RA"

<400> 43
Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
1 5 10 15

Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala

```
            20                  25                  30

Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45

Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60

Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80

Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95

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

Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125

Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140

Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160

Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175

Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190

Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205

Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220

Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
225                 230                 235                 240

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

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

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

Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
    290                 295                 300
```

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His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
305                 310                 315                 320

Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
                325                 330                 335

Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
            340                 345                 350

Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
        355                 360                 365

Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
    370                 375                 380

Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
385                 390                 395                 400

Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
                405                 410                 415

Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
            420                 425                 430

Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
        435                 440                 445

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

Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
465                 470                 475                 480

Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
                485                 490                 495

Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser
            500                 505                 510

Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
        515                 520                 525

Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
    530                 535                 540

Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
545                 550                 555                 560

Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
                565                 570                 575
```

Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
580 585 590

Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
595 600 605

Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
610 615 620

Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
625 630 635 640

Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser
645 650 655

Ser Cys Pro Thr Ser Ile
660

<210> 44
<211> 649
<212> PRT
<213> Macaca fascicularis

<220>
<221> source
<223> /note="Cynomolgus monkey IL-21RA"

<400> 44
Met Met Trp Thr Trp Ala Leu Trp Met Phe Pro Leu Leu Cys Lys Phe
1 5 10 15

Gly Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
20 25 30

Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
35 40 45

Ser Tyr Thr Gln Tyr Thr Ala Lys Arg Thr Tyr Ala Phe Gly Lys Lys
50 55 60

His Asp Asn Cys Thr Thr Ser Ser Ser Thr Ser Glu Asn Arg Ala Ser
65 70 75 80

Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
85 90 95

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser Asp Met Thr
100 105 110

Cys Trp Arg Leu Glu Asp Ile Ala Lys Thr Glu Pro Pro Glu Ile Phe
115 120 125

Ser Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Arg Ile Glu Trp
130 135 140

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Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Ala Leu
145                 150                 155                 160

Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
                165                 170                 175

Lys Asn Arg Lys Asp Thr Asn Gln Thr Tyr Asn Leu Met Gly Leu Gln
            180                 185                 190

Ala Phe Thr Glu Tyr Val Val Ala Leu Arg Cys Ala Val Lys Glu Ser
        195                 200                 205

Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
    210                 215                 220

Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Thr Glu
225                 230                 235                 240

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

Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Phe Pro
            260                 265                 270

Glu Asn Asn Thr Asn Leu Thr Glu Thr Val Asn Thr Thr Asn Gln Gln
        275                 280                 285

Leu Glu Leu His Leu Gly Gly Glu Ser Tyr Trp Val Ser Met Ile Ser
    290                 295                 300

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

Ile Gln Glu Lys Ser Phe Arg Cys Ile Glu Val Met Gln Ala Cys Leu
                325                 330                 335

Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
            340                 345                 350

Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Met Asp Ser Glu His Pro
        355                 360                 365

Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
    370                 375                 380

Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
385                 390                 395                 400

Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
                405                 410                 415
```

Lys Glu Gly Ile Pro Ser Lys Gly Pro Glu Thr Lys Val Glu Asn Ile
420 425 430

Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
435 440 445

Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
450 455 460

Gly Thr Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
465 470 475 480

Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Thr Val Arg Val Met Ala
485 490 495

Ser Thr Ser Ala Gly Gly Ile Asn Gly Thr Ser Ile Asn Phe Lys Thr
500 505 510

Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
515 520 525

Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
530 535 540

Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Ser Val Pro Asn Pro
545 550 555 560

Ala Glu Ser Ser Ile Ala Thr Trp Arg Gly Asp Asp Phe Lys Asp Lys
565 570 575

Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
580 585 590

Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Ser
595 600 605

Val Val Asn Phe Gly Asn Val Leu Gln Glu Met Phe Thr Asp Glu Ala
610 615 620

Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Glu Asn Arg
625 630 635 640

Ile Leu Ser Ser Cys Pro Thr Ser Ile
645

<210> 45
<211> 918
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Human gp130"

<400> 45

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Met Leu Thr Leu Gln Thr Trp Leu Val Gln Ala Leu Phe Ile Phe Leu
1               5                  10                  15

Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
            20                  25                  30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
        35                  40                  45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
    50                  55                  60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65                  70                  75                  80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
                85                  90                  95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
            100                 105                 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270
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Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335

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

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400

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

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460

Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480

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

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540
```

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Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
    610                 615                 620

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625                 630                 635                 640

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
                645                 650                 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
            660                 665                 670

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Ser Asn Phe
        675                 680                 685

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

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705                 710                 715                 720

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
                725                 730                 735

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
            740                 745                 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
        755                 760                 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
    770                 775                 780

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785                 790                 795                 800

His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys
                805                 810                 815

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
```

820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
865 870 875 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala
885 890 895

Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
900 905 910

Gly Gly Tyr Met Pro Gln
915

<210> 46
<211> 918
<212> PRT
<213> Macaca fascicularis

<220>
<221> source
<223> /note="Cynomolgus monkey gp130"

<400> 46
Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
1 5 10 15

Thr Thr Glu Ser Ile Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
20 25 30

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ser Ser
85 90 95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100 105 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115 120 125

```
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140

Glu Trp Asn Arg Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Arg Leu Lys
                245                 250                 255

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Cys Cys Met Lys Glu
    290                 295                 300

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Asn Gly Ile
305                 310                 315                 320

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335

Asp Pro Ser His Ala Gln Gly Tyr Arg Thr Val Gln Leu Met Trp Lys
            340                 345                 350

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Asp
    370                 375                 380

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Val Ala Thr Leu
385                 390                 395                 400

Thr Ala Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
```

405 410 415

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
420 425 430

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
435 440 445

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
450 455 460

Pro Cys Ile Ala Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465 470 475 480

His Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
485 490 495

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
500 505 510

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
515 520 525

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
530 535 540

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545 550 555 560

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
565 570 575

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
580 585 590

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
595 600 605

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
610 615 620

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625 630 635 640

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
645 650 655

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
660 665 670

Arg His Asn Phe Ser Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
675 680 685

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

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705 710 715 720

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
725 730 735

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
740 745 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
755 760 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
770 775 780

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785 790 795 800

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

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Glu
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Pro Phe Gly Pro Gly
865 870 875 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Ile Gly Met Glu Ala Ala
885 890 895

Ile Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
900 905 910

Gly Gly Tyr Met Pro Gln
915

<210> 47
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 47
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcaactgggt gcgacaggcc 120

actggacagg ggcttgagtg gatgggatgg atgaacccta atagtggtaa cacagactat 180

gcacagaagt tccagggcag agtcaccatg accagggaca tttccataag cacggcctac 240

attgagctga gcagcctgag atctgaggac acggccgttt attactgtgc gagagatatg 300

gtggctgcga atacggatta ctacttctac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccct ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggt 1353

<210> 48
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 48
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgaaa tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtggtta cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accagggaca cctccataag cacagcctac 240

atggaaatga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatata 300

gtggctgcga atacggatta ctacttctat tatggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcagc tagcaccaag ggcccatcgg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gctctgacca gcggcgtgca caccttccca 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagacag ttgagcgcaa atgttgtgtc gagtgcccac cgtgcccagc accacctgtg 720

gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacgtgcgt ggtggtggac gtgagccacg aagaccccga ggtccagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccacg ggaggagcag 900

ttcaacagca cgttccgtgt ggtcagcgtc ctcaccgttg tgcaccagga ctggctgaac 960

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cagccccat cgagaaaacc 1020

atctccaaaa ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacacct 1200

cccatgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggt 1353

<210> 49
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 49
caggttcatc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ctcagcactt acagtggtaa cacaaactat 180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagggaac 300

ttctactact acggtatgga cgtctggggc caggggacca cggtcaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa 660

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 900

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gt 1332

<210> 50
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 50
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser

```
        115                 120                 125

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
        195                 200                 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly
450

<210> 51
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 51
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

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

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

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

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

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

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
        195                 200                 205

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

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly
450

<210> 52
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 52
Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Leu Ser Thr Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

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

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

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

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

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

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

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

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

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

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

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300

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

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440


<210> 53
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 53
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Asp Met Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 54
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 54
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

```
Ala Arg Asp Ile Val Ala Ala Asn Thr Asp Tyr Tyr Phe Tyr Tyr Gly
            100                 105                 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
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