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<110> iCell Gene Therapeutics LLC

<120> Chimeric Antigen Receptors (CARs), Compositions and Methods of Use

<130> 2541-3 PCT

<140> 0000000
<141> 2016-06-24

<150> 62/184,321
<151> 2015-06-25

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<170> PatentIn version 3.5

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

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

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Val
100 105 110

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Arg Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Val Val
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Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
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Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
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Leu Asp Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Asp Tyr
        195                 200                 205

Asp Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Thr Ser Thr
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Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Glu Lys Asp Asn Tyr Ala Thr Gly Ala Trp
                245                 250                 255

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
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Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

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

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

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg
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Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
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Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
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Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
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Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
465                 470                 475                 480

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
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Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
            500                 505                 510

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
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Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
    530                 535                 540

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg
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Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
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Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
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Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
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Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
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Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
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Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
                645                 650                 655

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
            660                 665                 670

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
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Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
    690                 695                 700
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Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu
            740                 745                 750

Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys
        755                 760                 765

Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
    770                 775                 780

Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
785                 790                 795                 800

Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
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Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
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actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg      240

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tgaccagcga caccagcaca agcaccgcct acatggagct gtccagcctg aggtccgagg      720

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Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

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

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145                 150                 155                 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
                165                 170                 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
            180                 185                 190

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

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
    210                 215                 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225                 230                 235                 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270
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Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
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Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
                325                 330                 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
            340                 345                 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
        355                 360                 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
    370                 375                 380

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

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
                405                 410                 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

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

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
                485                 490                 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
            500                 505                 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
        515                 520                 525

Arg Pro Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser
    530                 535                 540
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Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser
545                 550                 555                 560

Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp
                565                 570                 575

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

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

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro
    610                 615                 620

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
                645                 650                 655

Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser
            660                 665                 670

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val
        675                 680                 685

Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro
    690                 695                 700

Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr
705                 710                 715                 720

Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser
                725                 730                 735

Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Tyr
            740                 745                 750

Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr Thr Val
        755                 760                 765

Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
    770                 775                 780

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
785                 790                 795                 800

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
                805                 810                 815
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Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
            820                 825                 830

Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu
        835                 840                 845

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
    850                 855                 860

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
865                 870                 875                 880

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
                885                 890                 895

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            900                 905                 910

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        915                 920                 925

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    930                 935                 940

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
945                 950                 955                 960

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
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agcagaaacc agatggaact gttaaactcc tgatctacca tacatcaaga ttacactcag      240

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Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
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Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
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Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
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Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln
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Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

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Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser
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Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp
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Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp
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Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe
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Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys
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Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg
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Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
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Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
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565 570 575

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580 585 590

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
595 600 605

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610 615 620

Phe Gln Gly Ser Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val
625 630 635 640

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
645 650 655

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
660 665 670

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Glu Phe Ser

675 680 685

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

Trp Val Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Ser Gly
705 710 715 720

Lys Phe Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr
725 730 735

Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
740 745 750

Tyr Cys Ala Arg Asp Gly Ser Ser Trp Asp Trp Tyr Phe Asp Val Trp
755 760 765

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
770 775 780

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
785 790 795 800

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
805 810 815

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
835 840 845

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
850 855 860

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
865 870 875 880

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
885 890 895

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
900 905 910

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
915 920 925

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
930 935 940

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr

945 950 955 960

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
965 970 975

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
980 985 990

Leu His Met Gln Ala Leu Pro Pro Arg
995 1000

<210> 6
<211> 3016
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 6
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60

ccgccaggcc ggacatccag atgacacaga ctacatcctc cctgtctgcc tctctgggag 120

acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc 180

agcagaaacc agatggaact gttaaactcc tgatctacca tacatcaaga ttacactcag 240

gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca 300

acctggagca agaagatatt gccacttact tttgccaaca gggtaatacg cttccgtaca 360

cgttcggagg ggggaccaag ctggagatca caggtggcgg tggctcgggc ggtggtgggt 420

cgggtggcgg cggatctgag gtgaaactgc aggagtcagg acctggcctg gtggcgccct 480

cacagagcct gtccgtcaca tgcactgtct caggggtctc attacccgac tatggtgtaa 540

gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg 600

aaaccacata ctataattca gctctcaaat ccagactgac catcatcaag gacaactcca 660

agagccaagt tttcttaaaa atgaacagtc tgcaaactga tgacacagcc atttactact 720

gtgccaaaca ttattactac ggtggtagct atgctatgga ctactggggc caaggaacct 780

cagtcaccgt ctcctcaacc acgacgccag cgccgcgacc accaacaccg gcgcccacca 840

tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag 900

tgcacacgag ggggctggac ttcgcctgtg atatctacat ctgggcgccc ttggccggga 960

cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg ggcagaaaga 1020

aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag 1080

atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt 1140

tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc tataacgagc 1200

tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg 1260

agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga 1320

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 1380

aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc tacgacgccc 1440

ttcacatgca ggccctgccc cctcgcggaa gcggagccac caacttcagc ctgctgaagc 1500

aggccggcga cgtggaggag aaccccggcc ccatggcctt accagtgacc gccttgctcc 1560

tgccgctggc cttgctgctc cacgccgcca ggccggatat ccagatgacc cagagcccca 1620

gctccctgtc cgcatccgtg ggcgacagag tgacaattac ctgtagaagc agccaaagca 1680

tcgtgcatag cgtcggcaac acttttctgg agtggtatca acagaagccc gggaaggccc 1740

ccaaactgct gatctacaag gtgagcaaca gattcagcgg ggtcccaagc agattctccg 1800

gcagcggctc cgggactgac ttcaccctga ccattagcag cctgcagcca gaggacttcg 1860

ccacatacta ctgcttccaa gggagccagt tcccctacac cttcggccaa ggcactaagg 1920

tggagatcaa agggggggga ggaagcggcg gaggagggag cggaggcggg ggatccgaag 1980

tgcaactggt cgaatccgga ggggggctgg tccagcctgg agggtccctg agactgagct 2040

gcgccgcaag cggctacgag ttctccaggt cctggatgaa ctgggtgagg caggccccag 2100

gaaaagggct ggaatgggtg ggcaggatct accctggcga cggcgatacc aactactccg 2160

gaaagttcaa gggcaggttc actatcagcg ccgacactag caagaatacc gcctacctgc 2220

agatgaatag cctgagggcc gaggacaccg ccgtgtatta ctgcgctaga gacggcagca 2280

gctgggattg gtacttcgac gtgtggggcc agggcactct ggtgactgtg agcagcacca 2340

cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc 2400

tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact 2460

tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtggggtc cttctcctgt 2520

cactggttat cacccтttac tgcaaacggg gcagaaagaa actcctgtat atattcaaac 2580

aaccatttat gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc 2640

cagaagaaga agaaggagga tgtgaactga gagtgaagtt cagcaggagc gcagacgccc 2700

ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga cgaagagagg 2760

agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga aagccgagaa 2820

ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg gcggaggcct 2880

acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc 2940

agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag gccctgcccc 3000

ctcgctaagt ttaaac 3016

<210> 7
<211> 990
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 7

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

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

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145                 150                 155                 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
                165                 170                 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
            180                 185                 190

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

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
    210                 215                 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225                 230                 235                 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270
```

```
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
                325                 330                 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
            340                 345                 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
        355                 360                 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
    370                 375                 380

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

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
                405                 410                 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

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

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
                485                 490                 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
            500                 505                 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
        515                 520                 525

Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser
    530                 535                 540
```

```
Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser
545                 550                 555                 560

Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu
                565                 570                 575

Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe
            580                 585                 590

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
        595                 600                 605

Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr
    610                 615                 620

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
                645                 650                 655

Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu
            660                 665                 670

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp
        675                 680                 685

Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp
    690                 695                 700

Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala
705                 710                 715                 720

Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
                725                 730                 735

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn
            740                 745                 750

Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr
        755                 760                 765

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
    770                 775                 780

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
785                 790                 795                 800

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
                805                 810                 815
```

```
Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
            820                 825                 830

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
        835                 840                 845

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
    850                 855                 860

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
865                 870                 875                 880

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
                885                 890                 895

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            900                 905                 910

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
        915                 920                 925

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    930                 935                 940

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
945                 950                 955                 960

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                965                 970                 975

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            980                 985                 990
```

<210> 8
<211> 2989
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 8

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gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg       60

ccgccaggcc ggacatccag atgacacaga ctacatcctc cctgtctgcc tctctgggag      120

acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc      180

agcagaaacc agatggaact gttaaactcc tgatctacca tacatcaaga ttacactcag      240

gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca      300

acctggagca agaagatatt gccacttact tttgccaaca gggtaatacg cttccgtaca      360

cgttcggagg ggggaccaag ctggagatca caggtggcgg tggctcgggc ggtggtgggt      420
```

cgggtggcgg cggatctgag gtgaaactgc aggagtcagg acctggcctg gtggcgccct 480

cacagagcct gtccgtcaca tgcactgtct caggggtctc attacccgac tatggtgtaa 540

gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg 600

aaaccacata ctataattca gctctcaaat ccagactgac catcatcaag gacaactcca 660

agagccaagt tttcttaaaa atgaacagtc tgcaaactga tgacacagcc atttactact 720

gtgccaaaca ttattactac ggtggtagct atgctatgga ctactggggc caaggaacct 780

cagtcaccgt ctcctcaacc acgacgccag cgccgcgacc accaacaccg gcgcccacca 840

tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag 900

tgcacacgag ggggctggac ttcgcctgtg atatctacat ctgggcgccc ttggccggga 960

cttgtggggt ccttctcctg tcactggtta tcacccttta ctgcaaacgg ggcagaaaga 1020

aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag 1080

atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt 1140

tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc tataacgagc 1200

tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg 1260

agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac aatgaactgc 1320

agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag cgccggaggg 1380

gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac acctacgacg 1440

cccttcacat gcaggccctg ccccctcgcg gaagcggagc caccaacttc agcctgctga 1500

agcaggccgg cgacgtggag gagaaccccg gccccatggc cttaccagtg accgccttgc 1560

tcctgccgct ggccttgctg ctccacgccg ccaggccgga cgtgcagatc acccagagcc 1620

ccagctacct ggccgccagc cccggcgaga ccatcaccat caactgcaga gccagcaaga 1680

gcatcagcaa ggacctggcc tggtaccagg agaagcccgg caagaccaac aagctgctga 1740

tctacagcgg cagcaccctg cagagcggca tccccagcag attcagcggc agcggcagcg 1800

gcaccgactt caccctgacc atcagcagcc tggagcccga ggacttcgcc atgtactact 1860

gccagcagca caacaagtac ccctacacct tcggcggcgg caccaagctg gagatcaagg 1920

gaggggggg atccggggga ggaggctccg gcggaggcgg aagccaggtg cagctgcagc 1980

agcccggcgc cgagctggtg agacccggcg ccagcgtgaa gctgagctgc aaggccagcg 2040

gctacacctt caccagctac tggatgaact gggtgaagca gagacccgac cagggcctgg 2100

agtggatcgg cagaatcgac ccctacgaca gcgagaccca ctacaaccag aagttcaagg 2160

acaaggccat cctgaccgtg gacaagagca gcagcaccgc ctacatgcag ctgagcagcc 2220

tgaccagcga ggacagcgcc gtgtactact gcgccagagg caactgggac gactactggg 2280

gccagggcac caccctgacc gtgagcagca ccacgacgcc agcgccgcga ccaccaacac 2340

cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 2400

cgggggcgc agtgcacacg aggggctgg acttcgcctg tgatatctac atctgggcgc 2460

ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcagga 2520

gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc 2580

ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc tatcgctcca 2640

gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct 2700

ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc 2760

gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca 2820

atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg aaaggcgagc 2880

gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca 2940

cctacgacgc ccttcacatg caggccctgc cccctcgcta agtttaaac 2989

<210> 9
<211> 1066
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 9

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
20 25 30

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
35 40 45

Ser Ile Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro
50 55 60

Lys Leu Trp Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
100 105 110

Thr Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
130 135 140

Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala Ser Val
145 150 155 160

```
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Arg Met
                165                 170                 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
            180                 185                 190

Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys Asp
        195                 200                 205

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
    210                 215                 220

Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225                 230                 235                 240

Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
                245                 250                 255

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
            260                 265                 270

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
        275                 280                 285

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

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
305                 310                 315                 320

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
                325                 330                 335

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
            340                 345                 350

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        355                 360                 365

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
    370                 375                 380

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
385                 390                 395                 400

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
                405                 410                 415

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
            420                 425                 430
```

```
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
        435                 440                 445

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
    450                 455                 460

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
465                 470                 475                 480

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
                485                 490                 495

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
            500                 505                 510

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn
        515                 520                 525

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

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
545                 550                 555                 560

His Ala Ala Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu
                565                 570                 575

Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys
            580                 585                 590

Ser Ile Ser Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr
        595                 600                 605

Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro
    610                 615                 620

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
625                 630                 635                 640

Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His
                645                 650                 655

Asn Lys Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            660                 665                 670

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
        675                 680                 685

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

```
Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp
705                 710                 715                 720

Met Asn Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly
                725                 730                 735

Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
            740                 745                 750

Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
        755                 760                 765

Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
    770                 775                 780

Arg Gly Asn Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
785                 790                 795                 800

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                805                 810                 815

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            820                 825                 830

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
        835                 840                 845

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
    850                 855                 860

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
865                 870                 875                 880

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
                885                 890                 895

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
            900                 905                 910

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
        915                 920                 925

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
    930                 935                 940

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
945                 950                 955                 960

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
                965                 970                 975
```

```
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            980                 985                 990

Arg Gly Arg Asp Pro Glu Met Gly  Gly Lys Pro Arg Arg  Lys Asn Pro
        995                 1000                1005

Gln Glu  Gly Leu Tyr Asn Glu  Leu Gln Lys Asp Lys  Met Ala Glu
    1010                1015                1020

Ala Tyr  Ser Glu Ile Gly Met  Lys Gly Glu Arg Arg  Arg Gly Lys
    1025                1030                1035

Gly His  Asp Gly Leu Tyr Gln  Gly Leu Ser Thr Ala  Thr Lys Asp
    1040                1045                1050

Thr Tyr  Asp Ala Leu His Met  Gln Ala Leu Pro Pro  Arg
    1055                1060                1065
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<210> 10
<211> 3217
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 10

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ccgccaggcc gcagatcgtg ctgacccaga gccccgccat catgagcgcc agccccggcg      120

agaaggtgac catcacctgc agcgccagca gcagcatcag ctacatgcac tggttccagc      180

agaagcccgg caccagcccc aagctgtgga tctacaccac cagcaacctg gccagcggcg      240

tgcccgccag attcagcggc agcggcagcg gcaccagcta cagcctgacc atcagcagaa      300

tggaggccga ggacgccgcc acctactact gccaccagag aagcacctac cccctgacct      360

tcggcagcgg caccaagctg gagctgaagg gaggggggg atccggggga ggaggctccg      420

gcggaggcgg aagccaggtg cagctgcagc agagcggcgc cgagctggcc aagcccggcg      480

ccagcgtgaa gatgagctgc aaggccagcg gctacacctt caccagctac agaatgcact      540

gggtgaagca gagacccggc cagggcctgg agtggatcgg ctacatcaac cccagcaccg      600

gctacaccga gtacaaccag aagttcaagg acaaggccac cctgaccgcc gacaagagca      660

gcagcaccgc ctacatgcag ctgagcagcc tgaccttcga ggacagcgcc gtgtactact      720

gcgccagagg cggcggcgtg ttcgactact ggggccaggg caccaccctg accgtgagca      780

gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc      840

tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac acgaggggc       900

tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt ggggtccttc      960

tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc ctgcacagtg     1020
```

actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac cagccctatg 1080

ccccaccacg cgacttcgca gcctatcgct ccaaacgggg cagaaagaaa ctcctgtata 1140

tattcaaaca accatttatg agaccagtac aaactactca agaggaagat ggctgtagct 1200

gccgatttcc agaagaagaa gaaggaggat gtgaactgag agtgaagttc agcaggagcg 1260

cagacgcccc cgcgtacaag cagggccaga accagctcta taacgagctc aatctaggac 1320

gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag atgggggaa 1380

agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa gataagatgg 1440

cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag gggcacgatg 1500

gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt cacatgcagg 1560

ccctgccccc tcgcggaagc ggagctacta acttcagcct gctgaagcag gctggagacg 1620

tggaggagaa ccctggacct atggccttac cagtgaccgc cttgctcctg ccgctggcct 1680

tgctgctcca cgccgccagg ccggacgtgc agatcaccca gagccccagc tacctggccg 1740

ccagccccgg cgagaccatc accatcaact gcagagccag caagagcatc agcaaggacc 1800

tggcctggta ccaggagaag cccggcaaga ccaacaagct gctgatctac agcggcagca 1860

ccctgcagag cggcatcccc agcagattca gcggcagcgg cagcggcacc gacttcaccc 1920

tgaccatcag cagcctggag cccgaggact tcgccatgta ctactgccag cagcacaaca 1980

agtaccccta caccttcggc ggcggcacca agctggagat caagggaggg gggggatccg 2040

ggggaggagg ctccggcgga ggcggaagcc aggtgcagct gcagcagccc ggcgccgagc 2100

tggtgagacc cggcgccagc gtgaagctga gctgcaaggc cagcggctac accttcacca 2160

gctactggat gaactgggtg aagcagagac ccgaccaggg cctggagtgg atcggcagaa 2220

tcgaccccta cgacagcgag acccactaca accagaagtt caaggacaag gccatcctga 2280

ccgtggacaa gagcagcagc accgcctaca tgcagctgag cagcctgacc agcgaggaca 2340

gcgccgtgta ctactgcgcc agaggcaact gggacgacta ctggggccag ggcaccaccc 2400

tgaccgtgag cagcaccacg acgccagcgc cgcgaccacc aacaccggcg cccaccatcg 2460

cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc 2520

acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg gccgggactt 2580

gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag aggagcaggc 2640

tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc cgcaagcatt 2700

accagcccta tgccccacca cgcgacttcg cagcctatcg ctccaaacgg ggcagaaaga 2760

aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag 2820

atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt 2880

tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc tataacgagc 2940

tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg 3000

agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga 3060

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 3120

aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc tacgacgccc 3180

ttcacatgca ggccctgccc cctcgctaag tttaaac 3217

<210> 11
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 11

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
20 25 30

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
35 40 45

Ser Ile Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro
50 55 60

Lys Leu Trp Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
100 105 110

Thr Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
130 135 140

Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Arg Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys Asp
195 200 205

```
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
    210                 215                 220

Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225                 230                 235                 240

Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
                245                 250                 255

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
            260                 265                 270

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
        275                 280                 285

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

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
305                 310                 315                 320

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
                325                 330                 335

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
            340                 345                 350

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
        355                 360                 365

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
    370                 375                 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385                 390                 395                 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
                405                 410                 415

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
            420                 425                 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
        435                 440                 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
    450                 455                 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465                 470                 475                 480
```

```
Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
                485                 490                 495

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
            500                 505                 510

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Val Gln
        515                 520                 525

Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile
    530                 535                 540

Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Asp Leu Ala Trp
545                 550                 555                 560

Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly
                565                 570                 575

Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser
            580                 585                 590

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
        595                 600                 605

Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr Pro Tyr Thr Phe Gly
    610                 615                 620

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Pro Gly Ala
                645                 650                 655

Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser
            660                 665                 670

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
        675                 680                 685

Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Tyr Asp Ser Glu
    690                 695                 700

Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp
705                 710                 715                 720

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
                725                 730                 735

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn Trp Asp Asp Tyr Trp
            740                 745                 750
```

```
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
        755                 760                 765

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
    770                 775                 780

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
785                 790                 795                 800

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
                805                 810                 815

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
            820                 825                 830

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
        835                 840                 845

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
    850                 855                 860

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
865                 870                 875                 880

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
                885                 890                 895

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
            900                 905                 910

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
        915                 920                 925

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
    930                 935                 940

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
945                 950                 955                 960

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
                965                 970                 975

Leu His Met Gln Ala Leu Pro Pro Arg
            980                 985
```

<210> 12
<211> 2974
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 12
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agaaggtgac catcacctgc agcgccagca gcagcatcag ctacatgcac tggttccagc 180
agaagcccgg caccagcccc aagctgtgga tctacaccac cagcaacctg gccagcggcg 240
tgcccgccag attcagcggc agcggcagcg gcaccagcta cagcctgacc atcagcagaa 300
tggaggccga ggacgccgcc acctactact gccaccagag aagcacctac cccctgacct 360
tcggcagcgg caccaagctg gagctgaagg gaggggggg atccggggga ggaggctccg 420
gcggaggcgg aagccaggtg cagctgcagc agagcggcgc cgagctggcc aagcccggcg 480
ccagcgtgaa gatgagctgc aaggccagcg gctacacctt caccagctac agaatgcact 540
gggtgaagca gagacccggc cagggcctgg agtggatcgg ctacatcaac cccagcaccg 600
gctacaccga gtacaaccag aagttcaagg acaaggccac cctgaccgcc gacaagagca 660
gcagcaccgc ctacatgcag ctgagcagcc tgaccttcga ggacagcgcc gtgtactact 720
gcgccagagg cggcggcgtg ttcgactact ggggccaggg caccaccctg accgtgagca 780
gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc 840
tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac acgaggggc 900
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tcctgtcact ggttatcacc ctttactgca aacggggcag aaagaaactc ctgtatatat 1020
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gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc aggagcgcag 1140
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gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg gggggaaagc 1260
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tgaccatcag cagcctggag cccgaggact tcgccatgta ctactgccag cagcacaaca 1860
agtaccccta caccttcggc ggcggcacca agctggagat caagggaggg gggggatccg 1920
ggggaggagg ctccggcgga ggcggaagcc aggtgcagct gcagcagccc ggcgccgagc 1980

tggtgagacc cggcgccagc gtgaagctga gctgcaaggc cagcggctac accttcacca 2040

gctactggat gaactgggtg aagcagagac ccgaccaggg cctggagtgg atcggcagaa 2100

tcgaccccta cgacagcgag acccactaca accagaagtt caaggacaag gccatcctga 2160

ccgtggacaa gagcagcagc accgcctaca tgcagctgag cagcctgacc agcgaggaca 2220

gcgccgtgta ctactgcgcc agaggcaact gggacgacta ctggggccag ggcaccaccc 2280

tgaccgtgag cagcaccacg acgccagcgc cgcgaccacc aacaccggcg cccaccatcg 2340

cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc 2400

acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg gccgggactt 2460

gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag aggagcaggc 2520

tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc cgcaagcatt 2580

accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagagtg aagttcagca 2640

ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac gagctcaatc 2700

taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac cctgagatgg 2760

ggggaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag 2820

ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg aggggcaagg 2880

ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac gacgcccttc 2940

acatgcaggc cctgcccccc cgctaagttt aaac 2974

<210> 13
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 13

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
20 25 30

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
35 40 45

Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu
65 70 75 80

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

```
Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr
        115                 120                 125

Lys Leu Glu Ile Lys Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                165                 170                 175

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg
            180                 185                 190

Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        195                 200                 205

Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr Pro Ser
    210                 215                 220

Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
225                 230                 235                 240

Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr
                245                 250                 255

Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp Tyr Trp
            260                 265                 270

Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
            340                 345                 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
        355                 360                 365
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```
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
    370                 375                 380

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
385                 390                 395                 400

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
                405                 410                 415

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
            420                 425                 430

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
        435                 440                 445

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
    450                 455                 460

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
465                 470                 475                 480

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
                485                 490                 495

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
            500                 505                 510

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
        515                 520                 525

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
    530                 535                 540

Pro Arg
545
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<210> 14
<211> 1657
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 14
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gccagagagc caccatcagc tgcagagcca gcaagagcgt gagcaccagc ggctacagct 180

acctgcactg gtaccagcag aagcccggcc agcccccaa gctgctgatc tacctggcca 240

gcaacctgga gagcggcgtg cccgccagat tcagcggcag cggcagcggc accgacttca 300

ccctgaacat ccaccccgtg gaggaggagg acgccgccac ctactactgc cagcacagca 360

gagagctgcc cttcaccttc ggcagcggca ccaagctgga gatcaagaag atcagcggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cggcggcggc ggcagcggcg 480

gcggcggcag ccaggtgcag ctggtggaga gcggcggcgg cctggtgcag cccggcggca 540

gcctgaagct gagctgcgcc gccagcggct tcgacttcag cagatactgg atgagctggg 600

tgagacaggc ccccggcaag ggcctggagt ggatcggcga gatcaacccc accagcagca 660

ccatcaactt caccccccagc ctgaaggaca aggtgttcat cagcagagac aacgccaaga 720

acaccctgta cctgcagatg agcaaggtga gaagcgagga caccgccctg tactactgcg 780

ccagaggcaa ctactacaga tacggcgacg ccatggacta ctggggccag ggcaccagcg 840

tgaccgtgag caccacgacg ccagcgccgc gaccaccaac accggcgccc accatcgcgt 900

cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc gcagtgcaca 960

cgaggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc gggacttgtg 1020

gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg agcaggctcc 1080

tgcacagtga ctacatgaac atgactcccc gccgccccgg gcccacccgc aagcattacc 1140

agccctatgc cccaccacgc gacttcgcag cctatcgctc caaacggggc agaaagaaac 1200

tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa gaggaagatg 1260

gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga gtgaagttca 1320

gcaggagcgc agacgccccc gcgtaccagc agggccagaa ccagctctat aacgagctca 1380

atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg gaccctgaga 1440

tgggggggaaa gccgcagaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga 1500

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 1560

aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc tacgacgccc 1620

ttcacatgca ggccctgccc cctcgctaag tttaaac 1657

<210> 15
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 15

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
20 25 30

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys
35 40 45

```
Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys
    50                  55                  60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65                  70                  75                  80

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
            100                 105                 110

Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
        115                 120                 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145                 150                 155                 160

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
                165                 170                 175

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr
        195                 200                 205

Pro Ser Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn
    210                 215                 220

Thr Leu Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu
225                 230                 235                 240

Tyr Tyr Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp
                245                 250                 255

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

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

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

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320
```

```
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

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

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro
            420                 425                 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465                 470                 475                 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 16
<211> 1489
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 16

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gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg       60

ccgccaggcc ggacatcgtg ctgacccaga gccccgccag cctggccgtg agcctgggcc      120

agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc      180

tgcactggta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca      240

acctggagag cggcgtgccc gccaggttca gcggcagcgg cagcggcacc gacttcaccc      300

tgaacatcca ccccgtggag gaggaggacg ccgccaccta ctactgccag cacagcaggg      360

agctgccctt caccttcggc agcggcacca agctggagat caagggaggg gggggatccg      420
```

ggggaggagg ctccggcgga ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480

tggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540

ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600

tcaaccccac cagcagcacc atcaacttca cccccagcct gaaggacaag gtgttcatca 660

gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtgagg agcgaggaca 720

ccgccctgta ctactgcgcc aggggcaact actacaggta cggcgacgcc atggactact 780

ggggccaggg caccagcgtg accgtgagca ccacgacgcc agcgccgcga ccaccaacac 840

cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 900

cgggggcgc agtgcacacg aggggctgg acttcgcctg tgatatctac atctgggcgc 960

ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcagga 1020

gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc 1080

ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc tatcgctcca 1140

gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct 1200

ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc 1260

gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca 1320

atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg aaaggcgagc 1380

gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca 1440

cctacgacgc ccttcacatg caggccctgc cccctcgcta agtttaaac 1489

<210> 17
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 17

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
20 25 30

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys
35 40 45

Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65 70 75 80

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

85 90 95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
100 105 110

Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145 150 155 160

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
165 170 175

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr
195 200 205

Pro Ser Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Thr Leu Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu
225 230 235 240

Tyr Tyr Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp
245 250 255

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

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

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

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe

355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 18
<211> 1492
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 18
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60

ccgccaggcc ggacatcgtg ctgacccaga gccccgccag cctggccgtg agcctgggcc 120

agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc 180

tgcactggta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca 240

acctggagag cggcgtgccc gccaggttca gcggcagcgg cagcggcacc gacttcaccc 300

tgaacatcca ccccgtggag gaggaggacg ccgccaccta ctactgccag cacagcaggg 360

agctgccctt caccttcggc agcggcacca agctggagat caagggaggg gggggatccg 420

ggggaggagg ctccggcgga ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480

tggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540

ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600

tcaaccccac cagcagcacc atcaacttca cccccagcct gaaggacaag gtgttcatca 660

gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtgagg agcgaggaca 720

ccgccctgta ctactgcgcc aggggcaact actacaggta cggcgacgcc atggactact 780

ggggccaggg caccagcgtg accgtgagca ccacgacgcc agcgccgcga ccaccaacac 840

cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 900

cgggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc 960

ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcaaac 1020

ggggcagaaa gaaactcctg tatatattca aacaaccatt tatgagacca gtacaaacta 1080

ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga ggatgtgaac 1140

tgagagtgaa gttcagcagg agcgcagacg cccccgcgta ccagcagggc cagaaccagc 1200

tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac aagagacgtg 1260

gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt 1320

acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg atgaaaggcg 1380

agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca gccaccaagg 1440

acacctacga cgcccttcac atgcaggccc tgcccccctcg ctaagtttaa ac 1492

<210> 19
<211> 997
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 19

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser His Arg Phe Met
20 25 30

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln
35 40 45

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

Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
65 70 75 80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
100 105 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    130                 135                 140

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

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe Gly
                165                 170                 175

Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala
            180                 185                 190

Trp Ile Asn Thr Thr Arg Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp
        195                 200                 205

Phe Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala
    210                 215                 220

Tyr Leu Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe
225                 230                 235                 240

Cys Ala Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr
                245                 250                 255

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

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

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

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400
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```
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
            420                 425                 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
        435                 440                 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
    450                 455                 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465                 470                 475                 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr
                485                 490                 495

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
            500                 505                 510

Pro Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
        515                 520                 525

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    530                 535                 540

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
545                 550                 555                 560

Asp Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
                565                 570                 575

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro
            580                 585                 590

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        595                 600                 605

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

Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
625                 630                 635                 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
                645                 650                 655

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
            660                 665                 670
```

```
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp
        675                 680                 685

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

Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys
705                 710                 715                 720

Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
                725                 730                 735

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            740                 745                 750

Arg Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
        755                 760                 765

Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
    770                 775                 780

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
785                 790                 795                 800

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
                805                 810                 815

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
            820                 825                 830

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser
        835                 840                 845

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
    850                 855                 860

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
865                 870                 875                 880

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
                885                 890                 895

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
            900                 905                 910

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
        915                 920                 925

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
    930                 935                 940
```

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
945 950 955 960

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
965 970 975

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
980 985 990

Ala Leu Pro Pro Arg
995

<210> 20
<211> 2994
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 20
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggatgtgg tgatgaccca gagccatcgc tttatgagca ccagcgtggg cgatcgcgtg 120

agcattacct gccgcgcgag ccaggatgtg aacaccgcgg tgagctggta tcagcagaaa 180

ccgggccaga gcccgaaact gctgattttt agcgcgagct atcgctatac cggcgtgccg 240

gatcgcttta ccggcagcgg cagcggcgcg gattttaccc tgaccattag cagcgtgcag 300

gcggaagatc tggcggtgta ttattgccag cagcattata gcaccccgtg gacctttggc 360

ggcggcacca aactggaaat taaaggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agattcagct ggtgcagagc ggcccggatc tgaaaaaacc gggcgaaacc 480

gtgaaactga gctgcaaagc gagcggctat acctttacca actttggcat gaactgggtg 540

aaacaggcgc cgggcaaagg ctttaaatgg atggcgtgga ttaacaccac ccgctatacc 600

ggcgaaagct attttgcgga tgattttaaa ggccgctttg cgtttagcgt ggaaaccagc 660

gcgaccaccg cgtatctgca gattaacaac ctgaaaaccg aagataccgc gacctatttt 720

tgcgcgcgcg gcgaaattta ttatggctat gatggcggct ttgcgtattg gggccagggc 780

accctggtga ccgtgagcgc gaccacgacg ccagcgccgc gaccaccaac accggcgccc 840

accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc 900

gcagtgcaca cgaggggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcaa acggggcaga 1020

aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag 1080

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gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 1260

cctgagatgg ggggaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa 1320

ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac 1440

gacgcccttc acatgcaggc cctgccccct cgcggaagcg gagccaccaa cttcagcctg 1500

ctgaagcagg ccggcgacgt ggaggagaac cccggccccg ccttaccagt gaccgccttg 1560

ctcctgccgc tggccttgct gctccacgcc gccaggccgg atattcagat gacccagagc 1620

ccgagcagcc tgagcgcgag cgtgggcgat cgcgtgacca ttacctgcaa agcgagccag 1680

gatgtgggca ttgcggtggc gtggtatcag cagaaaccgg gcaaagtgcc gaaactgctg 1740

atttattggg cgagcacccg ccataccggc gtgccggatc gctttagcgg cagcggcagc 1800

ggcaccgatt ttaccctgac cattagcagc ctgcagccgg aagatgtggc gacctattat 1860

tgccagcagt atagcagcta tccgtatacc tttggccagg gcaccaaagt ggaaattaaa 1920

ggaggggggg gatccggggg aggaggctcc ggcggaggcg gaagcgaagt gcagctggtg 1980

gaaagcggcg gcggcctggt gcagccgggc ggcagcctgc gcctgagctg cgcggcgagc 2040

ggctttgatt ttagccgcta ttggatgagc tgggtgcgcc aggcgccggg caaaggcctg 2100

gaatggattg gcgaaattaa cccggatagc agcaccatta actatgcgcc gagcctgaaa 2160

gataaattta ttattagccg cgataacgcg aaaaacagcc tgtatctgca gatgaacagc 2220

ctgcgcgcgg aagataccgc ggtgtattat tgcgcgcgcc cggatggcaa ctattggtat 2280

tttgatgtgt ggggccaggg caccctggtg accgtgagca gcaccacgac gccagcgccg 2340

cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg 2400

tgccggccag cggcgggggg cgcagtgcac acgaggggc tggacttcgc ctgtgatatc 2460

tacatctggg cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc 2520

ctttactgca ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc 2580

cgccgccccg ggcccacccg caagcattac cagccctatg ccccaccacg cgacttcgca 2640

gcctatcgct ccagagtgaa gttcagcagg agcgcagacg cccccgcgta ccagcagggc 2700

cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac 2760

aagagacgtg gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag 2820

gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 2880

atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca 2940

gccaccaagg acacctacga cgcccttcac atgcaggccc tgcccctcg ctaa 2994

<210> 21
<211> 997
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 21

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser His Arg Phe Met
            20                  25                  30

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln
        35                  40                  45

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

Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
65                  70                  75                  80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
            100                 105                 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
        115                 120                 125

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

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

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe Gly
                165                 170                 175

Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala
            180                 185                 190

Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe Lys
        195                 200                 205

Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr Leu
    210                 215                 220

Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
225                 230                 235                 240

Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr Trp Gly
                245                 250                 255

Gln Gly Thr Leu Val Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg
            260                 265                 270
```

```
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
        275                 280                 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
    290                 295                 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305                 310                 315                 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
                325                 330                 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
            340                 345                 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
        355                 360                 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
    370                 375                 380

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

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
                405                 410                 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
            420                 425                 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
        435                 440                 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450                 455                 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465                 470                 475                 480

Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe
                485                 490                 495

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
            500                 505                 510

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
        515                 520                 525

Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
    530                 535                 540
```

```
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
545                 550                 555                 560

Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro
                565                 570                 575

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
            580                 585                 590

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
        595                 600                 605

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

Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
625                 630                 635                 640

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
                645                 650                 655

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
            660                 665                 670

Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp Met
        675                 680                 685

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

Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp
705                 710                 715                 720

Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
                725                 730                 735

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            740                 745                 750

Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
        755                 760                 765

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
    770                 775                 780

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
785                 790                 795                 800

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
                805                 810                 815
```

```
Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
            820                 825                 830

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
        835                 840                 845

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
    850                 855                 860

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
865                 870                 875                 880

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
                885                 890                 895

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
            900                 905                 910

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
        915                 920                 925

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
    930                 935                 940

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
945                 950                 955                 960

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
                965                 970                 975

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
            980                 985                 990

Ala Leu Pro Pro Arg
        995
```

<210> 22
<211> 3009
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 22

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cgatcgcatg gccttaccag tgaccgcctt gctcctgccg ctggccttgc tgctccacgc       60

cgccaggccg gatgtggtga tgacccagag ccatcgcttt atgagcacca gcgtgggaga      120

tcgagtgagc attacctgcc gcgcgagcca ggatgtgaac accgcggtga gctggtatca      180

gcagaaaccg ggccagagcc cgaaactgct gatttttagc gcgagctatc gctataccgg      240

cgtgccggat cgctttaccg gcagcggcag cggcgcggat ttttaccctga ccattagcag      300
```

cgtgcaggcg gaagatctgg cggtgtatta ttgccagcag cattatagca ccccgtggac 360

ctttggcggc ggcaccaaac tggatattaa aggagggggg ggatccgggg gaggaggctc 420

cggcggaggc ggaagccaga ttcagctggt gcagagcggc ccggatctga aaaaaccggg 480

cgaaaccgtg aaactgagct gcaaagcgag cggctatacc tttaccaact ttggcatgaa 540

ctgggtgaaa caggcgccgg gcaaaggctt taaatggatg gcgtggatta acacctatac 600

cggcgaaagc tattttgcgg atgattttaa aggccgcttt gcgtttagcg tggaaaccag 660

cgcgaccacc gcgtatctgc agattaacaa cctgaaaacc gaagataccg cgacctattt 720

ttgcgcgcgc ggcgaaattt attatggcta tgatggcggc tttgcgtatt ggggccaggg 780

caccctggtg accgtgagcg cgaccacgac gccagcgccg cgaccaccaa caccggcgcc 840

caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg 900

cgcagtgcac acgaggggcc tggacttcgc ctgtgatatc tacatctggg cgcccttggc 960

cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca aacggggcag 1020

aaagaaactc ctgtatatat tcaagcaacc atttatgaga ccagtacaaa ctactcaaga 1080

ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt 1140

gaagttcagc aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa 1200

cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga 1260

ccctgagatg gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga 1320

actgcagaaa gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg 1380

gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta 1440

cgacgccctt cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct 1500

gctgaagcag gccggcgacg tggaggagaa ccccggcccc atggccttac cagtgaccgc 1560

cttgctcctg ccgctggcct tgctgctcca cgccgccagg ccggatattc agatgaccca 1620

gagcccgagc agcctgagcg cgagcgtggg cgaccgcgtg accattacct gcaaagcgag 1680

ccaggatgtg ggcattgcgg tggcgtggta tcagcagaaa ccgggcaaag tgccgaaact 1740

gctgatttat tgggcgagca cccgccatac cggcgtgccg gatcgcttta gcggcagcgg 1800

cagcggcacc gattttaccc tgaccattag cagcctgcag ccggaagatg tggcgaccta 1860

ttattgccag cagtatagca gctatccgta tacctttggc cagggcacca aagtggaaat 1920

taaaggaggg gggggatccg ggggaggagg ctccggcgga ggcggaagcg aagtgcagct 1980

ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc ctgcgcctga gctgcgcggc 2040

gagcggcttt gattttagcc gctattggat gagctgggtg cgccaggcgc cgggcaaagg 2100

cctggaatgg attggcgaaa ttaacccgga tagcagcacc attaactatg cgccgagcct 2160

gaaagataaa tttattatta gccgcgataa cgcgaaaaac agcctgtatc tgcagatgaa 2220

cagcctgcgc gcggaagata ccgcggtgta ttattgcgcg cgcccggatg gcaactattg 2280

gtattttgat gtgtggggcc agggcaccct ggtgaccgtg agcagcacca cgacgccagc 2340

gccgcgacca ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga 2400

ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga 2460

tatctacatc tgggcgccct tggccgggac ttgtggggtc cttctcctgt cactggttat 2520

caccctttac tgcaaacggg gcagaaagaa actcctgtat atattcaagc aaccatttat 2580

gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga 2640

agaaggagga tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca 2700

gcagggccag aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt 2760

tttggacaag agacgtggcc gggaccctga gatgggggga aagccgcaga gaaggaagaa 2820

ccctcaggaa ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga 2880

gattgggatg aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct 2940

cagtacagcc accaaggaca cctacgacgc ccttcacatg caggccctgc cccctcgcta 3000

agtttaaac 3009

<210> 23
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 23
agctagctgc agtaacgcca ttttgcaagg catggaaaaa taccaaacca agaatagaga 60

agttcagatc aagggcgggt acatgaaaat agctaacgtt gggccaaaca ggatatctgc 120

ggtgagcagt ttcggccccg gcccggggcc aagaacagat ggtcaccgca gtttcggccc 180

cggcccgagg ccaagaacag atggtcccca gatatggccc aaccctcagc agtttcttaa 240

gacccatcag atgtttccag gctcccccaa ggacctgaaa tgaccctgcg ccttatttga 300

attaaccaat cagcctgctt ctcgcttctg ttcgcgcgct tctgcttccc gagctctata 360

aaagagctca caacccctca ctcggcgcgc cagtcctccg acagactgag tcgcccgggt 420

acc 423

<210> 24
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 24

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

Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30

Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45

Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60

Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80

His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140

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

Ala Leu Val Tyr Ser
165

<210> 25
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 25

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45

Val Lys Gly Thr Asn Ala
50

<210> 26
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 26

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

Phe Pro Leu Lys Ser Lys Val Lys Gln Val Asp Ser Ile Val Trp Thr
            20                  25                  30

Phe Asn Thr Thr Pro Leu Val Thr Ile Gln Pro Glu Gly Gly Thr Ile
        35                  40                  45

Ile Val Thr Gln Asn Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly
    50                  55                  60

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

Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln
                85                  90                  95

Glu Tyr Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr
            100                 105                 110

Met Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
        115                 120                 125

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys Ala
    130                 135                 140

Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu Pro Ile
145                 150                 155                 160

Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys Val Ala Arg
                165                 170                 175

Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu Ala Arg Lys Leu
            180                 185                 190

Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser Met
        195                 200
```

<210> 27
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 27

```
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
```

1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys
35 40 45

<210> 28
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 28

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

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

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

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

```
Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
        195                 200                 205


Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
    210                 215                 220


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


Val His
```

<210> 29
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 29

```
Thr Lys Glu Asp Pro Asn Pro Pro Ile Thr Asn Leu Arg Met Lys Ala
1               5                   10                  15


Lys Ala Gln Gln Leu Thr Trp Asp Leu Asn Arg Asn Val Thr Asp Ile
            20                  25                  30


Glu Cys Val Lys Asp Ala Asp Tyr Ser Met Pro Ala Val Asn Asn Ser
        35                  40                  45


Tyr Cys Gln Phe Gly Ala Ile Ser Leu Cys Glu Val Thr Asn Tyr Thr
    50                  55                  60


Val Arg Val Ala Asn Pro Pro Phe Ser Thr Trp Ile Leu Phe Pro Glu
65                  70                  75                  80


Asn Ser Gly Lys Pro Trp Ala Gly Ala Glu Asn Leu Thr Cys Trp Ile
                85                  90                  95


His Asp Val Asp Phe Leu Ser Cys Ser Trp Ala Val Gly Pro Gly Ala
            100                 105                 110


Pro Ala Asp Val Gln Tyr Asp Leu Tyr Leu Asn Val Ala Asn Arg Arg
        115                 120                 125


Gln Gln Tyr Glu Cys Leu His Tyr Lys Thr Asp Ala Gln Gly Thr Arg
    130                 135                 140


Ile Gly Cys Arg Phe Asp Asp Ile Ser Arg Leu Ser Ser Gly Ser Gln
145                 150                 155                 160


Ser Ser His Ile Leu Val Arg Gly Arg Ser Ala Ala Phe Gly Ile Pro
```

165 170 175

Cys Thr Asp Lys Phe Val Val Phe Ser Gln Ile Glu Ile Leu Thr Pro
180 185 190

Pro Asn Met Thr Ala Lys Cys Asn Lys Thr His Ser Phe Met His Trp
195 200 205

Lys Met Arg Ser His Phe Asn Arg Lys Phe Arg Tyr Glu Leu Gln Ile
210 215 220

Gln Lys Arg Met Gln Pro Val Ile Thr Glu Gln Val Arg Asp Arg Thr
225 230 235 240

Ser Phe Gln Leu Leu Asn Pro Gly Thr Tyr Thr Val Gln Ile Arg Ala
245 250 255

Arg Glu Arg Val Tyr Glu Phe Leu Ser Ala Trp Ser Thr Pro Gln Arg
260 265 270

Phe Glu Cys Asp Gln Glu Glu Gly Ala Asn Thr Arg Ala Trp Arg
275 280 285

<210> 30
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 30

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val
1 5 10 15

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
20 25 30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
35 40 45

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
50 55 60

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
65 70 75 80

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
100 105 110

```
Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
        115                 120                 125


Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
    130                 135                 140


Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145                 150                 155                 160


Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
                165                 170                 175


Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
            180                 185                 190


Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
        195                 200                 205


Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
    210                 215                 220


Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
225                 230                 235                 240


Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
                245                 250                 255


Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys
            260                 265                 270


<210>  31
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic sequence

<400>  31

Pro Ile Cys Val Thr Val
1               5


<210>  32
<211>  47
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic sequence

<400>  32

Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala
1               5                   10                  15
```

His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
20 25 30

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
35 40 45

<210> 33
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 33

Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp
1 5 10 15

Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly
20 25 30

Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn
35 40 45

Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly
50 55 60

Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn
65 70 75 80

Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly
85 90 95

Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg
100 105 110

Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu
115 120 125

Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu
130 135 140

Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu
145 150 155 160

Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile
165 170 175

Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser
180 185 190

His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys

195 200 205

Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His Thr Pro Lys
210 215 220

Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg Glu Gly Asp
225 230 235 240

Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro Glu Tyr Thr
245 250 255

Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys Gln Asn Thr
260 265 270

Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser Gly Lys Tyr
275 280 285

Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser Glu Glu Val
290 295 300

Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val Gln Ile Leu
305 310 315 320

His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu Cys Met Ser
325 330 335

Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His Asn Gly Lys
340 345 350

Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro Lys Ile Leu
355 360 365

Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn Ile Leu Gly
370 375 380

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

Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly
405 410 415

Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val
420 425 430

Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu
435 440 445

Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala
450 455 460

Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu

465 470 475 480

<210> 34
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 34

Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys Met Pro
1 5 10 15

Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr Ala Phe
20 25 30

Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu Thr Thr
35 40 45

Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro Asp Ser
50 55 60

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

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

Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Ala Asn Ala Lys Leu Asn
100 105 110

Pro Thr Pro Gly Ser Asn Ala Ile Ser Asp Val Pro Gly Glu Arg Ser
115 120 125

Thr Ala Ser Thr Phe Pro Thr Asp Pro Val Ser Pro Leu Thr Thr Thr
130 135 140

Leu Ser Leu Ala His His Ser Ser Ala Ala Leu Pro Ala Arg Thr Ser
145 150 155 160

Asn Thr Thr Ile Thr Ala Asn Thr Ser Asp Ala Tyr Leu Asn Ala Ser
165 170 175

Glu Thr Thr Thr Leu Ser Pro Ser Gly Ser Ala Val Ile Ser Thr Thr
180 185 190

Thr Ile Ala Thr Thr Pro Ser Lys Pro Thr Cys Asp Glu Lys Tyr Ala
195 200 205

Asn Ile Thr Val Asp Tyr Leu Tyr Asn Lys Glu Thr Lys Leu Phe Thr
210 215 220

```
Ala Lys Leu Asn Val Asn Glu Asn Val Glu Cys Gly Asn Asn Thr Cys
225                 230                 235                 240

Thr Asn Asn Glu Val His Asn Leu Thr Glu Cys Lys Asn Ala Ser Val
                245                 250                 255

Ser Ile Ser His Asn Ser Cys Thr Ala Pro Asp Lys Thr Leu Ile Leu
            260                 265                 270

Asp Val Pro Pro Gly Val Glu Lys Phe Gln Leu His Asp Cys Thr Gln
        275                 280                 285

Val Glu Lys Ala Asp Thr Thr Ile Cys Leu Lys Trp Lys Asn Ile Glu
    290                 295                 300

Thr Phe Thr Cys Asp Thr Gln Asn Ile Thr Tyr Arg Phe Gln Cys Gly
305                 310                 315                 320

Asn Met Ile Phe Asp Asn Lys Glu Ile Lys Leu Glu Asn Leu Glu Pro
                325                 330                 335

Glu His Glu Tyr Lys Cys Asp Ser Glu Ile Leu Tyr Asn Asn His Lys
            340                 345                 350

Phe Thr Asn Ala Ser Lys Ile Ile Lys Thr Asp Phe Gly Ser Pro Gly
        355                 360                 365

Glu Pro Gln Ile Ile Phe Cys Arg Ser Glu Ala Ala His Gln Gly Val
    370                 375                 380

Ile Thr Trp Asn Pro Pro Gln Arg Ser Phe His Asn Phe Thr Leu Cys
385                 390                 395                 400

Tyr Ile Lys Glu Thr Glu Lys Asp Cys Leu Asn Leu Asp Lys Asn Leu
                405                 410                 415

Ile Lys Tyr Asp Leu Gln Asn Leu Lys Pro Tyr Thr Lys Tyr Val Leu
            420                 425                 430

Ser Leu His Ala Tyr Ile Ile Ala Lys Val Gln Arg Asn Gly Ser Ala
        435                 440                 445

Ala Met Cys His Phe Thr Thr Lys Ser Ala Pro Pro Ser Gln Val Trp
    450                 455                 460

Asn Met Thr Val Ser Met Thr Ser Asp Asn Ser Met His Val Lys Cys
465                 470                 475                 480
```

<210> 35
<211> 65
<212> PRT

<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 35

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
1 5 10 15

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
20 25 30

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
35 40 45

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
50 55 60

Arg
65

<210> 36
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 36

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
20 25 30

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
35 40 45

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
50 55 60

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
65 70 75 80

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
85 90 95

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
100 105 110

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
115 120 125

```
Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
    130                 135                 140

Ile Val Gln Met Phe Ile Asn Thr Ser
145                 150
```