SEQUENCE LISTING

<110> iCell Gene Therapeutics LLC

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

<130> 2541-3 P2

<160> 252

<170> PatentIn version 3.5

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


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


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
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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
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

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
                325                 330                 335

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
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Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

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

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
385                 390                 395                 400

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
                405                 410                 415

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            420                 425                 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        435                 440                 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    450                 455                 460

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
                485                 490                 495

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
        515                 520                 525

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
545                 550                 555                 560
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Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
                565                 570                 575

Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
            580                 585                 590

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
        595                 600                 605

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
    610                 615                 620

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
625                 630                 635                 640

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
        675                 680                 685

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
    690                 695                 700

Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
705                 710                 715                 720

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                725                 730                 735

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
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    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
                805                 810                 815

Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            820                 825                 830
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agagggtgac catgaactgc aaaagcagcc agtccctgct gtactccacc aaccagaaga 180

actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg 240

ccagcactag ggaaagcggc gtgcccgata ggttcagcgg cagcgggagc ggcacagact 300

tcactctgac cattagcagc gtgcaggctg aggatgtggc cgtctactac tgccagcagt 360

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            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
```

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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
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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

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

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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

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
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            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
                965                 970                 975

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
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Pro Pro Arg
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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

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gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg 600

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gtgccaaaca ttattactac ggtggtagct atgctatgga ctactggggc caaggaacct 780

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aacagtggac ctccaaccca cccacctttg gaggagggac aaaactggag atcaaagggg 1920

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ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag ggtctcagta 2940

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<213> Artificial Sequence

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            20                  25                  30


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


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


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


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


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


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
    130                 135                 140


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


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


Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp
            180                 185                 190
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Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu
        195                 200                 205

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

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

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

Gln Gly Thr Ser Val Thr Val Ser Ser 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
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                405                 410                 415

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

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

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

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

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

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

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

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

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

Val His Ser Val Gly Asn Thr Phe Leu Glu Trp Tyr Gln Gln Lys Pro
                565                 570                 575

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

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

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    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

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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

gagggggggg 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

cgggggggcgc agtgcacacg agggggctgg 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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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 atccgggga 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

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tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt ggggtccttc 960

tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc ctgcacagtg 1020

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gccgatttcc agaagaagaa gaaggaggat gtgaactgag agtgaagttc agcaggagcg 1260

cagacgcccc cgcgtacaag cagggccaga accagctcta taacgagctc aatctaggac 1320

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atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt 2880

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

<220>
<223> Synthetic Sequence

<400> 11

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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 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
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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

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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 atccgggga 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

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

<220>
<223> Synthetic Sequence

<400> 13

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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
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```
    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

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
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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

<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

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tgagacaggc ccccggcaag ggcctggagt ggatcggcga gatcaacccc accagcagca 660

ccatcaactt cacccccagc ctgaaggaca aggtgttcat cagcagagac aacgccaaga 720

acaccctgta cctgcagatg agcaaggtga gaagcgagga caccgccctg tactactgcg 780

ccagaggcaa ctactacaga tacggcgacg ccatggacta ctggggccag ggcaccagcg 840

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tgcacagtga ctacatgaac atgactcccc gccgccccgg gcccacccgc aagcattacc 1140

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gcaggagcgc agacgccccc gcgtaccagc agggccagaa ccagctctat aacgagctca 1380

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tgggggggaaa gccgcagaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga 1500

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 1560

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ttcacatgca ggccctgccc cctcgctaag tttaaac 1657

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

<220>
<223> Synthetic Sequence

<400> 15

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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 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
```

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    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
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

cgggggggcgc agtgcacacg agggggctgg 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

cgggggggcgc 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 tgcccctcg 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

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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aagttcagca ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac 1200

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 acgagggggc 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 tgcccccctcg ctaa 2994

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

<220>
<223> Synthetic Sequence

<400> 21

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
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 tttaccctga 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 acgagggggc 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 acgccccgc 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

cacccтttac 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> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 35

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
1   5   10   15

Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
            20   25   30

Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
        35   40   45

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
    50   55   60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp
65   70   75   80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
                85   90   95

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

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
        115   120   125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
    130   135   140

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Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
145                 150                 155                 160

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
                165                 170                 175

Leu Ala Phe Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu
            180                 185                 190

Gln Val Glu Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr
        195                 200                 205

Gly Ser Gly Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys
    210                 215                 220

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

Val Thr Gln Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His
                245                 250                 255

Leu Thr Leu Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu
            260                 265                 270

Thr Leu Ala Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn
        275                 280                 285

Leu Val Val Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu
    290                 295                 300

Val Trp Gly Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu
305                 310                 315                 320

Asn Lys Glu Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu
                325                 330                 335

Asn Pro Glu Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln
            340                 345                 350

Val Leu Leu Glu Ser Asn Ile Lys Val Leu Pro Thr Trp Ser Thr Pro
```

```
        355                 360                 365


Val Gln Pro
    370


<210>  36
<211>  219
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  36

Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys
1               5                   10                  15


Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
            20                  25                  30


Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly
        35                  40                  45


Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
    50                  55                  60


Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
65                  70                  75                  80


Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp
                85                  90                  95


Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
            100                 105                 110


Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr
        115                 120                 125


Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
    130                 135                 140


Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
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145 150 155 160

Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu Glu
165 170 175

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

Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala Thr
195 200 205

Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
210 215

<210> 37
<211> 3799
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 37
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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 gaggggggga 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 aacggggcag aaagaaactc ctgtatatat 1020

tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc 1080

gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc aggagcgcag 1140

acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat ctaggacgaa 1200

gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg gggggaaagc 1260

cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa gataagatgg 1320

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gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt cacatgcagg 1440

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ggggaggagg ctccggcgga ggcggaagcc aggtgcagct gcagcagccc ggcgccgagc 1980

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tgaccgtgag cagcaccacg acgccagcgc cgcgaccacc aacaccggcg cccaccatcg 2340

cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc 2400

acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg gccgggactt 2460

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tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc cgcaagcatt 2580

accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagagtg aagttcagca 2640

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cctgggccgt gtccggggct cgcgcctcgc ccggctccgc ggccagcccg agactccgcg 3240

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ctcggaactc ggccttcggt ttccagggcc gcttgctgca cctgagtgcc ggccagcgcc 3660

tgggcgtcca tcttcacact gaggccaggg cacgccatgc ctggcagctt acccagggcg 3720

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ggtcggaata agtttaaac 3799

<210> 38
<211> 1260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 38

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
```

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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 Gly Ser Gly Glu Gly Arg Gly
            980                 985                 990

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

Tyr Ala  Ser Asp Ala Ser Leu  Asp Pro Glu Ala Pro  Trp Pro Pro
    1010                1015                1020

Ala Pro  Arg Ala Arg Ala Cys  Arg Val Leu Pro Trp  Ala Leu Val
    1025                1030                1035

Ala Gly  Leu Leu Leu Leu Leu  Leu Leu Ala Ala Ala  Cys Ala Val
    1040                1045                1050

Phe Leu  Ala Cys Pro Trp Ala  Val Ser Gly Ala Arg  Ala Ser Pro
```

```
    1055                1060                1065

Gly Ser  Ala Ala Ser Pro Arg  Leu Arg Glu Gly Pro  Glu Leu Ser
    1070                1075                1080

Pro Asp  Asp Pro Ala Gly Leu  Leu Asp Leu Arg Gln  Gly Met Phe
    1085                1090                1095

Ala Gln  Leu Val Ala Gln Asn  Val Leu Leu Ile Asp  Gly Pro Leu
    1100                1105                1110

Ser Trp  Tyr Ser Asp Pro Gly  Leu Ala Gly Val Ser  Leu Thr Gly
    1115                1120                1125

Gly Leu  Ser Tyr Lys Glu Asp  Thr Lys Glu Leu Val  Val Ala Lys
    1130                1135                1140

Ala Gly  Val Tyr Tyr Val Phe  Phe Gln Leu Glu Leu  Arg Arg Val
    1145                1150                1155

Val Ala  Gly Glu Gly Ser Gly  Ser Val Ser Leu Ala  Leu His Leu
    1160                1165                1170

Gln Pro  Leu Arg Ser Ala Ala  Gly Ala Ala Ala Leu  Ala Leu Thr
    1175                1180                1185

Val Asp  Leu Pro Pro Ala Ser  Ser Glu Ala Arg Asn  Ser Ala Phe
    1190                1195                1200

Gly Phe  Gln Gly Arg Leu Leu  His Leu Ser Ala Gly  Gln Arg Leu
    1205                1210                1215

Gly Val  His Leu His Thr Glu  Ala Arg Ala Arg His  Ala Trp Gln
    1220                1225                1230

Leu Thr  Gln Gly Ala Thr Val  Leu Gly Leu Phe Arg  Val Thr Pro
    1235                1240                1245

Glu Ile  Pro Ala Gly Leu Pro  Ser Pro Arg Ser Glu
    1250                1255                1260
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<210> 39
<211> 3856
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 39
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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 gaggggggggg atccgggggga 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

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tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt ggggtccttc 960

tcctgtcact ggttatcacc ctttactgca aacggggcag aaagaaactc ctgtatatat 1020

tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc 1080

gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc aggagcgcag 1140

acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat ctaggacgaa 1200

gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg gggggaaagc 1260

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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

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gcgatgtgga agaaaacccg ggccccatgt acagaatgca gctgctgagc tgcatcgccc 3060

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aggacctgat ccagagcatg cacatcgacg ccaccctgta caccgagagc gacgtgcacc 3240

ccagctgcaa ggtgaccgcc atgaagtgct tcctgctgga gctgcaggtg atcagcctgg 3300

agagcggcga cgccagcatc cacgacaccg tggagaacct gatcatcctg gccaacaaca 3360

gcctgagcag caacggcaac gtgaccgaga gcggctgcaa ggagtgcgag gagctggagg 3420

agaagaacat caaggagttc ctgcagagct tcgtgcacat cgtgcagatg ttcatcaaca 3480

ccagctccgg cggcggctcc ggcggcggcg gctccggcgg cggcggctcc ggcggcggcg 3540

gctccggcgg cggctccctg caggccccca gaagagccag aggctgcaga accctgggcc 3600

tgcccgccct gctgctgctg ctgctgctga gacccccccgc caccagaggc atcacctgcc 3660

ccccccccat gagcgtggag cacgccgaca tctgggtgaa gagctacagc ctgtacagca 3720

gagagagata catctgcaac agcggcttca agagaaaggc cggcaccagc agcctgaccg 3780

agtgcgtgct gaacaaggcc accaacgtgg cccactggac cacccccagc ctgaagtgca 3840

tcagataagt ttaaac 3856

<210> 40
<211> 1279
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 40

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 Gly Ser Gly Glu Gly Arg Gly
            980                 985                 990

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

Arg Met  Gln Leu Leu Ser Cys  Ile Ala Leu Ser Leu  Ala Leu Val
    1010                1015                1020

Thr Asn  Ser Gly Ile His Val  Phe Ile Leu Gly Cys  Phe Ser Ala
    1025                1030                1035

Gly Leu  Pro Lys Thr Glu Ala  Asn Trp Val Asn Val  Ile Ser Asp
    1040                1045                1050

Leu Lys  Lys Ile Glu Asp Leu  Ile Gln Ser Met His  Ile Asp Ala
    1055                1060                1065

Thr Leu  Tyr Thr Glu Ser Asp  Val His Pro Ser Cys  Lys Val Thr
    1070                1075                1080

Ala Met  Lys Cys Phe Leu Leu  Glu Leu Gln Val Ile  Ser Leu Glu
    1085                1090                1095

Ser Gly  Asp Ala Ser Ile His  Asp Thr Val Glu Asn  Leu Ile Ile
    1100                1105                1110

Leu Ala  Asn Asn Ser Leu Ser  Ser Asn Gly Asn Val  Thr Glu Ser
```

```
    1115                1120                1125

Gly Cys  Lys Glu Cys Glu Glu  Leu Glu Glu Lys Asn  Ile Lys Glu
    1130                1135                1140

Phe Leu  Gln Ser Phe Val His  Ile Val Gln Met Phe  Ile Asn Thr
    1145                1150                1155

Ser Ser  Gly Gly Gly Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly
    1160                1165                1170

Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Ser Leu Gln  Ala Pro Arg
    1175                1180                1185

Arg Ala  Arg Gly Cys Arg Thr  Leu Gly Leu Pro Ala  Leu Leu Leu
    1190                1195                1200

Leu Leu  Leu Leu Arg Pro Pro  Ala Thr Arg Gly Ile  Thr Cys Pro
    1205                1210                1215

Pro Pro  Met Ser Val Glu His  Ala Asp Ile Trp Val  Lys Ser Tyr
    1220                1225                1230

Ser Leu  Tyr Ser Arg Glu Arg  Tyr Ile Cys Asn Ser  Gly Phe Lys
    1235                1240                1245

Arg Lys  Ala Gly Thr Ser Ser  Leu Thr Glu Cys Val  Leu Asn Lys
    1250                1255                1260

Ala Thr  Asn Val Ala His Trp  Thr Thr Pro Ser Leu  Lys Cys Ile
    1265                1270                1275

Arg
```

<210> 41
<211> 2314
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 41
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

cgggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc 960

ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcacccct 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 cccctcgcgg cagcggcgaa ggccgcggca 1500

gcctgctgac ctgcggcgat gtggaagaaa acccgggccc catggaatac gcctctgacg 1560

cttcactgga ccccgaagcc ccgtggcctc ccgcgccccg cgctcgcgcc tgccgcgtac 1620

tgccttgggc cctggtcgcg gggctgctgc tgctgctgct gctcgctgcc gcctgcgccg 1680

tcttcctcgc ctgcccctgg gccgtgtccg gggctcgcgc ctcgcccggc tccgcggcca 1740

gcccgagact ccgcgagggt cccgagcttt cgcccgacga tcccgccggc ctcttggacc 1800

tgcggcaggg catgtttgcg cagctggtgg cccaaaatgt tctgctgatc gatgggcccc 1860

tgagctggta cagtgaccca ggcctggcag gcgtgtccct gacgggggggc ctgagctaca 1920

aagaggacac gaaggagctg gtggtggcca aggctggagt ctactatgtc ttctttcaac 1980

tagagctgcg gcgcgtggtg gccggcgagg gctcaggctc cgtttcactt gcgctgcacc 2040

tgcagccact gcgctctgct gctggggccg ccgccctggc tttgaccgtg gacctgccac 2100

ccgcctcctc cgaggctcgg aactcggcct tcggtttcca gggccgcttg ctgcacctga 2160

gtgccggcca gcgcctgggc gtccatcttc acactgaggc cagggcacgc catgcctggc 2220

agcttaccca gggcgccaca gtcttgggac tcttccgggt gacccccgaa atcccagccg 2280

gactcccttc accgaggtcg gaataagttt aaac 2314

<210> 42
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 42

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 Gly Ser Gly Glu Gly Arg
                485                 490                 495

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
```

```
            500                 505                 510

Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro
        515                 520                 525

Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala
    530                 535                 540

Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu
545                 550                 555                 560

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
                565                 570                 575

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
            580                 585                 590

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
        595                 600                 605

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

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
625                 630                 635                 640

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
                645                 650                 655

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

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

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

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
705                 710                 715                 720
```

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
725 730 735

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
740 745 750

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

<210> 43
<211> 2371
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 43
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

cgggggggcgc agtgcacacg agggggctgg 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 cccctcgcgg cagcggcgaa ggccgcggca 1500

gcctgctgac ctgcggcgat gtggaagaaa acccgggccc catgtacaga atgcagctgc 1560

tgagctgcat cgccctgagc ctggccctgg tgaccaacag cggcatccac gtgttcatcc 1620

tgggctgctt cagcgccggc ctgcccaaga ccgaggccaa ctgggtgaac gtgatcagcg 1680

acctgaagaa gatcgaggac ctgatccaga gcatgcacat cgacgccacc ctgtacaccg 1740

agagcgacgt gcaccccagc tgcaaggtga ccgccatgaa gtgcttcctg ctggagctgc 1800

aggtgatcag cctggagagc ggcgacgcca gcatccacga caccgtggag aacctgatca 1860

tcctggccaa caacagcctg agcagcaacg gcaacgtgac cgagagcggc tgcaaggagt 1920

gcgaggagct ggaggagaag aacatcaagg agttcctgca gagcttcgtg cacatcgtgc 1980

agatgttcat caacaccagc tccggcggcg gctccggcgg cggcggctcc ggcggcggcg 2040

gctccggcgg cggcggctcc ggcggcggct ccctgcaggc ccccagaaga gccagaggct 2100

gcagaaccct gggcctgccc gccctgctgc tgctgctgct gctgagaccc cccgccacca 2160

gaggcatcac ctgccccccc cccatgagcg tggagcacgc cgacatctgg gtgaagagct 2220

acagcctgta cagcagagag agatacatct gcaacagcgg cttcaagaga aaggccggca 2280

ccagcagcct gaccgagtgc gtgctgaaca aggccaccaa cgtggcccac tggaccaccc 2340

ccagcctgaa gtgcatcaga taagtttaaa c 2371

<210> 44
<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 44

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 Gly Ser Gly Glu Gly Arg
                485                 490                 495

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

Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val
        515                 520                 525

Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly
    530                 535                 540

Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys
545                 550                 555                 560

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
                565                 570                 575

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
            580                 585                 590

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
        595                 600                 605

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
    610                 615                 620

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
```

625 630 635 640

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
645 650 655

Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly
660 665 670

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

Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro
690 695 700

Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile
705 710 715 720

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
725 730 735

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
740 745 750

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
755 760 765

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
770 775 780

<210> 45
<211> 2369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 45
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggatgtgg tgatgaccca gagccatcgc tttatgagca ccagcgtggg cgaccgagtg 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 aactggacat 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 cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcaa acggggcaga 1020

aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag 1080

gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg 1140

aagttcagca ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac 1200

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 cccggcccca tgtacagaat gcagctgctg 1560

agctgcatcg ccctgagcct ggccctggtg accaacagcg gcatccacgt gttcatcctg 1620

ggctgcttca gcgccggcct gcccaagacc gaggccaact gggtgaacgt gatcagcgac 1680

ctgaagaaga tcgaggacct gatccagagc atgcacatcg acgccaccct gtacaccgag 1740

agcgacgtgc accccagctg caaggtgacc gccatgaagt gcttcctgct ggagctgcag 1800

gtgatcagcc tggagagcgg cgacgccagc atccacgaca ccgtggagaa cctgatcatc 1860

ctggccaaca acagcctgag cagcaacggc aacgtgaccg agagcggctg caaggagtgc 1920

gaggagctgg aggagaagaa catcaaggag ttcctgcaga gcttcgtgca catcgtgcag 1980

atgttcatca acaccagctc cggcggcggc tccggcggcg gcggctccgg cggcggcggc 2040

tccggcggcg gcggctccgg cggcggctcc ctgcaggccc ccagaagagc cagaggctgc 2100

agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc tgagaccccc cgccaccaga 2160

ggcatcacct gccccccccc catgagcgtg gagcacgccg acatctgggt gaagagctac 2220

agcctgtaca gcagagagag atacatctgc aacagcggct tcaagagaaa ggccggcacc 2280

agcagcctga ccgagtgcgt gctgaacaag gccaccaacg tggcccactg gaccaccccc 2340

agcctgaagt gcatcagata agtttaaac 2369

<210> 46
<211> 786
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 46

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 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

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 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala
515 520 525

```
Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser
    530                 535                 540

Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp
545                 550                 555                 560

Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr
                565                 570                 575

Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
            580                 585                 590

Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp
        595                 600                 605

Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn
    610                 615                 620

Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys
625                 630                 635                 640

Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
                645                 650                 655

His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly
            660                 665                 670

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

Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly
    690                 695                 700

Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg
705                 710                 715                 720

Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
                725                 730                 735

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
```

740 745 750

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
755 760 765

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
770 775 780

Ile Arg
785

<210> 47
<211> 3019
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 47
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggatgtg gtgatgaccc agagccatcg ctttatgagc accagcgtgg 120

gcgaccgagt gagcattacc tgccgcgcga gccaggatgt gaacaccgcg gtgagctggt 180

atcagcagaa accgggccag agcccgaaac tgctgatttt tagcgcgagc tatcgctata 240

ccggcgtgcc ggatcgcttt accggcagcg gcagcggcgc ggattttacc ctgaccatta 300

gcagcgtgca ggcggaagat ctggcggtgt attattgcca gcagcattat agcaccccgt 360

ggacctttgg cggcggcacc aaactggaca ttaaaggagg gggggatcc gggggaggag 420

gctccggcgg aggcggaagc cagattcagc tggtgcagag cggcccggat ctgaaaaaac 480

cgggcgaaac cgtgaaactg agctgcaaag cgagcggcta tacctttacc aactttggca 540

tgaactgggt gaaacaggcg ccgggcaaag gctttaaatg gatggcgtgg attaacacca 600

cccgctatac cggcgaaagc tattttgcgg atgattttaa aggccgcttt gcgtttagcg 660

tggaaaccag cgcgaccacc gcgtatctgc agattaacaa cctgaaaacc gaagataccg 720

cgacctattt ttgcgcgcgc ggcgaaattt attatggcta tgatggcggc tttgcgtatt 780

ggggccaggg caccctggtg accgtgagcg cgaccacgac gccagcgccg cgaccaccaa 840

caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag 900

cggcgggggg cgcagtgcac acgaggggc tggacttcgc ctgtgatatc tacatctggg 960

cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca 1020

aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga ccagtacaaa 1080

ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg 1140

aactgagagt gaagttcagc aggagcgcag acgcccccgc gtaccagcag ggccagaacc 1200

agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac 1260

gtggccggga ccctgagatg gggggaaagc cgcagagaag gaagaaccct caggaaggcc 1320

tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt gggatgaaag 1380

gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca 1440

aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgcggaagc ggagccacca 1500

acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccggcccc atggccctgc 1560

ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg cccgatattc 1620

agatgaccca gagcccgagc agcctgagcg cgagcgtggg cgaccgggtg accattacct 1680

gcaaagcgag ccaggatgtg ggcattgcgg tggcgtggta tcagcagaaa ccgggcaaag 1740

tgccgaaact gctgatttat tgggcgagca cccgccatac cggcgtgccg gatcgcttta 1800

gcggcagcgg cagcggcacc gattttaccc tgaccattag cagcctgcag ccggaagatg 1860

tggcgaccta ttattgccag cagtatagca gctatccgta tacctttggc cagggcacca 1920

aagtggaaat taaaggaggg gggggatccg ggggaggagg ctccggcgga ggcggaagcg 1980

aagtgcagct ggtggaaagc ggcggcggcc tggtgcagcc gggcggcagc ctgcgcctga 2040

gctgcgcggc gagcggcttt gattttagcc gctattggat gagctgggtg cgccaggcgc 2100

cgggcaaagg cctggaatgg attggcgaaa ttaacccgga tagcagcacc attaactatg 2160

cgccgagcct gaaagataaa tttattatta gccgcgataa cgcgaaaaac agcctgtatc 2220

tgcagatgaa cagcctgcgc gcggaagata ccgcggtgta ttattgcgcg cgcccggatg 2280

gcaactattg gtattttgat gtgtggggcc agggcaccct ggtgaccgtg agcagcacca 2340

ccacccccgc ccccaggccc cccacccccg cccccaccat cgccagccag cccctgagcc 2400

tgaggcccga ggcctgcagg cccgccgccg gcggcgccgt gcacaccagg ggcctggact 2460

tcgcctgcga catctacatc tgggcccccc tggccggcac ctgcggcgtg ctgctgctga 2520

gcctggtgat caccctgtac tgcaagaggg gcaggaagaa gctgctgtac atcttcaagc 2580

agcccttcat gaggcccgtg cagaccaccc aggaggagga cggctgcagc tgcaggttcc 2640

ccgaggagga ggagggcggc tgcgagctga gggtgaagtt cagcaggagc gccgacgccc 2700

ccgcctacca gcagggccag aaccagctgt acaacgagct gaacctgggc aggagggagg 2760

agtacgacgt gctggacaag aggaggggca gggaccccga gatgggcggc aagccccaga 2820

ggaggaagaa cccccaggag ggcctgtaca acgagctgca gaaggacaag atggccgagg 2880

cctacagcga gatcggcatg aagggcgaga ggaggagggg caagggccac gacggcctgt 2940

accagggcct gagcaccgcc accaaggaca cctacgacgc cctgcacatg caggccctgc 3000

cccccaggta agtttaaac 3019

<210> 48
<211> 999
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 48

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 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

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

Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
```

```
    530                 535                 540

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

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

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

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

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

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

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
```

965 970 975

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

Met Gln Ala Leu Pro Pro Arg
995

<210> 49
<211> 3040
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 49
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acgccgccag gccggatgtg gtgatgaccc agagccatcg ctttatgagc accagcgtgg 120

gcgaccgagt gagcattacc tgccgcgcga gccaggatgt gaacaccgcg gtgagctggt 180

atcagcagaa accgggccag agcccgaaac tgctgatttt tagcgcgagc tatcgctata 240

ccggcgtgcc ggatcgcttt accggcagcg gcagcggcgc ggattttacc ctgaccatta 300

gcagcgtgca ggcggaagat ctggcggtgt attattgcca gcagcattat agcaccccgt 360

ggacctttgg cggcggcacc aaactggaca ttaaaggagg gggggatcc gggggaggag 420

gctccggcgg aggcggaagc cagattcagc tggtgcagag cggcccggat ctgaaaaaac 480

cgggcgaaac cgtgaaactg agctgcaaag cgagcggcta tacctttacc aactttggca 540

tgaactgggt gaaacaggcg ccgggcaaag gctttaaatg gatggcgtgg attaacacca 600

cccgctatac cggcgaaagc tattttgcgg atgattttaa aggccgcttt gcgtttagcg 660

tggaaaccag cgcgaccacc gcgtatctgc agattaacaa cctgaaaacc gaagataccg 720

cgacctattt ttgcgcgcgc ggcgaaattt attatggcta tgatggcggc tttgcgtatt 780

ggggccaggg caccctggtg accgtgagcg cgaccacgac gccagcgccg cgaccaccaa 840

caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag 900

cggcgggggg cgcagtgcac acgaggggc tggacttcgc ctgtgatatc tacatctggg 960

cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca 1020

aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga ccagtacaaa 1080

ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg 1140

aactgagagt gaagttcagc aggagcgcag acgcccccgc gtaccagcag ggccagaacc 1200

agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac 1260

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tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt gggatgaaag 1380

gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca 1440

aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgcggaagc ggagccacca 1500

acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccggcccc atggccctgc 1560

ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg cccgaggtcc 1620

agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag atgtcctgca 1680

aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag aagcctgggc 1740

agggccttga gtggattgga tatattaatc cttacaatga tggtactaag tacaatgaga 1800

agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc tacatggagc 1860

tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg acttattact 1920

acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc tcctcaggtg 1980

gagggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg atgactcagg 2040

ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc aggtctagta 2100

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gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 2640

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc agggtgaagt 2700

tcagcaggag cgccgacgcc cccgcctacc agcagggcca gaaccagctg tacaacgagc 2760

tgaacctggg caggagggag gagtacgacg tgctggacaa gaggaggggc agggaccccg 2820

agatgggcgg caagccccag aggaggaaga acccccagga gggcctgtac aacgagctgc 2880

agaaggacaa gatggccgag gcctacagcg agatcggcat gaagggcgag aggaggaggg 2940

gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggac acctacgacg 3000

ccctgcacat gcaggccctg ccccccaggt aagtttaaac 3040

<210> 50
<211> 1006
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 50

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 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

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

Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
    530                 535                 540

Leu Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
```

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545                 550                 555                 560

Tyr Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly
                565                 570                 575

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr
            580                 585                 590

Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys
        595                 600                 605

Ser Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp
    610                 615                 620

Ser Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg
625                 630                 635                 640

Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly
                645                 650                 655

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
            660                 665                 670

Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser
        675                 680                 685

Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly
    690                 695                 700

Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln
705                 710                 715                 720

Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg
                725                 730                 735

Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg
            740                 745                 750

Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu
        755                 760                 765
```

```
Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr
    770                 775                 780

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

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
                805                 810                 815

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

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
        835                 840                 845

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
    850                 855                 860

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
865                 870                 875                 880

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

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
            900                 905                 910

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

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

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
945                 950                 955                 960

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
                965                 970                 975

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

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
995 1000 1005

<210> 51
<211> 3022
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 51
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acgccgccag gccggatgtg gtgatgaccc agagccatcg ctttatgagc accagcgtgg 120

gcgaccgagt gagcattacc tgccgcgcga gccaggatgt gaacaccgcg gtgagctggt 180

atcagcagaa accgggccag agcccgaaac tgctgatttt tagcgcgagc tatcgctata 240

ccggcgtgcc ggatcgcttt accggcagcg gcagcggcgc ggattttacc ctgaccatta 300

gcagcgtgca ggcggaagat ctggcggtgt attattgcca gcagcattat agcaccccgt 360

ggacctttgg cggcggcacc aaactggaca ttaaaggagg gggggggatcc gggggaggag 420

gctccggcgg aggcggaagc cagattcagc tggtgcagag cggcccggat ctgaaaaaac 480

cgggcgaaac cgtgaaactg agctgcaaag cgagcggcta tacctttacc aactttggca 540

tgaactgggt gaaacaggcg ccgggcaaag gctttaaatg gatggcgtgg attaacacca 600

cccgctatac cggcgaaagc tattttgcgg atgattttaa aggccgcttt gcgtttagcg 660

tggaaaccag cgcgaccacc gcgtatctgc agattaacaa cctgaaaacc gaagataccg 720

cgacctattt ttgcgcgcgc ggcgaaattt attatggcta tgatggcggc tttgcgtatt 780

ggggccaggg caccctggtg accgtgagcg cgaccacgac gccagcgccg cgaccaccaa 840

caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag 900

cggcgggggg cgcagtgcac acgaggggggc tggacttcgc ctgtgatatc tacatctggg 960

cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca 1020

aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga ccagtacaaa 1080

ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg 1140

aactgagagt gaagttcagc aggagcgcag acgcccccgc gtaccagcag ggccagaacc 1200

agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac 1260

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gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca 1440

aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgcggaagc ggagccacca 1500

acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccggcccc atggccctgc 1560

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gcagggcaag tcaggacatt agtaaatatt taaattggta tcagcagaaa ccagatggaa 1740

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gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag caagaagata 1860

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agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc ggcggatctg 1980

aggtgaaact gcaggagtca ggacctggcc tggtggcgcc ctcacagagc ctgtccgtca 2040

catgcactgt ctcaggggtc tcattacccg actatggtgt aagctggatt cgccagcctc 2100

cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca tactataatt 2160

cagctctcaa atccagactg accatcatca aggacaactc caagagccaa gttttcttaa 2220

aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa cattattact 2280

acggtggtag ctatgctatg gactactggg gccaaggaac ctcagtcacc gtctcctcaa 2340

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gcctgaggcc cgaggcctgc aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg 2460

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cccccgccta ccagcagggc cagaaccagc tgtacaacga gctgaacctg ggcaggaggg 2760

aggagtacga cgtgctggac aagaggaggg gcagggaccc cgagatgggc ggcaagcccc 2820

agaggaggaa gaacccccag gagggcctgt acaacgagct gcagaaggac aagatggccg 2880

aggcctacag cgagatcggc atgaagggcg agaggaggag gggcaagggc cacgacggcc 2940

tgtaccaggg cctgagcacc gccaccaagg acacctacga cgccctgcac atgcaggccc 3000

tgcccccag gtaagtttaa ac 3022

<210> 52
<211> 1000
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 52

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

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    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

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

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

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

Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
```

```
                565                 570                 575

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

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

Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln
    610                 615                 620

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

Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

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

Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr
        675                 680                 685

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

Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys
705                 710                 715                 720

Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
                725                 730                 735

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
            740                 745                 750

Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln
        755                 760                 765

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Met Gln Ala Leu Pro Pro Arg
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995 1000

<210> 53
<211> 1483
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 53
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acgccgccag gcccgacatc cagatgacac agactacatc ctccctgtct gcctctctgg 120

gagacagagt caccatcagt tgcagggcaa gtcaggacat tagtaaatat ttaaattggt 180

atcagcagaa accagatgga actgttaaac tcctgatcta ccatacatca agattacact 240

caggagtccc atcaaggttc agtggcagtg ggtctggaac agattattct ctcaccatta 300

gcaacctgga gcaagaagat attgccactt actttgcca acagggtaat acgcttccgt 360

acacgttcgg agggggggacc aagctggaga tcacaggtgg cggtggctcg ggcggtggtg 420

ggtcgggtgg cggcggatct gaggtgaaac tgcaggagtc aggacctggc ctggtggcgc 480

cctcacagag cctgtccgtc acatgcactg tctcaggggt ctcattaccc gactatggtg 540

taagctggat tcgccagcct ccacgaaagg gtctggagtg gctgggagta atatggggta 600

gtgaaaccac atactataat tcagctctca aatccagact gaccatcatc aaggacaact 660

ccaagagcca agttttctta aaaatgaaca gtctgcaaac tgatgacaca gccatttact 720

actgtgccaa acattattac tacggtggta gctatgctat ggactactgg ggccaaggaa 780

cctcagtcac cgtctcctca accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa cggggcagaa 1020

agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact actcaagagg 1080

aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa ctgagagtga 1140

agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag ctctataacg 1200

agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt ggccgggacc 1260

ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg tacaatgaac 1320

tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc gagcgccgga 1380

ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag gacacctacg 1440

acgcccttca catgcaggcc ctgcccccctc gctaagttta aac 1483

<210> 54
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 54

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
                485
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<210> 55
<211> 1501
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 55
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60

ccgccaggcc ggaggtccag ctgcagcagt ctggacctga gctgataaag cctggggctt 120

cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg 180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg 240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca 300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg 360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc 420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg 480

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaaacg gggcagaaag aaactcctgt atatattcaa acaaccattt atgagaccag 1080

tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa gaagaaggag 1140

gatgtgaact gagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 1200

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1260

agagacgtgg ccgggaccct gagatggggg gaaagccgca gagaaggaag aaccctcagg 1320

aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt gagattggga 1380

tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt ctcagtacag 1440

ccaccaagga cacctacgac gcccttcaca tgcaggccct gcccccctcgc taagtttaaa 1500

c 1501

<210> 56
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 56

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
```

435 440 445

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

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

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

<210> 57
<211> 2293
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 57
gcgatcgcac catggccctg cccgtgaccg ccctgctgct gcccctggcc ctgctgctgc 60

acgccgccag gcccgacatt cagctgaccc agtctccagc aatcctttct gcatctccag 120

gggagaaggt cacaatgact tgcagggcca gctcaagttt aagtttcatg cactggtacc 180

agcagaagcc aggatcctcc cccaaaccct ggatttatgc cacatccaac ctggcttctg 240

gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc acaatcagca 300

cagtggaggc tgaagatgct gcctcttatt tctgccatca gtggagtagt aacccgctca 360

cgttcggtgc tgggaccaag ctggagatca gctcgggcgg cggcggctcg ggcggcggcg 420

gctccggaga cgtcatgggg gtggattctg ggggaggctt agtgcagcct ggagggtccc 480

ggaaactctc ctgtgcagcc cctggattca ctttcagtag ctttgggatg cactgggttc 540

gtcaggctcc agagaagggg ttggagtggg tcgcatacat tagtagtccc agtagtaccc 600

tccactatgc agacagagtg aagggccgat tcaccatctc cagagacaat cccaagaaca 660

ccctgttcct gcaaatgaaa ctaccctcac tatgctatgg actactgggg ccaagggacc 720

acgttcacac caccaccccc gcccccaggc cccccacccc cgcccccacc atcgccagcc 780

agcccctgag cctgaggccc gaggcctgca ggcccgccgc cggcggcgcc gtgcacacca 840

ggggcctgga cttcgcctgc gacatctaca tctgggcccc cctggccggc acctgcggcg 900

tgctgctgct gagcctggtg atcaccctgt actgcaggag taagaggagc aggctcctgc 960

acagtgacta catgaacatg actccccgcc gccccgggcc cacccgcaag cattaccagc 1020

cctatgcccc accacgcgac ttcgcagcct atcgctccag ggtgaagttc agcaggagcg 1080

ccgacgcccc cgcctaccag cagggccaga accagctgta caacgagctg aacctgggca 1140

ggagggagga gtacgacgtg ctggacaaga ggaggggcag ggaccccgag atgggcggca 1200

agccccagag gaggaagaac ccccaggagg gcctgtacaa cgagctgcag aaggacaaga 1260

tggccgaggc ctacagcgag atcggcatga agggcgagag gaggaggggc aagggccacg 1320

acggcctgta ccagggcctg agcaccgcca ccaaggacac ctacgacgcc ctgcacatgc 1380

aggccctgcc ccccagggga agcggagcca ccaacttcag cctgctgaag caggccggcg 1440

acgtggagga gaaccccggc cccatgtaca gaatgcagct gctgagctgc atcgccctga 1500

gcctggccct ggtgaccaac agcggcatcc acgtgttcat cctgggctgc ttcagcgccg 1560

gcctgcccaa gaccgaggcc aactgggtga acgtgatcag cgacctgaag aagatcgagg 1620

acctgatcca gagcatgcac atcgacgcca ccctgtacac cgagagcgac gtgcacccca 1680

gctgcaaggt gaccgccatg aagtgcttcc tgctggagct gcaggtgatc agcctggaga 1740

gcggcgacgc cagcatccac gacaccgtgg agaacctgat catcctggcc aacaacagcc 1800

tgagcagcaa cggcaacgtg accgagagcg gctgcaagga gtgcgaggag ctggaggaga 1860

agaacatcaa ggagttcctg cagagcttcg tgcacatcgt gcagatgttc atcaacacca 1920

gctccggcgg cggctccggc ggcggcggct ccggcggcgg cggctccggc ggcggcggct 1980

ccggcggcgg ctccctgcag gcccccagaa gagccagagg ctgcagaacc ctgggcctgc 2040

ccgccctgct gctgctgctg ctgctgagac cccccgccac cagaggcatc acctgccccc 2100

cccccatgag cgtggagcac gccgacatct gggtgaagag ctacagcctg tacagcagag 2160

agagatacat ctgcaacagc ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt 2220

gcgtgctgaa caaggccacc aacgtggccc actggaccac ccccagcctg aagtgcatca 2280

gataagttta aac 2293

<210> 58
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 58

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 Leu Thr Gln Ser Pro Ala Ile Leu
            20   25   30

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

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

Lys Pro Trp Ile Tyr Ala 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

Thr Val Glu Ala Glu Asp Ala Ala Ser Tyr Phe Cys His Gln Trp Ser
            100   105   110

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp Val Met Gly Val
    130   135   140

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

Cys Ala Ala Pro Gly Phe Thr Phe Ser Ser Phe Gly Met His Trp Val
                165   170   175

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

Pro Ser Ser Thr Leu His Tyr Ala Asp Arg Val Lys Gly Arg Phe Thr

```
        195                 200                 205

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

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

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
                245                 250                 255

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
            260                 265                 270

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
        275                 280                 285

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    290                 295                 300

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
305                 310                 315                 320

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
                325                 330                 335

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
            340                 345                 350

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        355                 360                 365

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    370                 375                 380

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
385                 390                 395                 400

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
                405                 410                 415
```

```
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            420                 425                 430

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

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser
    450                 455                 460

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
465                 470                 475                 480

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
                485                 490                 495

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
            500                 505                 510

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

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
    530                 535                 540

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
545                 550                 555                 560

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
                565                 570                 575

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
            580                 585                 590

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
        595                 600                 605

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
    610                 615                 620

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
```

625 630 635 640

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

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

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

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
690 695 700

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
705 710 715 720

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
725 730 735

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
740 745 750

Leu Lys Cys Ile Arg
755

<210> 59
<211> 2389
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 59
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggaggtc cagctgcagc agtctggacc tgagctgata aagcctgggg 120

cttcagtgaa gatgtcctgc aaggcttctg gatacacatt cactagctat gttatgcact 180

gggtgaagca gaagcctggg cagggccttg agtggattgg atatattaat ccttacaatg 240

atggtactaa gtacaatgag aagttcaaag gcaaggccac actgacttca gacaaatcct 300

ccagcacagc ctacatggag ctcagcagcc tgacctctga ggactctgcg gtctattact 360

gtgcaagagg gacttattac tacggtagta gggtatttga ctactggggc caaggcacca 420

ctctcacagt ctcctcaggt ggaggggct caggcggagg tggctctggg ggtggaggct 480

cggacattgt gatgactcag gctgcaccct ctatacctgt cactcctgga gagtcagtat 540

ccatctcctg caggtctagt aagagtctcc tgaatagtaa tggcaacact tacttgtatt 600

ggttcctgca gaggccaggc cagtctcctc agctcctgat atatcggatg tccaaccttg 660

cctcaggagt cccagacagg ttcagtggca gtgggtcagg aactgctttc acactgagaa 720

tcagtagagt ggaggctgag gatgtgggtg tttattactg tatgcaacat ctagaatatc 780

cgttcacgtt cggtgctggg accaagctgg agctgaaacg gaccacgacg ccagcgccgc 840

gaccaccaac accggcgccc accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt 900

gccggccagc ggcgggggc gcagtgcaca cgagggggct ggacttcgcc tgtgatatct 960

acatctgggc gcccttggcc gggacttgtg gggtccttct cctgtcactg gttatcaccc 1020

tttactgcaa acggggcaga aagaaactcc tgtatatatt caaacaacca tttatgagac 1080

cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa gaagaagaag 1140

gaggatgtga actgagagtg aagttcagca ggagcgcaga cgcccccgcg taccagcagg 1200

gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac gatgttttgg 1260

acaagagacg tggccgggac cctgagatgg ggggaaagcc gcagagaagg aagaaccctc 1320

aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac agtgagattg 1380

ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag ggtctcagta 1440

cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgccccct cgcggaagcg 1500

gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca 1560

tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctggtg accaacagcg 1620

gcatccacgt gttcatcctg ggctgcttca gcgccggcct gcccaagacc gaggccaact 1680

gggtgaacgt gatcagcgac ctgaagaaga tcgaggacct gatccagagc atgcacatcg 1740

acgccaccct gtacaccgag agcgacgtgc accccagctg caaggtgacc gccatgaagt 1800

gcttcctgct ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca 1860

ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg 1920

agagcggctg caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga 1980

gcttcgtgca catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg 2040

gcggctccgg cggcggcggc tccggcggcg gcggctccgg cggcggctcc ctgcaggccc 2100

ccagaagagc cagaggctgc agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc 2160

tgagaccccc cgccaccaga ggcatcacct gccccccccc catgagcgtg gagcacgccg 2220

acatctgggt gaagagctac agcctgtaca gcagagagag atacatctgc aacagcggct 2280

tcaagagaaa ggccggcacc agcagcctga ccgagtgcgt gctgaacaag gccaccaacg 2340

tggcccactg gaccaccccc agcctgaagt gcatcagata agtttaaac 2389

<210> 60
<211> 789
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 60

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65 70 75 80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
100 105 110

```
Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
```

```
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
    530                 535                 540
```

```
Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

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

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
                645                 650                 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
            660                 665                 670

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

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
    690                 695                 700

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro
705                 710                 715                 720

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
                725                 730                 735

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
            740                 745                 750

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
```

```
        755                 760                 765

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
    770                 775                 780

Leu Lys Cys Ile Arg
785
```

<210> 61
<211> 2389
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 61

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acgccgccag gcccgatatc cagatgaccc agagccccag ctccctgtcc gcatccgtgg      120

gcgacagagt gacaattacc tgtagaagca gccaaagcat cgtgcatagc gtcggcaaca      180

cttttctgga gtggtatcaa cagaagcccg ggaaggcccc caaactgctg atctacaagg      240

tgagcaacag attcagcggg gtcccaagca gattctccgg cagcggctcc gggactgact      300

tcaccctgac cattagcagc ctgcagccag aggacttcgc cacatactac tgcttccaag      360

ggagccagtt cccctacacc ttcggccaag gcactaaggt ggagatcaaa gggggggggag      420

gaagcggcgg aggagggagc ggaggcgggg gatccgaagt gcaactggtc gaatccggag      480

gggggctggt ccagcctgga gggtccctga gactgagctg cgccgcaagc ggctacgagt      540

tctccaggtc ctggatgaac tgggtgaggc aggccccagg aaaagggctg gaatgggtgg      600

gcaggatcta ccctggcgac ggcgatacca actactccgg aaagttcaag ggcaggttca      660

ctatcagcgc cgacactagc aagaataccg cctacctgca gatgaatagc ctgagggccg      720

aggacaccgc cgtgtattac tgcgctagag acggcagcag ctgggattgg tacttcgacg      780

tgtggggcca gggcactctg gtgactgtga gcagcaccac cacccccgcc cccaggcccc      840

ccacccccgc ccccaccatc gccagccagc ccctgagcct gaggcccgag gcctgcaggc      900

ccgccgccgg cggcgccgtg cacaccaggg gcctggactt cgcctgcgac ttttgggtgc      960

tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg gcctttatta     1020
```

ttttctgggt gaggagtaag aggagcaggc tcctgcacag tgactacatg aacatgactc 1080

cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca cgcgacttcg 1140

cagcctatcg ctccagggtg aagttcagca ggagcgccga cgcccccgcc taccagcagg 1200

gccagaacca gctgtacaac gagctgaacc tgggcaggag ggaggagtac gacgtgctgg 1260

acaagaggag gggcagggac cccgagatgg gcggcaagcc ccagaggagg aagaacccc 1320

aggagggcct gtacaacgag ctgcagaagg acaagatggc cgaggcctac agcgagatcg 1380

gcatgaaggg cgagaggagg aggggcaagg gccacgacgg cctgtaccag ggcctgagca 1440

ccgccaccaa ggacacctac gacgccctgc acatgcaggc cctgcccccc aggggaagcg 1500

gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca 1560

tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctggtg accaacagcg 1620

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gcttcctgct ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca 1860

ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg 1920

agagcggctg caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga 1980

gcttcgtgca catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg 2040

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ccagaagagc cagaggctgc agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc 2160

tgagaccccc cgccaccaga ggcatcacct gccccccccc catgagcgtg gagcacgccg 2220

acatctgggt gaagagctac agcctgtaca gcagagagag atacatctgc aacagcggct 2280

tcaagagaaa ggccggcacc agcagcctga ccgagtgcgt gctgaacaag gccaccaacg 2340

tggcccactg gaccaccccc agcctgaagt gcatcagata agtttaaac 2389

<210> 62
<211> 789
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 62

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

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

Ser Ile Val His Ser Val Gly Asn Thr Phe Leu Glu Trp Tyr Gln Gln
50 55 60

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

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

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

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

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Glu
165 170 175

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

Leu Glu Trp Val Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr
195 200 205

```
Ser Gly Lys Phe Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
    210                 215                 220

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

Val Tyr Tyr Cys Ala Arg Asp Gly Ser Ser Trp Asp Trp Tyr Phe Asp
                245                 250                 255

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

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

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

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

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

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
            340                 345                 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
        355                 360                 365

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

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

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

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
```

```
            420                 425                 430

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

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

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

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

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

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
    530                 535                 540

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
625                 630                 635                 640
```

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
645 650 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
660 665 670

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

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
690 695 700

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro
705 710 715 720

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
725 730 735

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
740 745 750

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
755 760 765

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
770 775 780

Leu Lys Cys Ile Arg
785

<210> 63
<211> 3049
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 63
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cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg 180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg 240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca 300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg 360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc 420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg 480

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaaacg gggcagaaag aaactcctgt atatattcaa acaaccattt atgagaccag 1080

tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa gaagaaggag 1140

gatgtgaact gagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 1200

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1260

agagacgtgg ccgggaccct gagatggggg gaaagccgca gagaaggaag aaccctcagg 1320

aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt gagattggga 1380

tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt ctcagtacag 1440

ccaccaagga cacctacgac gcccttcaca tgcaggccct gcccccctcgc ggaagcggag 1500

ccaccaactt cagcctgctg aagcaggccg gcgacgtgga ggagaacccc ggccccatgg 1560

ccctgcccgt gaccgccctg ctgctgcccc tggccctgct gctgcacgcc gccaggcccg 1620

atatccagat gacccagagc cccagctccc tgtccgcatc cgtgggcgac agagtgacaa 1680

ttacctgtag aagcagccaa agcatcgtgc atagcgtcgg caacactttt ctggagtggt 1740

atcaacagaa gcccgggaag gcccccaaac tgctgatcta caaggtgagc aacagattca 1800

gcggggtccc aagcagattc tccggcagcg gctccgggac tgacttcacc ctgaccatta 1860

gcagcctgca gccagaggac ttcgccacat actactgctt ccaagggagc cagttccct 1920

acaccttcgg ccaaggcact aaggtggaga tcaaaggggg gggaggaagc ggcggaggag 1980

ggagcggagg cgggggatcc gaagtgcaac tggtcgaatc cggaggggg ctggtccagc 2040

ctggagggtc cctgagactg agctgcgccg caagcggcta cgagttctcc aggtcctgga 2100

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ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc tatcgctcca 2700

gggtgaagtt cagcaggagc gccgacgccc ccgcctacca gcagggccag aaccagctgt 2760

acaacgagct gaacctgggc aggagggagg agtacgacgt gctggacaag aggaggggca 2820

gggaccccga gatgggcggc aagccccaga ggaggaagaa cccccaggag ggcctgtaca 2880

acgagctgca gaaggacaag atggccgagg cctacagcga gatcggcatg aagggcgaga 2940

ggaggagggg caagggccac gacggcctgt accagggcct gagcaccgcc accaaggaca 3000

cctacgacgc cctgcacatg caggccctgc cccccaggta agtttaaac 3049

<210> 64
<211> 1010
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 64

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

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
```

```
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

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

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

Arg Ser Ser Gln Ser Ile Val His Ser Val Gly Asn Thr Phe Leu Glu
                565                 570                 575

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys
            580                 585                 590

Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        595                 600                 605

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    610                 615                 620

Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gln Phe Pro Tyr Thr Phe
625                 630                 635                 640

Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
```

```
               645                 650                 655

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

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

Ser Gly Tyr Glu Phe Ser Arg Ser Trp Met Asn Trp Val Arg Gln Ala
    690                 695                 700

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

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

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

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

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    770                 775                 780

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
785                 790                 795                 800

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
               805                 810                 815

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val
            820                 825                 830

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
        835                 840                 845

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
    850                 855                 860
```

```
His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
865                 870                 875                 880

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
                885                 890                 895

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
            900                 905                 910

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
        915                 920                 925

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
    930                 935                 940

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
945                 950                 955                 960

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
                965                 970                 975

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
            980                 985                 990

Thr Ala Thr Lys Asp Thr Tyr Asp  Ala Leu His Met Gln  Ala Leu Pro
        995                 1000                1005

Pro Arg
    1010
```

<210> 65
<211> 2953
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 65
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ccgccaggcc ggaggtccag ctgcagcagt ctggacctga gctgataaag cctggggctt 120

cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg 180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg 240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca 300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg 360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc 420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg 480

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

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agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1260

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ccaccaagga cacctacgac gcccttcaca tgcaggccct gcccccctcgc ggaagcggag 1500

ccaccaactt cagcctgctg aagcaggccg gcgacgtgga ggagaacccc ggccccatgg 1560

ccctgcccgt gaccgccctg ctgctgcccc tggccctgct gctgcacgcc gccaggcccg 1620

acattcagct gacccagtct ccagcaatcc tttctgcatc tccaggggag aaggtcacaa 1680

tgacttgcag ggccagctca agtttaagtt tcatgcactg gtaccagcag aagccaggat 1740

cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc cctgctcgct 1800

tcagtggcag tgggtctggg acctcttact ctctcacaat cagcacagtg gaggctgaag 1860

atgctgcctc ttatttctgc catcagtgga gtagtaaccc gctcacgttc ggtgctggga 1920

ccaagctgga gatcagctcg ggcggcggcg gctcgggcgg cggcggctcc ggagacgtca 1980

tgggggtgga ttctgggggа ggcttagtgc agcctggagg gtcccggaaa ctctcctgtg 2040

cagcccctgg attcactttc agtagctttg ggatgcactg ggttcgtcag gctccagaga 2100

aggggttgga gtgggtcgca tacattagta gtcccagtag taccctccac tatgcagaca 2160

gagtgaaggg ccgattcacc atctccagag acaatcccaa gaacaccctg ttcctgcaaa 2220

tgaaactacc ctcactatgc tatggactac tggggccaag ggaccacgtt cacaccacca 2280

cccccgcccc caggcccccc acccccgccc ccaccatcgc cagccagccc ctgagcctga 2340

ggcccgaggc ctgcaggccc gccgccggcg gcgccgtgca caccaggggc ctggacttcg 2400

cctgcgacat ctacatctgg gccccccctgg ccggcacctg cggcgtgctg ctgctgagcc 2460

tggtgatcac cctgtactgc aggagtaaga ggagcaggct cctgcacagt gactacatga 2520

acatgactcc ccgccgcccc gggcccaccc gcaagcatta ccagccctat gccccaccac 2580

gcgacttcgc agcctatcgc tccagggtga agttcagcag gagcgccgac gcccccgcct 2640

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acgtgctgga caagaggagg ggcagggacc ccgagatggg cggcaagccc cagaggagga 2760

agaaccccca ggagggcctg tacaacgagc tgcagaagga caagatggcc gaggcctaca 2820

gcgagatcgg catgaagggc gagaggagga ggggcaaggg ccacgacggc ctgtaccagg 2880

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ggtaagttta aac 2953

<210> 66
<211> 978
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 66

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

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1               5                   10                  15

His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
```

```
        435                 440                 445

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

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

Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
545                 550                 555                 560

Arg Ala Ser Ser Ser Leu Ser Phe Met His Trp Tyr Gln Gln Lys Pro
                565                 570                 575

Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
            580                 585                 590

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
        595                 600                 605

Leu Thr Ile Ser Thr Val Glu Ala Glu Asp Ala Ala Ser Tyr Phe Cys
    610                 615                 620

His Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
625                 630                 635                 640

Glu Ile Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp
                645                 650                 655
```

```
Val Met Gly Val Asp Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
            660                 665                 670

Arg Lys Leu Ser Cys Ala Ala Pro Gly Phe Thr Phe Ser Ser Phe Gly
        675                 680                 685

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

Tyr Ile Ser Ser Pro Ser Ser Thr Leu His Tyr Ala Asp Arg Val Lys
705                 710                 715                 720

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

Gln Met Lys Leu Pro Ser Leu Cys Tyr Gly Leu Leu Gly Pro Arg Asp
            740                 745                 750

His Val His Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
        755                 760                 765

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

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
785                 790                 795                 800

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
                805                 810                 815

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

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

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
    850                 855                 860

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
```

865 870 875 880

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
885 890 895

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

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
915 920 925

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
930 935 940

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
945 950 955 960

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
965 970 975

Pro Arg

<210> 67
<211> 3010
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 67
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cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg 180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg 240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca 300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg 360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc 420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg 480

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaaacg gggcagaaag aaactcctgt atatattcaa acaaccattt atgagaccag 1080

tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa gaagaaggag 1140

gatgtgaact gagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 1200

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1260

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aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt gagattggga 1380

tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt ctcagtacag 1440

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gcaccaagct ggagatcaag ggaggggggg gatccggggg aggaggctcc ggcggaggcg 1980

gaagccaggt gcagctgcag cagcccggcg ccgagctggt gagacccggc gccagcgtga 2040

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agagacccga ccagggcctg gagtggatcg gcagaatcga cccctacgac agcgagaccc 2160

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gcaactggga cgactactgg ggccagggca ccaccctgac cgtgagcagc accaccaccc 2340

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tgctggacaa gaggaggggc agggaccccg agatgggcgg caagccccag aggaggaaga 2820

acccccagga gggcctgtac aacgagctgc agaaggacaa gatggccgag gcctacagcg 2880

agatcggcat gaagggcgag aggaggaggg gcaagggcca cgacggcctg taccagggcc 2940

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aagtttaaac 3010

<210> 68
<211> 997
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 68

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr

```
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255
```

```
Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
```

```
465                 470                 475                 480

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

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

Pro Ser Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys
545                 550                 555                 560

Arg Ala Ser Lys Ser Ile Ser Lys Asp Leu Ala Trp Tyr Gln Glu Lys
                565                 570                 575

Pro Gly Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln
            580                 585                 590

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

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr
    610                 615                 620

Cys Gln Gln His Asn Lys Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
625                 630                 635                 640

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

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

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        675                 680                 685
```

```
Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Asp Gln Gly Leu
    690                 695                 700

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

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

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

Tyr Tyr Cys Ala Arg Gly Asn Trp Asp Asp Tyr Trp Gly Gln Gly Thr
        755                 760                 765

Thr Leu 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>  69
<211>  1767
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  69
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tctggacaca gaagtatttg tgacagggga catccaggtg acccagagcc ccagcagcct      120

gagcgccagc ctgggcgaga gaatcagcct gacctgcaga accagccagg acatcagcaa      180

ctacctgaac tggttccagc agaagcccga cggcaccttc aagagactga tctacgccac      240

cagcagcctg gacagcggcg tgcccaagag attcagcggc agcggcagcg gcagcgacta      300

cagcctgacc atcagcagcc tggagagcga ggacttcgcc gactactact gcctgcagta      360

cgccagctac cccttcacct tcggcagcgg caccaagctg gagatcaagg gaggggggg       420

atccgggga ggaggctccg gcggaggcgg aagcgaggtg cagctgcagg agagcggccc      480

cggcctggtg aagcccagcc agaccctgag cctgacctgc agcgtgaccg gctacagcat      540
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caccagcggc tactactggc actggatcag acagttcccc ggcaacaagc tgcagtggat 600

gggctacatc agctacagcg gcttcaccaa ctacaagacc agcctgatca acagaatcag 660

catcacccac gacaccagcg agaaccagtt cttcctgaac ctgaacagcg tgaccaccga 720

ggacaccgcc acctactact gcgccggcga cagaaccggc agctggttcg cctactgggg 780

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cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaggag 1020

taagaggagc aggctcctgc acagtgacta catgaacatg actccccgcc gccccgggcc 1080

cacccgcaag cattaccagc cctatgcccc accacgcgac ttcgcagcct atcgctccag 1140

agtgaagttc agcaggagcg cagacgcccc cgcgtaccag cagggccaga accagctcta 1200

taacgagctc aatctaggac gaagagagga gtacgatgtt ttggacaaga gacgtggccg 1260

ggaccctgag atgggggggaa agccgcagag aaggaagaac cctcaggaag gcctgtacaa 1320

tgaactgcag aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg 1380

ccggaggggc aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac 1440

ctacgacgcc cttcacatgc aggccctgcc ccctcgcggc agcggcgaag gccgcggcag 1500

cctgctgacc tgcggcgatg tggaagaaaa cccgggcccc atgtacctgt ggctgaagct 1560

gctggccttc ggcttcgcct tcctggacac cgaggtgttc gtgaccggcg gccagaacga 1620

caccagccag accagcagcc ccagcagccc gctgtttccg ggcccgagca aaccgttttg 1680

ggtgctggtg gtggtgggcg gcgtgctggc gtgctatagc ctgctggtga ccgtggcgtt 1740

tattattttt tgggtgtaag tttaaac 1767

<210> 70
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 70

Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp

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Thr Glu Val Phe Val Thr Gly Asp Ile Gln Val Thr Gln Ser Pro Ser
            20                  25                  30

Ser Leu Ser Ala Ser Leu Gly Glu Arg Ile Ser Leu Thr Cys Arg Thr
        35                  40                  45

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

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

Val Pro Lys Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Ser Leu
                85                  90                  95

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

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

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

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

Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
                165                 170                 175

Gly Tyr Tyr Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Gln
            180                 185                 190

Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Asn Tyr Lys Thr Ser
        195                 200                 205

Leu Ile Asn Arg Ile Ser Ile Thr His Asp Thr Ser Glu Asn Gln Phe
    210                 215                 220
```

```
Phe Leu Asn Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr
225                 230                 235                 240

Cys Ala Gly Asp Arg Thr Gly Ser Trp Phe Ala Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Leu Val Thr Val Ser Ala 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 Arg Ser Lys Arg
                325                 330                 335

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

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

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

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

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

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

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
```

```
        435                 440                 445

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

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

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Leu Trp Leu
            500                 505                 510

Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
        515                 520                 525

Thr Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ser Pro
    530                 535                 540

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
545                 550                 555                 560

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                565                 570                 575

Phe Trp Val
```

<210> 71
<211> 1880
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 71
atgtacctgt ggctgaagct gctggccttc ggcttcgcct tcctggacac cgaggtgttc 60

gtgaccggcg acatccaggt gacccagagc cccagcagcc tgagcgccag cctgggcgag 120

agaatcagcc tgacctgcag aaccagccag gacatcagca actacctgaa ctggttccag 180

cagaagcccg acggcacctt caagagactg atctacgcca ccagcagcct ggacagcggc 240

gtgcccaaga gattcagcgg cagcggcagc ggcagcgact acagcctgac catcagcagc 300

ctggagagcg aggacttcgc cgactactac tgcctgcagt acgccagcta ccccttcacc 360

ttcggcagcg gcaccaagct ggagatcaag ggaggggggg gatccggggg aggaggctcc 420

ggcggaggcg gaagcgaggt gcagctgcag gagagcggcc ccggcctggt gaagcccagc 480

cagaccctga gcctgacctg cagcgtgacc ggctacagca tcaccagcgg ctactactgg 540

cactggatca gacagttccc cggcaacaag ctgcagtgga tgggctacat cagctacagc 600

ggcttcacca actacaagac cagcctgatc aacagaatca gcatcaccca cgacaccagc 660

gagaaccagt tcttcctgaa cctgaacagc gtgaccaccg aggacaccgc cacctactac 720

tgcgccggcg acagaaccgg cagctggttc gcctactggg gccagggcac cctggtgacc 780

gtgagcgcca ccacgacgcc agcgccgcga ccaccaacac cggcgcccac catcgcgtcg 840

cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg cgggggggcgc agtgcacacg 900

agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg 960

gtccttctcc tgtcactggt tatcaccctt tactgcagga gtaagaggag caggctcctg 1020

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080

ccctatgccc caccacgcga cttcgcagcc tatcgctcca aacggggcag aaagaaactc 1140

ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 1200

tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc 1260

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1320

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1380

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1440

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1500

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1560

cacatgcagg ccctgccccc tcgcatcgat ggcagcggcg agggcagggg cagcctgctg 1620

acctgcggcg acgtggagga gaaccccggc cccatggcct taccagtgac cgccttgctc 1680

ctgccgctgg ccttgctgct ccacgccgcc aggccgggcc agaacgacac cagccagacc 1740

agcagcccca gcagcccccc gttccccggc cccagcaagc ccttctgggt gctggtggtg 1800

gtgggcggcg tgctggcctg ctacagcctg ctggtgaccg tggccttcat catcttctgg 1860

gtgaggagct aagtttaaac 1880

<210> 72
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 72

Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp
1 5 10 15

Thr Glu Val Phe Val Thr Gly Asp Ile Gln Val Thr Gln Ser Pro Ser
20 25 30

Ser Leu Ser Ala Ser Leu Gly Glu Arg Ile Ser Leu Thr Cys Arg Thr
35 40 45

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

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

Val Pro Lys Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Ser Leu
85 90 95

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

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

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

```
Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser
                165                 170                 175

Gly Tyr Tyr Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Gln
            180                 185                 190

Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Asn Tyr Lys Thr Ser
        195                 200                 205

Leu Ile Asn Arg Ile Ser Ile Thr His Asp Thr Ser Glu Asn Gln Phe
    210                 215                 220

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

Cys Ala Gly Asp Arg Thr Gly Ser Trp Phe Ala Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Leu Val Thr Val Ser Ala 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 Arg Ser Lys Arg
                325                 330                 335

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

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

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
```

```
    370                 375                 380

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
385                 390                 395                 400

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

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
            420                 425                 430

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
        435                 440                 445

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
    450                 455                 460

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
465                 470                 475                 480

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
                485                 490                 495

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        515                 520                 525

Ile Asp Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
    530                 535                 540

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
545                 550                 555                 560

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Gln Asn Asp
                565                 570                 575

Thr Ser Gln Thr Ser Ser Pro Ser Ser Pro Leu Phe Pro Gly Pro Ser
            580                 585                 590
```

Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
595 600 605

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
610 615 620

<210> 73
<211> 2314
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 73
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

cgggggggcgc agtgcacacg agggggctgg 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 cccctcgcgg cagcggcgaa ggccgcggca 1500

gcctgctgac ctgcggcgat gtggaagaaa acccgggccc catggaatac gcctctgacg 1560

cttcactgga ccccgaagcc ccgtggcctc ccgcgccccg cgctcgcgcc tgccgcgtac 1620

tgccttgggc cctggtcgcg gggctgctgc tgctgctgct gctcgctgcc gcctgcgccg 1680

tcttcctcgc ctgcccctgg gccgtgtccg gggctcgcgc ctcgcccggc tccgcggcca 1740

gcccgagact ccgcgagggt cccgagcttt cgcccgacga tcccgccggc ctcttggacc 1800

tgcggcaggg catgtttgcg cagctggtgg cccaaaatgt tctgctgatc gatgggcccc 1860

tgagctggta cagtgaccca ggcctggcag gcgtgtccct gacgggggggc ctgagctaca 1920

aagaggacac gaaggagctg gtggtggcca aggctggagt ctactatgtc ttctttcaac 1980

tagagctgcg gcgcgtggtg gccggcgagg gctcaggctc cgtttcactt gcgctgcacc 2040

tgcagccact gcgctctgct gctggggccg ccgccctggc tttgaccgtg gacctgccac 2100

ccgcctcctc cgaggctcgg aactcggcct tcggtttcca gggccgcttg ctgcacctga 2160

gtgccggcca gcgcctgggc gtccatcttc acactgaggc cagggcacgc catgcctggc 2220

agcttaccca gggcgccaca gtcttgggac tcttccgggt gacccccgaa atcccagccg 2280

gactcccttc accgaggtcg gaataagttt aaac 2314

<210> 74
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 74

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 Gly Ser Gly Glu Gly Arg
                485                 490                 495

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

Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro
        515                 520                 525

Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala
    530                 535                 540

Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu
545                 550                 555                 560

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
                565                 570                 575

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
            580                 585                 590

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
        595                 600                 605

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

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
625                 630                 635                 640

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
                645                 650                 655
```

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

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

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

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
705 710 715 720

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
725 730 735

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
740 745 750

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

<210> 75
<211> 2371
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 75
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

cgggggggcgc agtgcacacg agggggctgg 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 cccctcgcgg cagcggcgaa ggccgcggca 1500

gcctgctgac ctgcggcgat gtggaagaaa acccgggccc catgtacaga atgcagctgc 1560

tgagctgcat cgccctgagc ctggccctgg tgaccaacag cggcatccac gtgttcatcc 1620

tgggctgctt cagcgccggc ctgcccaaga ccgaggccaa ctgggtgaac gtgatcagcg 1680

acctgaagaa gatcgaggac ctgatccaga gcatgcacat cgacgccacc ctgtacaccg 1740

agagcgacgt gcaccccagc tgcaaggtga ccgccatgaa gtgcttcctg ctggagctgc 1800

aggtgatcag cctggagagc ggcgacgcca gcatccacga caccgtggag aacctgatca 1860

tcctggccaa caacagcctg agcagcaacg gcaacgtgac cgagagcggc tgcaaggagt 1920

gcgaggagct ggaggagaag aacatcaagg agttcctgca gagcttcgtg cacatcgtgc 1980

agatgttcat caacaccagc tccggcggcg gctccggcgg cggcggctcc ggcggcggcg 2040

gctccggcgg cggcggctcc ggcggcggct ccctgcaggc ccccagaaga gccagaggct 2100

gcagaaccct gggcctgccc gccctgctgc tgctgctgct gctgagaccc cccgccacca 2160

gaggcatcac ctgccccccc cccatgagcg tggagcacgc cgacatctgg gtgaagagct 2220

acagcctgta cagcagagag agatacatct gcaacagcgg cttcaagaga aaggccggca 2280

ccagcagcct gaccgagtgc gtgctgaaca aggccaccaa cgtggcccac tggaccaccc 2340

ccagcctgaa gtgcatcaga taagtttaaa c 2371

<210> 76
<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 76

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 Gly Ser Gly Glu Gly Arg
                485                 490                 495

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

Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val
        515                 520                 525

Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly
    530                 535                 540

Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys
545                 550                 555                 560

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
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                565                 570                 575

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
            580                 585                 590

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
        595                 600                 605

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
    610                 615                 620

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
625                 630                 635                 640

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
                645                 650                 655

Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly
            660                 665                 670

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

Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro
    690                 695                 700

Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile
705                 710                 715                 720

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
                725                 730                 735

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
            740                 745                 750

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
        755                 760                 765

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
    770                 775                 780
```

<210> 77
<211> 1223
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 77
gcgatcgctg ccatcgatac catgtatttg tggcttaaac tcttggcatt tggctttgcc 60

tttctggaca cagaagtatt tgtgacaggg gccgttcagg gtccagaaga aacagtcact 120

caagactgct tgcaactgat tgcagacagt gaaacaccaa ctatacaaaa aggatcttac 180

acatttgttc catggcttct cagctttaaa aggggaagtg ccctagaaga aaaagagaat 240

aaaatattgg tcaaagaaac tggttacttt tttatatatg gtcaggtttt atatactgat 300

aagacctacg ccatgggaca tctaattcag aggaagaagg tccatgtctt tggggatgaa 360

ttgagtctgg tgactttgtt tcgatgtatt caaaatatgc ctgaaacact acccaataat 420

tcctgctatt cagctggcat tgcaaaactg gaagaaggag atgaactcca acttgcaata 480

ccaagagaaa atgcacaaat atcactggat ggagatgtca catttttgg tgcattgaaa 540

ctgctgacca cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgcag 600

cccctgtccc tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg 660

gggctggact tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtggggtc 720

cttctcctgt cactggttat cacccтttac tgcaggagta agaggagcag gctcctgcac 780

agtgactaca tgaacatgac tccccgccgc cccgggccca cccgcaagca ttaccagccc 840

tatgccccac cacgcgactt cgcagcctat cgctccagag tgaagttcag caggagcgca 900

gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga 960

agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat gggggggaaag 1020

ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 1080

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 1140

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 1200

ctgccccctc gctaagttta aac 1223

<210> 78

<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 78

Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp
1 5 10 15

Thr Glu Val Phe Val Thr Gly Ala Val Gln Gly Pro Glu Glu Thr Val
20 25 30

Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile
35 40 45

Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg
50 55 60

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

Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr
85 90 95

Ala Met Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp
100 105 110

Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu
115 120 125

Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu
130 135 140

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

Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu Thr
165 170 175

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser

```
            180                 185                 190

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        195                 200                 205

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    210                 215                 220

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
225                 230                 235                 240

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
                245                 250                 255

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
            260                 265                 270

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
        275                 280                 285

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
    290                 295                 300

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
305                 310                 315                 320

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
                325                 330                 335

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
            340                 345                 350

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
        355                 360                 365

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
    370                 375                 380

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
385                 390                 395
```

<210> 79
<211> 1214
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 79
gcgatcgctg ccatcgatac catggcctta ccagtgaccg ccttgctcct gccgctggcc 60

ttgctgctcc acgccgccag gccggttcag ggtccagaag aaacagtcac tcaagactgc 120

ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 180

ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 240

gtcaaagaaa ctggttactt ttttatatat ggtcaggttt tatatactga taagacctac 300

gccatgggac atctaattca gaggaagaag gtccatgtct ttggggatga attgagtctg 360

gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 420

tcagctggca ttgcaaaact ggaagaagga gatgaactcc aacttgcaat accaagagaa 480

aatgcacaaa tatcactgga tggagatgtc acatttttg gtgcattgaa actgctgacc 540

acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca gcccctgtcc 600

ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag tgcacacgag ggggctggac 660

ttcgcctgtg atatctacat ctgggcgccc ttggccggga cttgtggggt ccttctcctg 720

tcactggtta tcacccttta ctgcaggagt aagaggagca ggctcctgca cagtgactac 780

atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgcccca 840

ccacgcgact tcgcagccta tcgctccaga gtgaagttca gcaggagcgc agacgccccc 900

gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag 960

tacgatgttt tggacaagag acgtggccgg gaccctgaga tgggggggaaa gccgagaagg 1020

aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac 1080

agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag 1140

ggtctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgcccccc 1200

cgctaagttt aaac 1214

<210> 80

<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 80

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 Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp
20 25 30

Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly
35 40 45

Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala
50 55 60

Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe
65 70 75 80

Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly
85 90 95

His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser
100 105 110

Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro
115 120 125

Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp
130 135 140

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

Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu Thr Thr Thr Pro
165 170 175

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu

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            180                 185                 190

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

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
    210                 215                 220

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
225                 230                 235                 240

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
                245                 250                 255

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
            260                 265                 270

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
        275                 280                 285

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
    290                 295                 300

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
305                 310                 315                 320

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
                325                 330                 335

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
            340                 345                 350

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
        355                 360                 365

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
    370                 375                 380

Ala Leu His Met Gln Ala Leu Pro Pro Arg
385                 390
```

<210> 81
<211> 2039
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 81
gcgatcgctg ccatcgatac catggcctta ccagtgaccg ccttgctcct gccgctggcc 60

ttgctgctcc acgccgccag gccggttcag ggtccagaag aaacagtcac tcaagactgc 120

ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 180

ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 240

gtcaaagaaa ctggttactt ttttatatat ggtcaggttt tatatactga taagacctac 300

gccatgggac atctaattca gaggaagaag gtccatgtct ttggggatga attgagtctg 360

gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 420

tcagctggca ttgcaaaact ggaagaagga gatgaactcc aacttgcaat accaagagaa 480

aatgcacaaa tatcactgga tggagatgtc acatttttg gtgcattgaa actgctgacc 540

acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca gcccctgtcc 600

ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag tgcacacgag ggggctggac 660

ttcgcctgtg atatctacat ctgggcgccc ttggccggga cttgtggggt ccttctcctg 720

tcactggtta tcacccttta ctgcaggagt aagaggagca ggctcctgca cagtgactac 780

atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgcccca 840

ccacgcgact tcgcagccta tcgctccaga gtgaagttca gcaggagcgc agacgccccc 900

gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag 960

tacgatgttt tggacaagag acgtggccgg gaccctgaga tgggggggaaa gccgagaagg 1020

aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac 1080

agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag 1140

ggtctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgcccccc 1200

cgcggcagcg gcgaaggccg cggcagcctg ctgacctgcg gcgatgtgga agaaaacccg 1260

ggccccatgg aatacgcctc tgacgcttca ctggaccccg aagccccgtg gcctcccgcg 1320

ccccgcgctc gcgcctgccg cgtactgcct tgggccctgg tcgcggggct gctgctgctg 1380

ctgctgctcg ctgccgcctg cgccgtcttc ctcgcctgcc cctgggccgt gtccggggct 1440

cgcgcctcgc ccggctccgc ggccagcccg agactccgcg agggtcccga gctttcgccc 1500

gacgatcccg ccggcctctt ggacctgcgg cagggcatgt ttgcgcagct ggtggcccaa 1560

aatgttctgc tgatcgatgg gcccctgagc tggtacagtg acccaggcct ggcaggcgtg 1620

tccctgacgg ggggcctgag ctacaaagag gacacgaagg agctggtggt ggccaaggct 1680

ggagtctact atgtcttctt tcaactagag ctgcggcgcg tggtggccgg cgagggctca 1740

ggctccgttt cacttgcgct gcacctgcag ccactgcgct ctgctgctgg ggccgccgcc 1800

ctggctttga ccgtggacct gccacccgcc tcctccgagg ctcggaactc ggccttcggt 1860

ttccagggcc gcttgctgca cctgagtgcc ggccagcgcc tgggcgtcca tcttcacact 1920

gaggccaggg cacgccatgc ctggcagctt acccagggcg ccacagtctt gggactcttc 1980

cgggtgaccc ccgaaatccc agccggactc ccttcaccga ggtcggaata agtttaaac 2039

<210> 82
<211> 669
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 82

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 Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp
20 25 30

Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly
35 40 45

Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala
50 55 60

Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe
65 70 75 80

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Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly
                85                  90                  95

His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser
            100                 105                 110

Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro
        115                 120                 125

Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp
    130                 135                 140

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

Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu Thr Thr Thr Pro
                165                 170                 175

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
            180                 185                 190

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

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
    210                 215                 220

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
225                 230                 235                 240

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
                245                 250                 255

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
            260                 265                 270

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
        275                 280                 285

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
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    290                 295                 300

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
305                 310                 315                 320

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
                325                 330                 335

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
            340                 345                 350

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
        355                 360                 365

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
    370                 375                 380

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
385                 390                 395                 400

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
                405                 410                 415

Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro
            420                 425                 430

Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala
        435                 440                 445

Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu
    450                 455                 460

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
465                 470                 475                 480

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
                485                 490                 495

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
            500                 505                 510
```

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Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
        515                 520                 525

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
    530                 535                 540

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
545                 550                 555                 560

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
                565                 570                 575

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
            580                 585                 590

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
        595                 600                 605

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
    610                 615                 620

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
625                 630                 635                 640

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
                645                 650                 655

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
            660                 665
```

<210> 83
<211> 2096
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 83
gcgatcgctg ccatcgatac catggcctta ccagtgaccg ccttgctcct gccgctggcc 60

ttgctgctcc acgccgccag gccggttcag ggtccagaag aaacagtcac tcaagactgc 120

ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 180

ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 240

gtcaaagaaa ctggttactt ttttatatat ggtcaggttt tatatactga taagacctac 300

gccatgggac atctaattca gaggaagaag gtccatgtct ttggggatga attgagtctg 360

gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 420

tcagctggca ttgcaaaact ggaagaagga gatgaactcc aacttgcaat accaagagaa 480

aatgcacaaa tatcactgga tggagatgtc acatttttg gtgcattgaa actgctgacc 540

acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca gcccctgtcc 600

ctgcgcccag aggcgtgccg gccagcggcg gggggcgcag tgcacacgag ggggctggac 660

ttcgcctgtg atatctacat ctgggcgccc ttggccggga cttgtggggt ccttctcctg 720

tcactggtta tcacccttta ctgcaggagt aagaggagca ggctcctgca cagtgactac 780

atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgcccca 840

ccacgcgact tcgcagccta tcgctccaga gtgaagttca gcaggagcgc agacgccccc 900

gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag 960

tacgatgttt tggacaagag acgtggccgg gaccctgaga tgggggggaaa gccgagaagg 1020

aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac 1080

agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag 1140

ggtctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgcccccc 1200

cgcggcagcg gcgaaggccg cggcagcctg ctgacctgcg gcgatgtgga agaaaacccg 1260

ggccccatgt acagaatgca gctgctgagc tgcatcgccc tgagcctggc cctggtgacc 1320

aacagcggca tccacgtgtt catcctgggc tgcttcagcg ccggcctgcc caagaccgag 1380

gccaactggg tgaacgtgat cagcgacctg aagaagatcg aggacctgat ccagagcatg 1440

cacatcgacg ccaccctgta caccgagagc gacgtgcacc ccagctgcaa ggtgaccgcc 1500

atgaagtgct tcctgctgga gctgcaggtg atcagcctgg agagcggcga cgccagcatc 1560

cacgacaccg tggagaacct gatcatcctg gccaacaaca gcctgagcag caacggcaac 1620

gtgaccgaga gcggctgcaa ggagtgcgag gagctggagg agaagaacat caaggagttc 1680

ctgcagagct tcgtgcacat cgtgcagatg ttcatcaaca ccagctccgg cggcggctcc 1740

ggcggcggcg gctccggcgg cggcggctcc ggcggcggcg gctccggcgg cggctccctg 1800

caggccccca gaagagccag aggctgcaga accctgggcc tgcccgccct gctgctgctg 1860

ctgctgctga gacccccccgc caccagaggc atcacctgcc ccccccccat gagcgtggag 1920

cacgccgaca tctgggtgaa gagctacagc ctgtacagca gagagagata catctgcaac 1980

agcggcttca agagaaaggc cggcaccagc agcctgaccg agtgcgtgct gaacaaggcc 2040

accaacgtgg cccactggac caccccccagc ctgaagtgca tcagataagt ttaaac 2096

<210> 84
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 84

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 Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp
20 25 30

Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly
35 40 45

Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala
50 55 60

Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe
65 70 75 80

Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly
85 90 95

His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser
100 105 110

Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro
115 120 125

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Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp
    130                 135                 140

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

Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu Thr Thr Thr Pro
                165                 170                 175

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
            180                 185                 190

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

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
    210                 215                 220

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
225                 230                 235                 240

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
                245                 250                 255

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
            260                 265                 270

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
        275                 280                 285

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
    290                 295                 300

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
305                 310                 315                 320

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
                325                 330                 335

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

```
            340                 345                 350

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
        355                 360                 365

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
    370                 375                 380

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
385                 390                 395                 400

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
                405                 410                 415

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

Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly
        435                 440                 445

Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys
    450                 455                 460

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
465                 470                 475                 480

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
                485                 490                 495

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
            500                 505                 510

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
        515                 520                 525

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
    530                 535                 540

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
545                 550                 555                 560
```

Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly
565 570 575

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro
595 600 605

Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile
610 615 620

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
625 630 635 640

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
645 650 655

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

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
675 680 685

<210> 85
<211> 2755
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 85
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acgccgccag gcccgccgtt cagggtccag aagaaacagt cactcaagac tgcttgcaac 120

tgattgcaga cagtgaaaca ccaactatac aaaaaggatc ttacacattt gttccatggc 180

ttctcagctt taaaagggga agtgccctag aagaaaaaga gaataaaata ttggtcaaag 240

aaactggtta ctttttttata tatggtcagg ttttatatac tgataagacc tacgccatgg 300

gacatctaat tcagaggaag aaggtccatg tctttgggga tgaattgagt ctggtgactt 360

tgtttcgatg tattcaaaat atgcctgaaa cactacccaa taattcctgc tattcagctg 420

gcattgcaaa actggaagaa ggagatgaac tccaacttgc aataccaaga gaaaatgcac 480

aaatatcact ggatggagat gtcacatttt ttggtgcatt gaaactgctg accacgacgc 540

cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc 600

cagaggcgtg ccggccagcg gcgggggggcg cagtgcacac gagggggctg gacttcgcct 660

gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc ctgtcactgg 720

ttatcaccct ttactgcagg agtaagagga gcaggctcct gcacagtgac tacatgaaca 780

tgactccccg ccgccccggg cccacccgca agcattacca gccctatgcc ccaccacgcg 840

acttcgcagc ctatcgctcc agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc 900

agcagggcca gaaccagctc tataacgagc tcaatctagg acgaagagag gagtacgatg 960

ttttggacaa gagacgtggc cgggaccctg agatgggggg aaagccgaga aggaagaacc 1020

ctcaggaagg cctgtacaat gaactgcaga aagataagat ggcggaggcc tacagtgaga 1080

ttgggatgaa aggcgagcgc cggaggggca aggggcacga tggcctttac cagggtctca 1140

gtacagccac caaggacacc tacgacgccc ttcacatgca ggccctgccc cctcgcggaa 1200

gcggagccac caacttcagc ctgctgaagc aggccggcga cgtggaggag aaccccggcc 1260

ccatggcctt accagtgacc gccttgctcc tgccgctggc cttgctgctc cacgccgcca 1320

ggccggaggt ccagctgcag cagtctggac ctgagctgat aaagcctggg gcttcagtga 1380

agatgtcctg caaggcttct ggatacacat tcactagcta tgttatgcac tgggtgaagc 1440

agaagcctgg gcagggcctt gagtggattg gatatattaa tccttacaat gatggtacta 1500

agtacaatga gaagttcaaa ggcaaggcca cactgacttc agacaaatcc tccagcacag 1560

cctacatgga gctcagcagc ctgacctctg aggactctgc ggtctattac tgtgcaagag 1620

ggacttatta ctacggtagt agggtatttg actactgggg ccaaggcacc actctcacag 1680

tctcctcagg tggaggggggc tcaggcggag gtggctctgg gggtggaggc tcggacattg 1740

tgatgactca ggctgcaccc tctatacctg tcactcctgg agagtcagta tccatctcct 1800

gcaggtctag taagagtctc ctgaatagta atggcaacac ttacttgtat tggttcctgc 1860

agaggccagg ccagtctcct cagctcctga tatatcggat gtccaacctt gcctcaggag 1920

tcccagacag gttcagtggc agtgggtcag gaactgcttt cacactgaga atcagtagag 1980

tggaggctga ggatgtgggt gtttattact gtatgcaaca tctagaatat ccgttcacgt 2040

tcggtgctgg gaccaagctg gagctgaaac ggaccacgac gccagcgccg cgaccaccaa 2100

caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag 2160

cggcgggggg cgcagtgcac acgagggggc tggacttcgc ctgtgatatc tacatctggg 2220

cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca 2280

aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga ccagtacaaa 2340

ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg 2400

aactgagagt gaagttcagc aggagcgcag acgccccgc gtaccagcag ggccagaacc 2460

agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac 2520

gtggccggga ccctgagatg gggggaaagc cgcagagaag gaagaaccct caggaaggcc 2580

tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt gggatgaaag 2640

gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca 2700

aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgctaagtt taaac 2755

<210> 86
<211> 911
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 86

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 Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
20 25 30

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
35 40 45

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

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr

```
65                  70                  75                  80

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
                85                  90                  95

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
            100                 105                 110

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
        115                 120                 125

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
    130                 135                 140

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

Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu Thr Thr Thr
                165                 170                 175

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            180                 185                 190

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        195                 200                 205

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    210                 215                 220

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
225                 230                 235                 240

Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
                245                 250                 255

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
            260                 265                 270

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
        275                 280                 285
```

```
Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
    290                 295                 300

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
305                 310                 315                 320

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
                325                 330                 335

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
            340                 345                 350

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
        355                 360                 365

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
    370                 375                 380

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr
385                 390                 395                 400

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
                405                 410                 415

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
            420                 425                 430

Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
        435                 440                 445

Leu Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
    450                 455                 460

Tyr Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly
465                 470                 475                 480

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr
                485                 490                 495

Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys
```

```
            500                 505                 510

Ser Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp
        515                 520                 525

Ser Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg
    530                 535                 540

Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly
545                 550                 555                 560

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                565                 570                 575

Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser
            580                 585                 590

Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly
        595                 600                 605

Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln
    610                 615                 620

Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg
625                 630                 635                 640

Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg
                645                 650                 655

Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu
            660                 665                 670

Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr
        675                 680                 685

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
    690                 695                 700

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
705                 710                 715                 720
```

```
Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
                725                 730                 735

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
            740                 745                 750

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        755                 760                 765

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    770                 775                 780

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
785                 790                 795                 800

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
                805                 810                 815

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            820                 825                 830

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln
        835                 840                 845

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    850                 855                 860

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
865                 870                 875                 880

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                885                 890                 895

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            900                 905                 910
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<210> 87
<211> 2734
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 87
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acgccgccag gccggtgctc acccaaaaac agaagaagca gcactctgtc ctgcacctgg 120

ttcccattaa cgccacctcc aaggatgact ccgatgtgac agaggtgatg tggcaaccag 180

ctcttaggcg tgggagaggc ctacaggccc aaggatatgg tgtccgaatc caggatgctg 240

gagtttatct gctgtatagc caggtcctgt ttcaagacgt gactttcacc atgggtcagg 300

tggtgtctcg agaaggccaa ggaaggcagg agactctatt ccgatgtata agaagtatgc 360

cctcccaccc ggaccgggcc tacaacagct gctatagcgc aggtgtcttc catttacacc 420

aaggggatat tctgagtgtc ataattcccc gggcaagggc gaaacttaac ctctctccac 480

atggaacctt cctggggttt gtgaaactga ccacgacgcc agcgccgcga ccaccaacac 540

cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 600

cgggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc 660

ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcagga 720

gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc 780

ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc tatcgctcca 840

gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct 900

ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc 960

gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg 1020

aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc 1080

ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc aaggacacct 1140

acgacgccct tcacatgcag gccctgcccc ctcgcggaag cggagccacc aacttcagcc 1200

tgctgaagca ggccggcgac gtggaggaga accccggccc catggcctta ccagtgaccg 1260

ccttgctcct gccgctggcc ttgctgctcc acgccgccag gccggaggtc cagctgcagc 1320

agtctggacc tgagctgata aagcctgggg cttcagtgaa gatgtcctgc aaggcttctg 1380

gatacacatt cactagctat gttatgcact gggtgaagca gaagcctggg cagggccttg 1440

agtggattgg atatattaat ccttacaatg atggtactaa gtacaatgag aagttcaaag 1500

gcaaggccac actgacttca gacaaatcct ccagcacagc ctacatggag ctcagcagcc 1560

tgacctctga ggactctgcg gtctattact gtgcaagagg gacttattac tacggtagta 1620

gggtatttga ctactggggc caaggcacca ctctcacagt ctcctcaggt ggagggggct 1680

caggcggagg tggctctggg ggtggaggct cggacattgt gatgactcag gctgcaccct 1740

ctatacctgt cactcctgga gagtcagtat ccatctcctg caggtctagt aagagtctcc 1800

tgaatagtaa tggcaacact tacttgtatt ggttcctgca gaggccaggc cagtctcctc 1860

agctcctgat atatcggatg tccaaccttg cctcaggagt cccagacagg ttcagtggca 1920

gtgggtcagg aactgctttc acactgagaa tcagtagagt ggaggctgag gatgtgggtg 1980

tttattactg tatgcaacat ctagaatatc cgttcacgtt cggtgctggg accaagctgg 2040

agctgaaacg gaccacgacg ccagcgccgc gaccaccaac accggcgccc accatcgcgt 2100

cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc gcagtgcaca 2160

cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc gggacttgtg 2220

gggtccttct cctgtcactg gttatcaccc tttactgcaa acggggcaga aagaaactcc 2280

tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag gaagatggct 2340

gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg aagttcagca 2400

ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac gagctcaatc 2460

taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac cctgagatgg 2520

ggggaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag 2580

ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg aggggcaagg 2640

ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac gacgcccttc 2700

acatgcaggc cctgcccccc cgctaagttt aaac 2734

<210> 88
<211> 904
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 88

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 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser
            20                  25                  30

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

Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu
    50                  55                  60

Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu
65                  70                  75                  80

Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
                85                  90                  95

Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg Cys
            100                 105                 110

Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser Cys Tyr
        115                 120                 125

Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser Val Ile
    130                 135                 140

Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly Thr Phe
145                 150                 155                 160

Leu Gly Phe Val Lys Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                165                 170                 175

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            180                 185                 190

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        195                 200                 205

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
    210                 215                 220
```

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Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser
225                 230                 235                 240

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

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            260                 265                 270

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        275                 280                 285

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    290                 295                 300

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
305                 310                 315                 320

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                325                 330                 335

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            340                 345                 350

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        355                 360                 365

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    370                 375                 380

Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
385                 390                 395                 400

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
                405                 410                 415

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Glu
            420                 425                 430

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile Lys Pro Gly Ala Ser
```

```
        435                 440                 445

Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val
    450                 455                 460

Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly
465                 470                 475                 480

Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys
                485                 490                 495

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

Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
        515                 520                 525

Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe Asp Tyr Trp Gly Gln
    530                 535                 540

Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
545                 550                 555                 560

Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ala Ala Pro
                565                 570                 575

Ser Ile Pro Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser
            580                 585                 590

Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe
        595                 600                 605

Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser
    610                 615                 620

Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
625                 630                 635                 640

Thr Ala Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly
                645                 650                 655
```

```
Val Tyr Tyr Cys Met Gln His Leu Glu Tyr Pro Phe Thr Phe Gly Ala
            660                 665                 670

Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr Thr Pro Ala Pro Arg Pro
        675                 680                 685

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    690                 695                 700

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
705                 710                 715                 720

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                725                 730                 735

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
            740                 745                 750

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
        755                 760                 765

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
    770                 775                 780

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
785                 790                 795                 800

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                805                 810                 815

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            820                 825                 830

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
        835                 840                 845

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
    850                 855                 860

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
```

865 870 875 880

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
885 890 895

His Met Gln Ala Leu Pro Pro Arg
900

<210> 89
<211> 1498
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 89
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ccgccaggcc ggacatcgtg atgacccaaa gccccgacag cctggccgtg agcctgggcg 120

agagggtgac catgaactgc aaaagcagcc agtccctgct gtactccacc aaccagaaga 180

actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg 240

ccagcactag ggaaagcggc gtgcccgata ggttcagcgg cagcgggagc ggcacagact 300

tcactctgac cattagcagc gtgcaggctg aggatgtggc cgtctactac tgccagcagt 360

actacagcta caggaccttt gggggcggaa ctaagctgga gatcaaggga gggggggat 420

ccgggggagg aggctccggc ggaggcggaa gccaagtgca actgcagcag agcggcccag 480

aggtggtcaa acctggggca agcgtgaaga tgagctgcaa ggctagcggc tataccttca 540

ccagctatgt gatccactgg gtgaggcaga aaccaggaca gggcctggac tggatcggct 600

acatcaaccc ctacaatgac ggcaccgatt atgacgaaaa attcaagggg aaggccaccc 660

tgaccagcga caccagcaca agcaccgcct acatggagct gtccagcctg aggtccgagg 720

acaccgccgt gtattactgt gccagggaga aggacaatta cgccaccggc gcttggttcg 780

cctactgggg ccagggcaca ctggtgacag tgagcagcac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg actccccgcc 1080

gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac ttcgcagcct 1140

atcgctccag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag cagggccaga 1200

accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt ttggacaaga 1260

gacgtggccg ggaccctgag atgggggaa agccgcagag aaggaagaac cctcaggaag 1320

gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagtgag attgggatga 1380

aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc agtacagcca 1440

ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgctaa gtttaaac 1498

<210> 90
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 90

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 Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

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

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
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

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
```

```
                325                 330                 335

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
        355                 360                 365

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

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

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

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

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

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

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

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


<210>  91
<211>  2560
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  91
gcgatcgcat gtatttgtgg cttaaactct tggcatttgg ctttgccttt ctggacacag       60
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aagtatttgt gacaggggac atcgtgatga cccaaagccc cgacagcctg gccgtgagcc 120

tgggcgagag ggtgaccatg aactgcaaaa gcagccagtc cctgctgtac tccaccaacc 180

agaagaacta cctggcttgg tatcaacaga agcccggaca gagccccaag ctgctgatct 240

attgggccag cactagggaa agcggcgtgc ccgataggtt cagcggcagc gggagcggca 300

cagacttcac tctgaccatt agcagcgtgc aggctgagga tgtggccgtc tactactgcc 360

agcagtacta cagctacagg acctttgggg gcggaactaa gctggagatc aagggagggg 420

ggggatccgg gggaggaggc tccggcggag gcggaagcca agtgcaactg cagcagagcg 480

gcccagaggt ggtcaaacct ggggcaagcg tgaagatgag ctgcaaggct agcggctata 540

ccttcaccag ctatgtgatc cactgggtga ggcagaaacc aggacagggc ctggactgga 600

tcggctacat caacccctac aatgacggca ccgattatga cgaaaaattc aaggggaagg 660

ccaccctgac cagcgacacc agcacaagca ccgcctacat ggagctgtcc agcctgaggt 720

ccgaggacac cgccgtgtat tactgtgcca gggagaagga caattacgcc accggcgctt 780

ggttcgccta ctggggccag ggcacactgg tgacagtgag cagcaccacg acgccagcgc 840

cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg 900

cgtgccggcc agcggcgggg ggcgcagtgc acacgagggg gctggacttc gcctgtgata 960

tctacatctg ggcgcccttg gccgggactt gtggggtcct tctcctgtca ctggttatca 1020

ccctttactg cagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 1080

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1140

agagacgtgg ccgggaccct gagatggggg gaaagccgag aaggaagaac cctcaggaag 1200

gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagtgag attgggatga 1260

aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc agtacagcca 1320

ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgcgga agcggagcca 1380

ccaacttcag cctgctgaag caggccggcg acgtggagga gaaccccggc ccctacctgt 1440

ggctgaagct gctggccttc ggcttcgcct tcctggacac cgaggtgttc gtgaccggcg 1500

acatccagat gacccagagc cccagcaccc tgagcgccag cgtgggcgac agggtgacca 1560

tcacctgcag cgccagcagc agcatcagct acatgcactg gtaccagcag aagcccggca 1620

aggcccccaa gctgctgatc tacaccacca gcaacctggc cagcggcgtg cccgccaggt 1680

tcagcggcag cggcagcggc accgagttca ccctgaccat cagcagcctg cagcccgacg 1740

acttcgccac ctactactgc caccagagga gcacctaccc cctgaccttc ggccagggca 1800

ccaaggtgga ggtgaagggc ggcggcggca gcggcggcgg cggcagcggc ggcggcggca 1860

gccaggtgca gctggtgcag agcggcgccg aggtgaagaa gcccggcagc agcgtgaagg 1920

tgagctgcaa ggccagcggc tacaccttca ccagctacag gatgcactgg gtgaggcagg 1980

cccccggcca gggcctggag tggatcggct acatcaaccc cagcaccggc tacaccgagt 2040

acaaccagaa gttcaaggac aaggccacca tcaccgccga cgagagcacc aacaccgcct 2100

acatggagct gagcagcctg aggagcgagg acaccgccgt gtactactgc gccaggggcg 2160

gcggcgtgtt cgactactgg ggccagggca ccctggtgac cgtgagcagc accaccaccc 2220

ccgcccccag gccccccacc cccgccccca ccatcgccag ccagccctg agcctgaggc 2280

ccgaggcctg caggcccgcc gccggcggcg ccgtgcacac caggggcctg gacttcgcct 2340

gcgacttttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc ttgctagtaa 2400

cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg cacagtgact 2460

acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag ccctatgccc 2520

caccacgcga cttcgcagcc tatcgctcct aagtttaaac 2560

<210> 92
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 92

Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp
1 5 10 15

Thr Glu Val Phe Val Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp
20 25 30

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

Ser Gln Ser Leu Leu Tyr Ser Thr Asn Gln Lys Asn Tyr Leu Ala Trp

```
    50                  55                  60

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

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

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

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

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

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

Val Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
                165                 170                 175

Tyr Thr Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly
            180                 185                 190

Gln Gly Leu Asp Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr
        195                 200                 205

Asp Tyr Asp Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Thr
    210                 215                 220

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

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

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

```
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

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

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

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
                325                 330                 335

Ile Thr Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
            340                 345                 350

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
        355                 360                 365

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
    370                 375                 380

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
385                 390                 395                 400

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
                405                 410                 415

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
            420                 425                 430

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
        435                 440                 445

Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
    450                 455                 460

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Tyr Leu Trp Leu Lys
465                 470                 475                 480

Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val Thr
```

```
                485                 490                 495

Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
            500                 505                 510

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr
        515                 520                 525

Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    530                 535                 540

Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
545                 550                 555                 560

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                565                 570                 575

Asp Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr Tyr Pro Leu
            580                 585                 590

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Gly Gly Gly Gly Ser
        595                 600                 605

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln
    610                 615                 620

Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys
625                 630                 635                 640

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Arg Met His Trp Val Arg
                645                 650                 655

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
            660                 665                 670

Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Ile
        675                 680                 685

Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu
    690                 695                 700
```

```
Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Gly Val
705                 710                 715                 720


Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr
                725                 730                 735


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


Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        755                 760                 765


Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val
    770                 775                 780


Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
785                 790                 795                 800


Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
                805                 810                 815


Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            820                 825                 830


Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        835                 840                 845


<210>  93
<211>  2551
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  93
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg       60

ccgccaggcc ggacatcgtg atgacccaaa gccccgacag cctggccgtg agcctgggcg      120

agagggtgac catgaactgc aaaagcagcc agtccctgct gtactccacc aaccagaaga      180

actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg      240
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ccagcactag ggaaagcggc gtgcccgata ggttcagcgg cagcgggagc ggcacagact 300

tcactctgac cattagcagc gtgcaggctg aggatgtggc cgtctactac tgccagcagt 360

actacagcta caggaccttt gggggcggaa ctaagctgga gatcaaggga ggggggggat 420

ccgggggagg aggctccggc ggaggcggaa gccaagtgca actgcagcag agcggcccag 480

aggtggtcaa acctggggca agcgtgaaga tgagctgcaa ggctagcggc tataccttca 540

ccagctatgt gatccactgg gtgaggcaga aaccaggaca gggcctggac tggatcggct 600

acatcaaccc ctacaatgac ggcaccgatt atgacgaaaa attcaagggg aaggccaccc 660

tgaccagcga caccagcaca agcaccgcct acatggagct gtccagcctg aggtccgagg 720

acaccgccgt gtattactgt gccagggaga aggacaatta cgccaccggc gcttggttcg 780

cctactgggg ccagggcaca ctggtgacag tgagcagcac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggcgcga gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcagagt gaagttcagc aggagcgcag acgccccgc gtaccagcag ggccagaacc 1080

agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac 1140

gtggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt 1200

acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg atgaaaggcg 1260

agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca gccaccaagg 1320

acacctacga cgcccttcac atgcaggccc tgcccctcg cggaagcgga gccaccaact 1380

tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggccccatg gccctgcccg 1440

tgaccgccct gctgctgccc ctggccctgc tgctgcacgc cgccaggccc gacatccaga 1500

tgacccagag ccccagcacc ctgagcgcca gcgtgggcga cagggtgacc atcacctgca 1560

gcgccagcag cagcatcagc tacatgcact ggtaccagca gaagcccggc aaggccccca 1620

agctgctgat ctacaccacc agcaacctgg ccagcggcgt gcccgccagg ttcagcggca 1680

gcggcagcgg caccgagttc accctgacca tcagcagcct gcagcccgac gacttcgcca 1740

cctactactg ccaccagagg agcacctacc ccctgacctt cggccagggc accaaggtgg 1800

aggtgaaggg cggcggcggc agcggcggcg gcggcagcgg cggcggcggc agccaggtgc 1860

agctggtgca gagcggcgcc gaggtgaaga agcccggcag cagcgtgaag gtgagctgca 1920

aggccagcgg ctacaccttc accagctaca ggatgcactg ggtgaggcag gcccccggcc 1980

agggcctgga gtggatcggc tacatcaacc ccagcaccgg ctacaccgag tacaaccaga 2040

agttcaagga caaggccacc atcaccgccg acgagagcac caacaccgcc tacatggagc 2100

tgagcagcct gaggagcgag gacaccgccg tgtactactg cgccaggggc ggcggcgtgt 2160

tcgactactg gggccagggc accctggtga ccgtgagcag caccaccacc cccgccccca 2220

ggcccccac ccccgccccc accatcgcca gccagcccct gagcctgagg cccgaggcct 2280

gcaggcccgc cgccggcggc gccgtgcaca ccaggggcct ggacttcgcc tgcgactttt 2340

gggtgctggt ggtggttggt ggagtcctgg cttgctatag cttgctagta acagtggcct 2400

ttattatttt ctgggtgagg agtaagagga gcaggctcct gcacagtgac tacatgaaca 2460

tgactccccg ccgccccggg cccacccgca agcattacca gccctatgcc ccaccacgcg 2520

acttcgcagc ctatcgctcc taagtttaaa c 2551

<210> 94
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 94

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 Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

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

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
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

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
                325                 330                 335

Leu Tyr Cys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
            340                 345                 350

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
        355                 360                 365

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
    370                 375                 380

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

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

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
            420                 425                 430

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

Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
    450                 455                 460

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
465                 470                 475                 480

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile
                485                 490                 495

Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg
            500                 505                 510
```

```
Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp
        515                 520                 525

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Thr
    530                 535                 540

Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
545                 550                 555                 560

Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe
                565                 570                 575

Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr Tyr Pro Leu Thr Phe Gly
            580                 585                 590

Gln Gly Thr Lys Val Glu Val Lys Gly Gly Gly Gly Ser Gly Gly Gly
        595                 600                 605

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
    610                 615                 620

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
625                 630                 635                 640

Gly Tyr Thr Phe Thr Ser Tyr Arg Met His Trp Val Arg Gln Ala Pro
                645                 650                 655

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Thr Gly Tyr
            660                 665                 670

Thr Glu Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp
        675                 680                 685

Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
    690                 695                 700

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Gly Val Phe Asp Tyr
705                 710                 715                 720

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
```

```
               725                 730                 735

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

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
        755                 760                 765

Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly
    770                 775                 780

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
785                 790                 795                 800

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
               805                 810                 815

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
            820                 825                 830

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        835                 840
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<210> 95
<211> 2149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 95
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60

ccgccaggcc ggacatcgtg atgacccaaa gccccgacag cctggccgtg agcctgggcg 120

agagggtgac catgaactgc aaaagcagcc agtccctgct gtactccacc aaccagaaga 180

actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg 240

ccagcactag ggaaagcggc gtgcccgata ggttcagcgg cagcgggagc ggcacagact 300

tcactctgac cattagcagc gtgcaggctg aggatgtggc cgtctactac tgccagcagt 360

actacagcta caggaccttt gggggcggaa ctaagctgga gatcaaggga gggggggat 420

ccgggggagg aggctccggc ggaggcggaa gccaagtgca actgcagcag agcggcccag 480

aggtggtcaa acctggggca agcgtgaaga tgagctgcaa ggctagcggc tataccttca 540

ccagctatgt gatccactgg gtgaggcaga aaccaggaca gggcctggac tggatcggct 600

acatcaaccc ctacaatgac ggcaccgatt atgacgaaaa attcaagggg aaggccaccc 660

tgaccagcga caccagcaca agcaccgcct acatggagct gtccagcctg aggtccgagg 720

acaccgccgt gtattactgt gccagggaga aggacaatta cgccaccggc gcttggttcg 780

cctactgggg ccagggcaca ctggtgacag tgagcagcac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg actccccgcc 1080

gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac ttcgcagcct 1140

atcgctccaa acggggcaga aagaaactcc tgtatatatt caaacaacca tttatgagac 1200

cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa gaagaagaag 1260

gaggatgtga actgagagtg aagttcagca ggagcgcaga cgcccccgcg taccagcagg 1320

gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac gatgttttgg 1380

acaagagacg tggccgggac cctgagatgg ggggaaagcc gcagagaagg aagaaccctc 1440

aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac agtgagattg 1500

ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag ggtctcagta 1560

cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgcccccc cgcggaagcg 1620

gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca 1680

tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctggtg accaacagcg 1740

gcatccacgt gttcatcctg ggctgcttca gcgccggcct gcccaagacc gaggccaact 1800

gggtgaacgt gatcagcgac ctgaagaaga tcgaggacct gatccagagc atgcacatcg 1860

acgccaccct gtacaccgag agcgacgtgc accccagctg caaggtgacc gccatgaagt 1920

gcttcctgct ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca 1980

ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg 2040

agagcggctg caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga 2100

gcttcgtgca catcgtgcag atgttcatca acaccagcta agtttaaac 2149

<210> 96
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 96

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 Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

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

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
145 150 155 160

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Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

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
                325                 330                 335

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
        355                 360                 365

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

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
385                 390                 395                 400

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
                405                 410                 415

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            420                 425                 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        435                 440                 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    450                 455                 460

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
                485                 490                 495

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
        515                 520                 525

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
545                 550                 555                 560

Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
                565                 570                 575

Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
            580                 585                 590
```

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
595 600 605

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
610 615 620

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
625 630 635 640

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
675 680 685

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
690 695 700

Met Phe Ile Asn Thr Ser
705 710

<210> 97
<211> 2623
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 97
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ccgccaggcc ggacatcgtg atgacccaaa gccccgacag cctggccgtg agcctgggcg 120

agagggtgac catgaactgc aaaagcagcc agtccctgct gtactccacc aaccagaaga 180

actacctggc ttggtatcaa cagaagcccg gacagagccc caagctgctg atctattggg 240

ccagcactag ggaaagcggc gtgcccgata ggttcagcgg cagcgggagc ggcacagact 300

tcactctgac cattagcagc gtgcaggctg aggatgtggc cgtctactac tgccagcagt 360

actacagcta caggaccttt gggggcggaa ctaagctgga gatcaaggga gggggggat 420

ccgggggagg aggctccggc ggaggcggaa gccaagtgca actgcagcag agcggcccag 480

aggtggtcaa acctggggca agcgtgaaga tgagctgcaa ggctagcggc tataccttca 540

ccagctatgt gatccactgg gtgaggcaga aaccaggaca gggcctggac tggatcggct 600

acatcaaccc ctacaatgac ggcaccgatt atgacgaaaa attcaagggg aaggccaccc 660

tgaccagcga caccagcaca agcaccgcct acatggagct gtccagcctg aggtccgagg 720

acaccgccgt gtattactgt gccagggaga aggacaatta cgccaccggc gcttggttcg 780

cctactgggg ccagggcaca ctggtgacag tgagcagcac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc ggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg actccccgcc 1080

gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac ttcgcagcct 1140

atcgctccaa acggggcaga aagaaactcc tgtatatatt caaacaacca tttatgagac 1200

cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa gaagaagaag 1260

gaggatgtga actgagagtg aagttcagca ggagcgcaga cgcccccgcg taccagcagg 1320

gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac gatgttttgg 1380

acaagagacg tggccgggac cctgagatgg ggggaaagcc gcagagaagg aagaaccctc 1440

aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac agtgagattg 1500

ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag ggtctcagta 1560

cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgcccccc cgcggaagcg 1620

gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca 1680

tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctggtg accaacagcg 1740

gcatccacgt gttcatcctg ggctgcttca gcgccggcct gcccaagacc gaggccaact 1800

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gcttcctgct ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca 1980

ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg 2040

agagcggctg caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga 2100

gcttcgtgca catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg 2160

gcggctccgg cggcggcggc tccggcggcg gcggctccgg cggcggctcc ctgcagatca 2220

cctgcccccc ccccatgagc gtggagcacg ccgacatctg ggtgaagagc tacagcctgt 2280

acagcagaga gagatacatc tgcaacagcg gcttcaagag aaaggccggc accagcagcc 2340

tgaccgagtg cgtgctgaac aaggccacca acgtggccca ctggaccacc cccagcctga 2400

agtgcatcag aaccaccacc cccgccccca ggccccccac ccccgccccc accatcgcca 2460

gccagcccct gagcctgagg cccgaggcct gcaggcccgc cgccggcggc gccgtgcaca 2520

ccaggggcct ggacttcgcc tgcgacgtgg ctatctccac gtccactgtc ctgctgtgtg 2580

ggctgagcgc tgtgtctctc ctggcatgct actaagttta aac 2623

<210> 98
<211> 868
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 98

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 Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

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

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

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                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
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300
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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
                325                 330                 335

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
        355                 360                 365

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

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
385                 390                 395                 400

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
                405                 410                 415

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            420                 425                 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        435                 440                 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    450                 455                 460

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
                485                 490                 495

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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        515                 520                 525

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
545                 550                 555                 560

Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
                565                 570                 575

Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
            580                 585                 590

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
        595                 600                 605

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
    610                 615                 620

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
625                 630                 635                 640

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
        675                 680                 685

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
    690                 695                 700

Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
705                 710                 715                 720

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

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
755 760 765

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
770 775 780

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
785 790 795 800

Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
805 810 815

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

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

Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu
850 855 860

Leu Ala Cys Tyr
865

<210> 99
<211> 2389
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 99
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acgccgccag gccggacatc gtgatgagcc agagccccag cagcctggcc gtgagcgtgg 120

gcgagaagtt caccgtgaac tgcaagagca gccagagcct gctgtacagc agcaaccaga 180

agaacttcct ggcctggtac cagcagaagc ccggccagag ccccaagctg ctgatctact 240

gggccagcac cagagagagc ggcgtgcccg acagattcat cggcagcggc agcggcaccg 300

acttcaccct gaccatcagc agcgtgaagg ccgaggacct ggccgtgtac tactgccagc 360

agcactacag ataccctgg accttcggcg gcggcaccaa gctggagatc aagagagcca 420

gaggaggggg gggatccggg ggaggaggct ccggcggagg cggaagccag gtgaccctga 480

aggagagcgg ccccggcatc ctgcagccca gccagaccct gagcctgacc tgcagcttca 540

gcggcttcag cctgaacacc agcggcgtgg gcgtgggctg gatcagacag cccagcggca 600

agggcctgga gtggctggcc cacatctggt gggacgacga cgagagatac aaccccgtgc 660

tgaagagcag actgaccatc agcaaggaca ccagcagcaa ccaggtgttc ctgaagatcg 720

ccaacgtgga caccgccgac agcgccacct actactgcgt gagaagcatg gtggcctggt 780

tcttccccta ctggggcaga ggcaccctgg tgaccgtgag cgccaccacg acgccagcgc 840

cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg 900

cgtgccggcc agcggcgggg ggcgcagtgc acacgagggg gctggacttc gcctgtgata 960

tctacatctg ggcgcccttg gccgggactt gtggggtcct tctcctgtca ctggttatca 1020

ccctttactg caggagtaag aggagcaggc tcctgcacag tgactacatg aacatgactc 1080

cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca cgcgacttcg 1140

cagcctatcg ctccagggtg aagttcagca ggagcgccga cgcccccgcc taccagcagg 1200

gccagaacca gctgtacaac gagctgaacc tgggcaggag ggaggagtac gacgtgctgg 1260

acaagaggag gggcagggac cccgagatgg gcggcaagcc ccagaggagg aagaacccc 1320

aggagggcct gtacaacgag ctgcagaagg acaagatggc cgaggcctac agcgagatcg 1380

gcatgaaggg cgagaggagg aggggcaagg gccacgacgg cctgtaccag ggcctgagca 1440

ccgccaccaa ggacacctac gacgccctgc acatgcaggc cctgcccccc aggggaagcg 1500

gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca 1560

tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctggtg accaacagcg 1620

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gggtgaacgt gatcagcgac ctgaagaaga tcgaggacct gatccagagc atgcacatcg 1740

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gcttcctgct ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca 1860

ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg 1920

agagcggctg caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga 1980

gcttcgtgca catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg 2040

gcggctccgg cggcggcggc tccggcggcg gcggctccgg cggcggctcc ctgcaggccc 2100

ccagaagagc cagaggctgc agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc 2160

tgagaccccc cgccaccaga ggcatcacct gccccccccc catgagcgtg gagcacgccg 2220

acatctgggt gaagagctac agcctgtaca gcagagagag atacatctgc aacagcggct 2280

tcaagagaaa ggccggcacc agcagcctga ccgagtgcgt gctgaacaag gccaccaacg 2340

tggcccactg gaccaccccc agcctgaagt gcatcagata agtttaaac 2389

<210> 100
<211> 789
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 100

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 Met Ser Gln Ser Pro Ser Ser Leu
20 25 30

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

Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Phe 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 Ile Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val

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            100                 105                 110

Tyr Tyr Cys Gln Gln His Tyr Arg Tyr Pro Trp Thr Phe Gly Gly Gly
        115                 120                 125

Thr Lys Leu Glu Ile Lys Arg Ala Arg Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

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

Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe
                165                 170                 175

Ser Gly Phe Ser Leu Asn Thr Ser Gly Val Gly Val Gly Trp Ile Arg
            180                 185                 190

Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp
        195                 200                 205

Asp Asp Glu Arg Tyr Asn Pro Val Leu Lys Ser Arg Leu Thr Ile Ser
    210                 215                 220

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

Thr Ala Asp Ser Ala Thr Tyr Tyr Cys Val Arg Ser Met Val Ala Trp
                245                 250                 255

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

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

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

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305                 310                 315                 320
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Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
                325                 330                 335

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
            340                 345                 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
        355                 360                 365

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
```

```
    530                 535                 540

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

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

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
                645                 650                 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
            660                 665                 670

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

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
    690                 695                 700

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro
705                 710                 715                 720

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
                725                 730                 735

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
            740                 745                 750
```

```
Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
        755                 760                 765


Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
    770                 775                 780


Leu Lys Cys Ile Arg
785
```

<210> 101
<211> 2371
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 101

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gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc       60

acgccgccag gccggacatt atgatgacac agtcgccatc atctctggct gtgtctgcag      120

gagaaaaggt cactatgacc tgtaagtcca gtcaaagtgt tttatacagt tcaaatcaga      180

agaactactt ggcctggtac cagcagaaac cagggcagtc tcctaaacta ctgatctact      240

gggcatccac tagggaatct ggtgtccctg atcgcttcac aggcagtgga tctgggacag      300

attttactct taccatcagc agtgtgcaac ctgaagacct ggcagtttat tactgtcatc      360

aatacctctc ctcgcacacg ttcggagggg ggaccaagct ggaaataaaa cggggtggcg      420

gtggctcggg cggtggtggg tcgggtggcg gcggatctca actgcagcag cctggggctg      480

agctggtgag gcctgggtct tcagtgaagc tgtcctgcaa ggcttctggc tacaccttca      540

ccaggtactg gatacattgg gtgaagcaga ggcctataca aggccttgaa tggattggta      600

acattgatcc ttctgatagt gaaactcact acaatcaaaa gttcaaggac aaggccacat      660

tgactgtaga caaatcctcc ggcacagcct acatgcagct cagcagcctg acatctgagg      720

actctgcggt ctattactgt gcaacagagg atctttacta tgctatggag tactggggtc      780

aaggaacctc agtcaccgtc tcctctacca cgacgccagc gccgcgacca ccaacaccgg      840

cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg ccagcggcgg      900

ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatctacatc tgggcgccct      960
```

tggccgggac ttgtggggtc cttctcctgt cactggttat cacccтttac tgcaggagta 1020

agaggagcag gctcctgcac agtgactaca tgaacatgac tccccgccgc cccgggccca 1080

cccgcaagca ttaccagccc tatgccccac cacgcgactt cgcagcctat cgctccagag 1140

tgaagttcag caggagcgca gacgcccccg cgtaccagca gggccagaac cagctctata 1200

acgagctcaa tctaggacga agagaggagt acgatgtttt ggacaagaga cgtggccggg 1260

accctgagat ggggggaaag ccgcagagaa ggaagaaccc tcaggaaggc ctgtacaatg 1320

aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc 1380

ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc aaggacacct 1440

acgacgccct tcacatgcag gccctgcccc ctcgcggaag cggagccacc aacttcagcc 1500

tgctgaagca ggccggcgac gtggaggaga accccggccc catgtacaga atgcagctgc 1560

tgagctgcat cgccctgagc ctggccctgg tgaccaacag cggcatccac gtgttcatcc 1620

tgggctgctt cagcgccggc ctgcccaaga ccgaggccaa ctgggtgaac gtgatcagcg 1680

acctgaagaa gatcgaggac ctgatccaga gcatgcacat cgacgccacc ctgtacaccg 1740

agagcgacgt gcaccccagc tgcaaggtga ccgccatgaa gtgcttcctg ctggagctgc 1800

aggtgatcag cctggagagc ggcgacgcca gcatccacga caccgtggag aacctgatca 1860

tcctggccaa caacagcctg agcagcaacg gcaacgtgac cgagagcggc tgcaaggagt 1920

gcgaggagct ggaggagaag aacatcaagg agttcctgca gagcttcgtg cacatcgtgc 1980

agatgttcat caacaccagc tccggcggcg gctccggcgg cggcggctcc ggcggcggcg 2040

gctccggcgg cggcggctcc ggcggcggct ccctgcaggc ccccagaaga gccagaggct 2100

gcagaaccct gggcctgccc gccctgctgc tgctgctgct gctgagaccc cccgccacca 2160

gaggcatcac ctgccccccc cccatgagcg tggagcacgc cgacatctgg gtgaagagct 2220

acagcctgta cagcagagag agatacatct gcaacagcgg cttcaagaga aaggccggca 2280

ccagcagcct gaccgagtgc gtgctgaaca aggccaccaa cgtggcccac tggaccaccc 2340

ccagcctgaa gtgcatcaga taagtttaaa c 2371

<210> 102
<211> 783
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 102

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 Met Met Thr Gln Ser Pro Ser Ser Leu
            20   25   30

Ala Val Ser Ala Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln
        35   40   45

Ser Val Leu Tyr Ser Ser 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 Thr Gly Ser Gly Ser Gly Thr
                85   90   95

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

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

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

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

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

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

Glu Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn

```
        195                 200                 205

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Gly
    210                 215                 220

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

Tyr Tyr Cys Ala Thr Glu Asp Leu Tyr Tyr Ala Met Glu Tyr Trp Gly
                245                 250                 255

Gln Gly Thr Ser Val Thr Val Ser Ser 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 Arg Ser
                325                 330                 335

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

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

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

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

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

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

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

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

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

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

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

Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr
        515                 520                 525

Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
    530                 535                 540

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
545                 550                 555                 560

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                565                 570                 575

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            580                 585                 590

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        595                 600                 605

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    610                 615                 620

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
```

625 630 635 640

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
645 650 655

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
660 665 670

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
675 680 685

Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala
690 695 700

Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr
705 710 715 720

Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
725 730 735

Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys
740 745 750

Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
755 760 765

Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
770 775 780

<210> 103
<211> 2356
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 103
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acgccgccag gccggacatc cagatgaccc agagccccag cagcctgagc gccagcgtgg 120

gcgacagagt gaccatcacc tgcagcgcca gcagcagcgt gagctacatg aactggtacc 180

agcagacccc cggcaaggcc cccaagagat ggatctacga caccagcaag ctggccagcg 240

gcgtgcccag cagattcagc ggcagcggca gcggcaccga ctacaccttc accatcagca 300

gcctgcagcc cgaggacatc gccacctact actgccagca gtggagcagc aacccccttca 360

ccttcggcca gggcaccaag ctgcagatcg gcggcggcgg cagcggcggc ggcggcagcg 420

gcggcggcgg cagccaggtg cagctggtgc agagcggcgg cggcgtggtg cagcccggca 480

gaagcctgag actgagctgc aaggccagcg gctacacctt caccagatac accatgcact 540

gggtgagaca ggcccccggc aagggcctgg agtggatcgg ctacatcaac cccagcagag 600

gctacaccaa ctacaaccag aaggtgaagg acagattcac catcagcaga gacaacagca 660

agaacaccgc cttcctgcag atggacagcc tgagacccga ggacaccggc gtgtacttct 720

gcgccagata ctacgacgac cactactgcc tggactactg gggccagggc acccccgtga 780

ccgtgagcag caccacgacg ccagcgccgc gaccaccaac accggcgccc accatcgcgt 840

cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc gcagtgcaca 900

cgaggggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc gggacttgtg 960

gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg agcaggctcc 1020

tgcacagtga ctacatgaac atgactcccc gccgccccgg gcccacccgc aagcattacc 1080

agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag ttcagcagga 1140

gcgcagacgc ccccgcgtac cagcagggcc agaaccagct ctataacgag ctcaatctag 1200

gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct gagatggggg 1260

gaaagccgca gagaaggaag aaccctcagg aaggcctgta caatgaactg cagaaagata 1320

agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg ggcaaggggc 1380

acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac gcccttcaca 1440

tgcaggccct gcccccctcgc ggaagcggag ccaccaactt cagcctgctg aagcaggccg 1500

gcgacgtgga ggagaacccc ggccccatgt acagaatgca gctgctgagc tgcatcgccc 1560

tgagcctggc cctggtgacc aacagcggca tccacgtgtt catcctgggc tgcttcagcg 1620

ccggcctgcc caagaccgag gccaactggg tgaacgtgat cagcgacctg aagaagatcg 1680

aggacctgat ccagagcatg cacatcgacg ccaccctgta caccgagagc gacgtgcacc 1740

ccagctgcaa ggtgaccgcc atgaagtgct tcctgctgga gctgcaggtg atcagcctgg 1800

agagcggcga cgccagcatc cacgacaccg tggagaacct gatcatcctg gccaacaaca 1860

gcctgagcag caacggcaac gtgaccgaga gcggctgcaa ggagtgcgag gagctggagg 1920

agaagaacat caaggagttc ctgcagagct tcgtgcacat cgtgcagatg ttcatcaaca 1980

ccagctccgg cggcggctcc ggcggcggcg gctccggcgg cggcggctcc ggcggcggcg 2040

gctccggcgg cggctccctg caggccccca gaagagccag aggctgcaga accctgggcc 2100

tgcccgccct gctgctgctg ctgctgctga gacccccgc caccagaggc atcacctgcc 2160

ccccccccat gagcgtggag cacgccgaca tctgggtgaa gagctacagc ctgtacagca 2220

gagagagata catctgcaac agcggcttca agagaaaggc cggcaccagc agcctgaccg 2280

agtgcgtgct gaacaaggcc accaacgtgg cccactggac cacccccagc ctgaagtgca 2340

tcagataagt ttaaac 2356

<210> 104
<211> 777
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 104

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 Ser Pro Ser Ser Leu
20 25 30

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

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

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

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

```
Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            100                 105                 110

Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Gly Gly
        115                 120                 125

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

Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
145                 150                 155                 160

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

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

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val Lys Asp Arg
        195                 200                 205

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

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

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val
                245                 250                 255

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

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

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

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

```
305                 310                 315                 320

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

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

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

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

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

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

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

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

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

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

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

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu
            500                 505                 510

Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His
        515                 520                 525
```

```
Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
    530                 535                 540

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
545                 550                 555                 560

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
                565                 570                 575

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
            580                 585                 590

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
        595                 600                 605

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
    610                 615                 620

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

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
                645                 650                 655

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            660                 665                 670

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

Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu
    690                 695                 700

Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met
705                 710                 715                 720

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser
                725                 730                 735

Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr
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740 745 750

Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His
755 760 765

Trp Thr Thr Pro Ser Leu Lys Cys Ile
770 775

<210> 105
<211> 2401
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 105
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccgggcgcc cagcccgcca tggccgccta caaggacatc cagatgaccc 120

agaccaccag cagcctgagc gccagcctgg gcgacagagt gaccatcagc tgcagcgcca 180

gccagggcat cagcaactac ctgaactggt accagcagaa gcccgacggc accaacaagc 240

tgctgatcta ctacaccagc agcctgcaca gcggcgtgcc cagcagattc agcggcagcg 300

gcagcggcac cgactacagc ctgcacagca acctggagcc cgaggacatc gccacctact 360

actgccagca gtacagcaag ctgccctaca ccttcggcgg cggcaccaag ctggagatca 420

agagaggcgg cggcggcagc ggcggcggcg gcagcggcgg cggcggcagc ggcggcggcg 480

gcagcgaggt gcagctggtg gagagcggcg gcggcctggt gaagcccggc ggcagcctga 540

agctgagctg cgccgccagc ggcctgacct tcagcagcta cgccatgagc tggaacagac 600

agaccccga gaagagactg gagtgggtgg ccagcatcag cagcggcggc ttcacctact 660

accccgacag caacaagggc agattcacca tcagcagaga caacgccaga aacatcctgt 720

acctgcagat gagcagcctg agaagcgagg acaccgccat gtactactgc gccagagacg 780

aggtgagagg ctacctggac gtgtggggcg ccggcaccac cgtgaccgtg agcagcacca 840

cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc 900

tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact 960

tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtggggtc cttctcctgt 1020

cactggttat cacccttac tgcaggagta agaggagcag gctcctgcac agtgactaca 1080

tgaacatgac tccccgccgc cccgggccca cccgcaagca ttaccagccc tatgccccac 1140

cacgcgactt cgcagcctat cgctccagag tgaagttcag caggagcgca gacgcccccg 1200

cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga agagaggagt 1260

acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag ccgcagagaa 1320

ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg gcggaggcct 1380

acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc 1440

agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag gccctgcccc 1500

ctcgcggaag cggagccacc aacttcagcc tgctgaagca ggccggcgac gtggaggaga 1560

accccggccc catgtacaga atgcagctgc tgagctgcat cgccctgagc ctggccctgg 1620

tgaccaacag cggcatccac gtgttcatcc tgggctgctt cagcgccggc ctgcccaaga 1680

ccgaggccaa ctgggtgaac gtgatcagcg acctgaagaa gatcgaggac ctgatccaga 1740

gcatgcacat cgacgccacc ctgtacaccg agagcgacgt gcaccccagc tgcaaggtga 1800

ccgccatgaa gtgcttcctg ctggagctgc aggtgatcag cctggagagc ggcgacgcca 1860

gcatccacga caccgtggag aacctgatca tcctggccaa caacagcctg agcagcaacg 1920

gcaacgtgac cgagagcggc tgcaaggagt gcgaggagct ggaggagaag aacatcaagg 1980

agttcctgca gagcttcgtg cacatcgtgc agatgttcat caacaccagc tccggcggcg 2040

gctccggcgg cggcggctcc ggcggcggcg gctccggcgg cggcggctcc ggcggcggct 2100

ccctgcaggc ccccagaaga gccagaggct gcagaaccct gggcctgccc gccctgctgc 2160

tgctgctgct gctgagaccc cccgccacca gaggcatcac ctgccccccc cccatgagcg 2220

tggagcacgc cgacatctgg gtgaagagct acagcctgta cagcagagag agatacatct 2280

gcaacagcgg cttcaagaga aaggccggca ccagcagcct gaccgagtgc gtgctgaaca 2340

aggccaccaa cgtggcccac tggaccaccc ccagcctgaa gtgcatcaga taagtttaaa 2400

c 2401

<210> 106
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 106

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 Gly Ala Gln Pro Ala Met Ala Ala Tyr Lys Asp
            20   25   30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
        35   40   45

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

Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Asn Lys Leu Leu Ile Tyr
65   70   75   80

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

Gly Ser Gly Thr Asp Tyr Ser Leu His Ser Asn Leu Glu Pro Glu Asp
            100   105   110

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Tyr Thr Phe
        115   120   125

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

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

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

Lys Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Ser Tyr Ala Met
            180   185   190

Ser Trp Asn Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala Ser

```
        195                 200                 205

Ile Ser Ser Gly Gly Phe Thr Tyr Tyr Pro Asp Ser Asn Lys Gly Arg
    210                 215                 220

Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu Gln Met
225                 230                 235                 240

Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Asp
                245                 250                 255

Glu Val Arg Gly Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr Val Thr
            260                 265                 270

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

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

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

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

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

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
        355                 360                 365

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
    370                 375                 380

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415
```

```
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser
        515                 520                 525

Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val
    530                 535                 540

Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn
545                 550                 555                 560

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
                565                 570                 575

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
            580                 585                 590

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
        595                 600                 605

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
    610                 615                 620

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
```

625 630 635 640

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
645 650 655

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
660 665 670

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

Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala
690 695 700

Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu
705 710 715 720

Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser
725 730 735

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
740 745 750

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
755 760 765

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
770 775 780

Thr Thr Pro Ser Leu Lys Cys Ile Arg
785 790

<210> 107
<211> 2359
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 107
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggacatc caggtgaccc agagccccag cagcctgagc gccagcctgg 120

gcgagagaat cagcctgacc tgcagaacca gccaggacat cagcaactac ctgaactggt 180

tccagcagaa gcccgacggc accttcaaga gactgatcta cgccaccagc agcctggaca 240

gcggcgtgcc caagagattc agcggcagcg gcagcggcag cgactacagc ctgaccatca 300

gcagcctgga gagcgaggac ttcgccgact actactgcct gcagtacgcc agctacccct 360

tcaccttcgg cagcggcacc aagctggaga tcaagggagg gggggatcc gggggaggag 420

gctccggcgg aggcggaagc gaggtgcagc tgcaggagag cggccccggc ctggtgaagc 480

ccagccagac cctgagcctg acctgcagcg tgaccggcta cagcatcacc agcggctact 540

actggcactg gatcagacag ttccccggca acaagctgca gtggatgggc tacatcagct 600

acagcggctt caccaactac aagaccagcc tgatcaacag aatcagcatc acccacgaca 660

ccagcgagaa ccagttcttc ctgaacctga acagcgtgac caccgaggac accgccacct 720

actactgcgc cggcgacaga accggcagct ggttcgccta ctggggccag ggcaccctgg 780

tgaccgtgag cgccaccacg acgccagcgc cgcgaccacc aacaccggcg cccaccatcg 840

cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc 900

acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg gccgggactt 960

gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag aggagcaggc 1020

tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc cgcaagcatt 1080

accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagagtg aagttcagca 1140

ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac gagctcaatc 1200

taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac cctgagatgg 1260

ggggaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag 1320

ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg aggggcaagg 1380

ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac gacgcccttc 1440

acatgcaggc cctgcccccc cgcggaagcg gagccaccaa cttcagcctg ctgaagcagg 1500

ccggcgacgt ggaggagaac cccggcccca tgtacagaat gcagctgctg agctgcatcg 1560

ccctgagcct ggccctggtg accaacagcg gcatccacgt gttcatcctg ggctgcttca 1620

gcgccggcct gcccaagacc gaggccaact gggtgaacgt gatcagcgac ctgaagaaga 1680

tcgaggacct gatccagagc atgcacatcg acgccaccct gtacaccgag agcgacgtgc 1740

accccagctg caaggtgacc gccatgaagt gcttcctgct ggagctgcag gtgatcagcc 1800

tggagagcgg cgacgccagc atccacgaca ccgtggagaa cctgatcatc ctggccaaca 1860

acagcctgag cagcaacggc aacgtgaccg agagcggctg caaggagtgc gaggagctgg 1920

aggagaagaa catcaaggag ttcctgcaga gcttcgtgca catcgtgcag atgttcatca 1980

acaccagctc cggcggcggc tccggcggcg gcggctccgg cggcggcggc tccggcggcg 2040

gcggctccgg cggcggctcc ctgcaggccc ccagaagagc cagaggctgc agaaccctgg 2100

gcctgcccgc cctgctgctg ctgctgctgc tgagaccccc cgccaccaga ggcatcacct 2160

gccccccccc catgagcgtg gagcacgccg acatctgggt gaagagctac agcctgtaca 2220

gcagagagag atacatctgc aacagcggct tcaagagaaa ggccggcacc agcagcctga 2280

ccgagtgcgt gctgaacaag gccaccaacg tggcccactg gaccaccccc agcctgaagt 2340

gcatcagata agtttaaac 2359

<210> 108
<211> 779
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 108

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 Val Thr Gln Ser Pro Ser Ser Leu
20 25 30

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

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

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

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

Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr
            100                 105                 110

Ala Ser Tyr Pro Phe Thr Phe Gly Ser 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 Glu
    130                 135                 140

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

Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr
                165                 170                 175

Tyr Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Gln Trp Met
            180                 185                 190

Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Asn Tyr Lys Thr Ser Leu Ile
        195                 200                 205

Asn Arg Ile Ser Ile Thr His Asp Thr Ser Glu Asn Gln Phe Phe Leu
    210                 215                 220

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

Gly Asp Arg Thr Gly Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
                245                 250                 255

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

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

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
```

```
    290                 295                 300

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

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

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

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
        355                 360                 365

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

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

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

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

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

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

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

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

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu
            500                 505                 510
```

```
Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile
        515                 520                 525

His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu
    530                 535                 540

Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655

Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            660                 665                 670

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

Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu
    690                 695                 700

Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro
705                 710                 715                 720

Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr
```

```
                725                 730                 735


Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly
            740                 745                 750


Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala
        755                 760                 765


His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
    770                 775


<210>  109
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  109

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
            20


<210>  110
<211>  116
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  110

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


Glu Lys Phe Thr Val Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
            20                  25                  30


Ser Asn Gln Lys Asn Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
```

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

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

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85   90   95

His Tyr Arg Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110

Lys Arg Ala Arg
        115

<210> 111
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 111

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 112
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 112

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Asn Thr Ser
            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu

```
        35                  40                  45

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Glu Arg Tyr Asn Pro Val
    50                  55                  60

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

Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr
                85                  90                  95

Cys Val Arg Ser Met Val Ala Trp Phe Phe Pro Tyr Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ala
        115
```

<210> 113
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 113

```
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20                  25                  30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        35                  40                  45
```

<210> 114
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 114

```
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1               5                   10                  15


Ser Leu Val Ile Thr Leu Tyr Cys
            20


<210>  115
<211>  41
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  115

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1               5                   10                  15


Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20                  25                  30


Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        35                  40


<210>  116
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Sequence

<400>  116

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1               5                   10                  15


Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20                  25                  30


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35                  40                  45


Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
```

50 55 60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
100 105 110

Arg

<210> 117
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 117

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 118
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 118

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

Val Thr Asn Ser
20

<210> 119
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 119

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
1 5 10 15

Thr Glu Ala Asn Trp
20

<210> 120
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 120

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
1 5 10 15

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
20 25 30

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
35 40 45

Ser Leu
50

<210> 121
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 121

```
Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
1               5                   10                  15


Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
            20                  25                  30


Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
        35                  40                  45


Gln Ser
    50
```

<210> 122
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 122

```
Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
1               5                   10
```

<210> 123
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 123

```
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1               5                   10                  15


Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
            20                  25
```

<210> 124
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 124

Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu
1   5   10   15

Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly
            20   25

<210> 125
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 125

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> 126
<211> 787
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19b-28-IL-15/IL-15sushi CAR amino acid sequence)

<400> 126

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220
```

```
Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

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
        355                 360                 365

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

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

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

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

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
```

```
        435                 440                 445

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

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

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

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

Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu
        515                 520                 525

Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe
    530                 535                 540

Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser
545                 550                 555                 560

Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala
                565                 570                 575

Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala
            580                 585                 590

Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly
        595                 600                 605

Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn
    610                 615                 620

Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu
625                 630                 635                 640

Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe
                645                 650                 655
```

Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser
660 665 670

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

Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu
690 695 700

Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr
705 710 715 720

Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile
725 730 735

Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn
740 745 750

Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val
755 760 765

Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys
770 775 780

Cys Ile Arg
785

<210> 127
<211> 2372
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-28-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 127
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gaggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg 1020

agtaagagga gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg 1080

cccacccgca agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 1140

agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260

cgggaccctg agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac 1320

aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 1380

cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 1440

acctacgacg cccttcacat gcaggccctg ccccctcgcg gcagcggcga aggccgcggc 1500

agcctgctga cctgcggcga tgtggaagaa aacccgggcc ccatgtacag aatgcagctg 1560

ctgagctgca tcgccctgag cctggccctg gtgaccaaca gcggcatcca cgtgttcatc 1620

ctgggctgct tcagcgccgg cctgcccaag accgaggcca actgggtgaa cgtgatcagc 1680

gacctgaaga agatcgagga cctgatccag agcatgcaca tcgacgccac cctgtacacc 1740

gagagcgacg tgcaccccag ctgcaaggtg accgccatga agtgcttcct gctggagctg 1800

caggtgatca gcctggagag cggcgacgcc agcatccacg acaccgtgga gaacctgatc 1860

atcctggcca acaacagcct gagcagcaac ggcaacgtga ccgagagcgg ctgcaaggag 1920

tgcgaggagc tggaggagaa gaacatcaag gagttcctgc agagcttcgt gcacatcgtg 1980

cagatgttca tcaacaccag ctccggcggc ggctccggcg gcggcggctc cggcggcggc 2040

ggctccggcg gcggcggctc cggcggcggc tccctgcagg cccccagaag agccagaggc 2100

tgcagaaccc tgggcctgcc cgccctgctg ctgctgctgc tgctgagacc ccccgccacc 2160

agaggcatca cctgcccccc ccccatgagc gtggagcacg ccgacatctg ggtgaagagc 2220

tacagcctgt acagcagaga gagatacatc tgcaacagcg gcttcaagag aaaggccggc 2280

accagcagcc tgaccgagtg cgtgctgaac aaggccacca acgtggccca ctggaccacc 2340

cccagcctga agtgcatcag ataagtttaa ac 2372

<210> 128
<211> 1024
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19b-BBpre-P2A-CD123b-2G CAR amino acid sequence)

<400> 128

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65 70 75 80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser

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            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
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Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

Ala Leu Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile
```

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    530                 535                 540

Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg
545                 550                 555                 560

Val Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala
                565                 570                 575

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr Ser
            580                 585                 590

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

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
    610                 615                 620

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe
625                 630                 635                 640

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
            660                 665                 670

Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
        675                 680                 685

Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met
    690                 695                 700

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

Ile Arg Ser Lys Ala Asp Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val
                725                 730                 735

Lys Gly Arg Phe Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr
            740                 745                 750
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Leu Gln Met Asn Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys
        755                 760                 765

Ala Arg Asp Ala Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met
    770                 775                 780

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Gly
785                 790                 795                 800

Ala Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
                805                 810                 815

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

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

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

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

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

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

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
        915                 920                 925

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

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
945                 950                 955                 960

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
```

965 970 975

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
980 985 990

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
995 1000 1005

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
1010 1015 1020

Arg

<210> 129
<211> 3083
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-BBpre-P2A-CD123b-2G CAR nucleotide sequence)

<400> 129
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccgaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gaggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accaccaccc ccgcccccag gccccccacc 840

cccgccccca ccatcgccag ccagcccctg agcctgaggc ccgaggcctg caggcccgcc 900

gccggcggcg ccgtgcacac caggggcctg gacttcgcct gcgacatcta catctgggcc 960

cccctggccg gcacctgcgg cgtgctgctg ctgagcctgg tgatcaccct gtactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagggtga agttcagcag gagcgccgac gcccccgcct accagcaggg ccagaaccag 1200

ctgtacaacg agctgaacct gggcaggagg gaggagtacg acgtgctgga caagaggagg 1260

ggcagggacc ccgagatggg cggcaagccc cagaggagga agaaccccca ggagggcctg 1320

tacaacgagc tgcagaagga caagatggcc gaggcctaca gcgagatcgg catgaagggc 1380

gagaggagga ggggcaaggg ccacgacggc ctgtaccagg gcctgagcac cgccaccaag 1440

gacacctacg acgccctgca catgcaggcc ctgccccccа ggggaagcgg agccaccaac 1500

ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggccccat ggccttacca 1560

gtgaccgcct tgctcctgcc gctggccttg ctgctccacg ccgccaggcc gatggccgac 1620

tacaaggaca tcgtgatgac ccagagccac aagttcatga gcaccagcgt gggcgacagg 1680

gtgaacatca cctgcaaggc cagccagaac gtggacagcg ccgtggcctg gtaccagcag 1740

aagcccggcc agagccccaa ggccctgatc tacagcgcca gctacaggta cagcggcgtg 1800

cccgacaggt tcaccggcag gggcagcggc accgacttca ccctgaccat cagcagcgtg 1860

caggccgagg acctggccgt gtactactgc cagcagtact acagcacccc ctggaccttc 1920

ggcggcggca ccaagctgga gatcaagagg ggcggcggcg gcagcggcgg cggcggcagc 1980

ggcggcggcg gcagcggcgg cggcggcagc gaggtgaagc tggtggagag cggcggcggc 2040

ctggtgcagc ccggcggcag cctgagcctg agctgcgccg ccagcggctt caccttcacc 2100

gactactaca tgagctgggt gaggcagccc cccggcaagg ccctggagtg gctggccctg 2160

atcaggagca aggccgacgg ctacaccacc gagtacagcg ccagcgtgaa gggcaggttc 2220

accctgagca gggacgacag ccagagcatc ctgtacctgc agatgaacgc cctgaggccc 2280

gaggacagcg ccacctacta ctgcgccagg gacgccgcct actacagcta ctacagcccc 2340

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gccccaccac gcgacttcgc agcctatcgc tccagagtga agttcagcag gagcgcagac 2760

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cagagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 2940

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 3000

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 3060

ctgccccctc gctaagttta aac 3083

<210> 130
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD22b-28-2G CAR amino acid sequence)

<400> 130

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 Val Gln Leu Gln Glu Ser Gly Ala Glu Leu
20 25 30

Ser Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu
65 70 75 80

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Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser
                85                  90                  95

Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

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

Ser Ser Leu Ala Val Ser Ala Gly Glu Asn Val Thr Met Ser Cys Lys
                165                 170                 175

Ser Ser Gln Ser Val Leu Tyr Ser Ala Asn His Lys Asn Tyr Leu Ala
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
        195                 200                 205

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
    210                 215                 220

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

Ile Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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
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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 Arg Ser Lys Arg
325 330 335

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

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

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

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

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

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

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

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

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

Ala Leu Pro Pro Arg
485

<210> 131
<211> 1466
<212> DNA

<213> Artificial Sequence

<220>
<223> (CD22b-28-2G CAR nucleotide sequence)

<400> 131
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ccccaggtgc agctgcagga gagcggcgcc gagctgagca agcccggcgc cagcgtgaag 120

atgagctgca aggccagcgg ctacaccttc accagctact ggctgcactg gatcaagcag 180

aggcccggcc agggcctgga gtggatcggc tacatcaacc ccaggaacga ctacaccgag 240

tacaaccaga acttcaagga caaggccacc ctgaccgccg acaagagcag cagcaccgcc 300

tacatgcagc tgagcagcct gaccagcgag gacagcgccg tgtactactg cgccaggagg 360

gacatcacca ccttctactg gggccagggc accaccctga ccgtgagcag cggagggggg 420

ggatccgggg gaggaggctc cggcggaggc ggaagcgaca tccagctgac ccagagcccc 480

agcagcctgg ccgtgagcgc cggcgagaac gtgaccatga gctgcaagag cagccagagc 540

gtgctgtaca gcgccaacca caagaactac ctggcctggt accagcagaa gcccggccag 600

agccccaagc tgctgatcta ctgggccagc accagggaga gcggcgtgcc cgacaggttc 660

accggcagcg gcaccgactt caccctgacc atcagcaggg tgcaggtgga ggacctggcc 720

atctactact gccaccagta cctgagcagc tggaccttcg gcggcggcac caagctggag 780

atcaagagga ccaccacccc cgcccccagg ccccccaccc ccgcccccac catcgccagc 840

cagcccctga gcctgaggcc cgaggcctgc aggcccgccg ccggcggcgc cgtgcacacc 900

aggggcctgg acttcgcctg cgacatctac atctgggccc ccctggccgg cacctgcggc 960

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cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080

ccctatgccc caccacgcga cttcgcagcc tatcgctcca gggtgaagtt cagcaggagc 1140

gccgacgccc ccgcctacca gcagggccag aaccagctgt acaacgagct gaacctgggc 1200

aggagggagg agtacgacgt gctggacaag aggaggggca gggaccccga gatgggcggc 1260

aagcccagga ggaagaaccc ccaggagggc ctgtacaacg agctgcagaa ggacaagatg 1320

gccgaggcct acagcgagat cggcatgaag ggcgagagga ggaggggcaa gggccacgac 1380

ggcctgtacc agggcctgag caccgccacc aaggacacct acgacgccct gcacatgcag 1440

gccctgcccc ccaggtaagt ttaaac 1466

<210> 132
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD33b-BB-2G CAR amino acid sequence)

<400> 132

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
50 55 60

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

Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
85 90 95

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

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

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

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

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys

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                165                 170                 175

Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp
        195                 200                 205

Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser
    210                 215                 220

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn Leu Gln
225                 230                 235                 240

Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr Tyr Pro
                245                 250                 255

Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

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

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

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

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
        355                 360                 365

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
    370                 375                 380
```

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385 390 395 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
405 410 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
420 425 430

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
435 440 445

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

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

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
485 490 495

Arg

<210> 133
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD33b-BB-2G CAR nucleotide sequence)

<400> 133
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccatggccg actacaagga catcgtgatg acccagagcc acaagttcct gctggtgagc 120

gtgggcgaca gggtgagcat cacctgcaag gccagccagg acgtgagcac cgccgtggcc 180

tggtaccagc agaagcccgg ccagagcccc aagctgctga tctacagcgc cagctacagg 240

tacaccggcg tgcccgacag gttcatcggc agcggcagcg gcaccgactt caccctgacc 300

atcagcagcg tgcaggccga ggacctggcc gactacttct gccagcagca ctacagcacc 360

```
cccctgacct tcggcgccgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc      420

ggcggcggca gcggcggcgg cggcagcagc ggcggcggca gcgaggtgca gctgaaggag      480

agcggccccg gcctggtggc ccccagccag agcctgagca tcacctgcac cgtgagcggc      540

ttccccctga ccagctacgg cgtgagctgg gtgaggcagc cccccggcaa gggcctggag      600

tggctgggcg tgatctgggg cgacggcagc accaactacc acagcgccct gatcagcagg      660

ctgagcatca gcaaggacaa cagcaagagc caggtgttcc tgaagctgaa caacctgcag      720

accgacgaca ccgccaccta ctactgcgcc agggacacct actaccccta ctacgccatg      780

gactactggg gccagggcac cagcgtgacc gtgagcagca ccaccacccc cgcccccagg      840

ccccccaccc ccgcccccac catcgccagc cagcccctga gcctgaggcc cgaggcctgc      900

aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg acttcgcctg cgacatctac      960

atctgggccc ccctggccgg cacctgcggc gtgctgctgc tgagcctggt gatcaccctg     1020

tactgcaaac ggggcagaaa gaaactcctg tatatattca aacaaccatt tatgagacca     1080

gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga     1140

ggatgtgaac tgagggtgaa gttcagcagg agcgccgacg cccccgccta ccagcagggc     1200

cagaaccagc tgtacaacga gctgaacctg ggcaggaggg aggagtacga cgtgctggac     1260

aagaggaggg gcagggaccc cgagatgggc ggcaagcccc agaggaggaa gaacccccag     1320

gagggcctgt acaacgagct gcagaaggac aagatggccg aggcctacag cgagatcggc     1380

atgaagggcg agaggaggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc     1440

gccaccaagg acacctacga cgccctgcac atgcaggccc tgcccccag gtaa            1494
```

<210> 134
<211> 1060
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD45-28-2G-4-1BBL-IL15RA "super" CAR amino acid sequence)

<400> 134

```
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
```

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    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 Gly Ser Gly Glu Gly Arg
                485                 490                 495

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

Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro
        515                 520                 525

Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala
    530                 535                 540

Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu
545                 550                 555                 560

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
                565                 570                 575

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
            580                 585                 590

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
        595                 600                 605

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

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
625                 630                 635                 640

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
                645                 650                 655

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
            660                 665                 670
```

```
Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
        675                 680                 685

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

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
705                 710                 715                 720

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
                725                 730                 735

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
            740                 745                 750

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

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

Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser
785                 790                 795                 800

Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys
                805                 810                 815

Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile
            820                 825                 830

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
        835                 840                 845

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
    850                 855                 860

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
865                 870                 875                 880

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
```

885 890 895

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
900 905 910

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
915 920 925

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly
930 935 940

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
945 950 955 960

Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr
965 970 975

Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala
980 985 990

Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp
995 1000 1005

Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
1010 1015 1020

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
1025 1030 1035

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr
1040 1045 1050

Pro Ser Leu Lys Cys Ile Arg
1055 1060

<210> 135
<211> 3191
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD45-28-2G-4-1BBL-IL15RA sequence, "super" CAR nucleotide

sequence)

<400> 135
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcg tgctgaccca gagccccgcc agcctggccg tgagcctggg ccagagggcc 120

accatcagct gcagggccag caagagcgtg agcaccagcg gctacagcta cctgcactgg 180

taccagcaga agcccggcca gccccccaag ctgctgatct acctggccag caacctggag 240

agcggcgtgc ccgccaggtt cagcggcagc ggcagcggca ccgacttcac cctgaacatc 300

caccccgtgg aggaggagga cgccgccacc tactactgcc agcacagcag ggagctgccc 360

ttcaccttcg gcagcggcac caagctggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag ccaggtgcag ctggtggaga gcggcggcgg cctggtgcag 480

cccggcggca gcctgaagct gagctgcgcc gccagcggct tcgacttcag caggtactgg 540

atgagctggg tgaggcaggc ccccggcaag ggcctggagt ggatcggcga gatcaacccc 600

accagcagca ccatcaactt caccccccagc ctgaaggaca aggtgttcat cagcagggac 660

aacgccaaga acaccctgta cctgcagatg agcaaggtga ggagcgagga caccgccctg 720

tactactgcg ccaggggcaa ctactacagg tacggcgacg ccatggacta ctggggccag 780

ggcaccagcg tgaccgtgag caccacgacg ccagcgccgc gaccaccaac accggcgccc 840

accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc 900

gcagtgcaca cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg 1020

agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gcccacccgc 1080

aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag 1140

ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc agaaccagct ctataacgag 1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1260

gagatggggg gaaagccgca gagaaggaag aaccctcagg aaggcctgta caatgaactg 1320

cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg 1380

ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac 1440

gcccttcaca tgcaggccct gcccccctcgc ggcagcggcg aaggccgcgg cagcctgctg 1500

acctgcggcg atgtggaaga aaacccgggc cccatggaat acgcctctga cgcttcactg 1560

gaccccgaag ccccgtggcc tcccgcgccc cgcgctcgcg cctgccgcgt actgccttgg 1620

gccctggtcg cggggctgct gctgctgctg ctgctcgctg ccgcctgcgc cgtcttcctc 1680

gcctgcccct gggccgtgtc cggggctcgc gcctcgcccg gctccgcggc cagcccgaga 1740

ctccgcgagg gtcccgagct ttcgcccgac gatcccgccg gcctcttgga cctgcggcag 1800

ggcatgtttg cgcagctggt ggcccaaaat gttctgctga tcgatgggcc cctgagctgg 1860

tacagtgacc caggcctggc aggcgtgtcc ctgacggggg gcctgagcta caaagaggac 1920

acgaaggagc tggtggtggc caaggctgga gtctactatg tcttctttca actagagctg 1980

cggcgcgtgg tggccggcga gggctcaggc tccgtttcac ttgcgctgca cctgcagcca 2040

ctgcgctctg ctgctggggc cgccgccctg gctttgaccg tggacctgcc acccgcctcc 2100

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cagcgcctgg gcgtccatct tcacactgag gccagggcac gccatgcctg gcagcttacc 2220

cagggcgcca cagtcttggg actcttccgg gtgacccccg aaatcccagc cggactccct 2280

tcaccgaggt cggaaggaag cggagctact aacttcagcc tgctgaagca ggctggagac 2340

gtggaggaga accctggacc tatgtacaga atgcagctgc tgagctgcat cgccctgagc 2400

ctggccctgg tgaccaacag cggcatccac gtgttcatcc tgggctgctt cagcgccggc 2460

ctgcccaaga ccgaggccaa ctgggtgaac gtgatcagcg acctgaagaa gatcgaggac 2520

ctgatccaga gcatgcacat cgacgccacc ctgtacaccg agagcgacgt gcaccccagc 2580

tgcaaggtga ccgccatgaa gtgcttcctg ctggagctgc aggtgatcag cctggagagc 2640

ggcgacgcca gcatccacga caccgtggag aacctgatca tcctggccaa caacagcctg 2700

agcagcaacg gcaacgtgac cgagagcggc tgcaaggagt gcgaggagct ggaggagaag 2760

aacatcaagg agttcctgca gagcttcgtg cacatcgtgc agatgttcat caacaccagc 2820

tccggcggcg gctccggcgg cggcggctcc ggcggcggcg gctccggcgg cggcggctcc 2880

ggcggcggct ccctgcaggc ccccagaaga gccagaggct gcagaaccct gggcctgccc 2940

gccctgctgc tgctgctgct gctgagaccc cccgccacca gaggcatcac ctgccccccc 3000

cccatgagcg tggagcacgc cgacatctgg gtgaagagct acagcctgta cagcagagag 3060

agatacatct gcaacagcgg cttcaagaga aaggccggca ccagcagcct gaccgagtgc 3120

gtgctgaaca aggccaccaa cgtggcccac tggaccaccc ccagcctgaa gtgcatcaga 3180

taagtttaaa c 3191

<210> 136
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD123b-2G CAR amino acid sequence)

<400> 136

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Asn Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala Trp Tyr Gln Gln
50 55 60

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

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

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

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr
115 120 125

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

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

```
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Ser Leu Ser Cys
                165                 170                 175

Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Leu Ile Arg Ser Lys
        195                 200                 205

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

Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn
225                 230                 235                 240

Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Asp Ala
                245                 250                 255

Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met Asp Tyr Trp Gly
            260                 265                 270

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

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

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

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

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
        355                 360                 365

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
    370                 375                 380
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```
Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
385                 390                 395                 400


Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
                405                 410                 415


Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
            420                 425                 430


Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys
        435                 440                 445


Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
    450                 455                 460


Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465                 470                 475                 480


Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                485                 490                 495


Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  137
<211>  1535
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (CD123b-2G CAR nucleotide sequence)

<400>  137
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccgatggccg actacaagga catcgtgatg acccagagcc acaagttcat gagcaccagc      120

gtgggcgaca gggtgaacat cacctgcaag gccagccaga acgtggacag cgccgtggcc      180

tggtaccagc agaagcccgg ccagagcccc aaggccctga tctacagcgc cagctacagg      240

tacagcggcg tgcccgacag gttcaccggc aggggcagcg gcaccgactt caccctgacc      300

atcagcagcg tgcaggccga ggacctggcc gtgtactact gccagcagta ctacagcacc      360
```

ccctggacct tcggcggcgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420

ggcggcggca gcggcggcgg cggcagcggc ggcggcggca gcgaggtgaa gctggtggag 480

agcggcggcg gcctggtgca gcccggcggc agcctgagcc tgagctgcgc cgccagcggc 540

ttcaccttca ccgactacta catgagctgg gtgaggcagc cccccggcaa ggccctggag 600

tggctggccc tgatcaggag caaggccgac ggctacacca ccgagtacag cgccagcgtg 660

aagggcaggt tcaccctgag cagggacgac agccagagca tcctgtacct gcagatgaac 720

gccctgaggc ccgaggacag cgccacctac tactgcgcca gggacgccgc ctactacagc 780

tactacagcc ccgagggcgc catggactac tggggccagg gcaccagcgt gaccgtgagc 840

agcgccagcg gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 900

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 960

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 1020

tgtggggtcc ttctcctgtc actggttatc acccctttact gcaggagtaa gaggagcagg 1080

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1140

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1200

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1260

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1320

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1380

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1440

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1500

cacatgcagg ccctgccccc tcgctaagtt taaac 1535

<210> 138
<211> 1027
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD123b-CD33b-2G CAR amino acid sequence)

<400> 138

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
            20                  25                  30

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Asn Ile Thr
        35                  40                  45

Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala Trp Tyr Gln Gln
    50                  55                  60

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

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

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

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr
        115                 120                 125

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

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

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

Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Leu Ile Arg Ser Lys
        195                 200                 205

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

```
Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn
225                 230                 235                 240

Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Asp Ala
                245                 250                 255

Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met Asp Tyr Trp Gly
            260                 265                 270

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

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

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

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

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
        355                 360                 365

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
    370                 375                 380

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
385                 390                 395                 400

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
                405                 410                 415

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
            420                 425                 430

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys
        435                 440                 445
```

```
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
    450                 455                 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465                 470                 475                 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                485                 490                 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala
            500                 505                 510

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
        515                 520                 525

Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
    530                 535                 540

Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile Val Met
545                 550                 555                 560

Thr Gln Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser
                565                 570                 575

Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr
            580                 585                 590

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser
        595                 600                 605

Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly
    610                 615                 620

Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
625                 630                 635                 640

Asp Tyr Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala
                645                 650                 655
```

```
Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
            660                 665                 670

Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Glu Val Gln Leu
        675                 680                 685

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

Thr Cys Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp
705                 710                 715                 720

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

Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser
            740                 745                 750

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn
        755                 760                 765

Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr
    770                 775                 780

Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
785                 790                 795                 800

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

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

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

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

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

```
Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
                885                 890                 895


Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
            900                 905                 910


Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
        915                 920                 925


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


Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
945                 950                 955                 960


Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
                965                 970                 975


Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
            980                 985                 990


Gly Glu Arg Arg Arg Gly Lys Gly  His Asp Gly Leu Tyr  Gln Gly Leu
        995                 1000                1005


Ser Thr  Ala Thr Lys Asp Thr  Tyr Asp Ala Leu His  Met Gln Ala
    1010                1015                1020


Leu Pro  Pro Arg
    1025
```

<210> 139
<211> 3084
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD123b-CD33b-2G CAR nucleotide sequence)

<400> 139
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatggccg actacaagga catcgtgatg acccagagcc acaagttcat gagcaccagc 120

gtgggcgaca gggtgaacat cacctgcaag gccagccaga acgtggacag cgccgtggcc 180

tggtaccagc agaagcccgg ccagagcccc aaggccctga tctacagcgc cagctacagg 240

tacagcggcg tgcccgacag gttcaccggc aggggcagcg gcaccgactt caccctgacc 300

atcagcagcg tgcaggccga ggacctggcc gtgtactact gccagcagta ctacagcacc 360

ccctggacct tcggcggcgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420

ggcggcggca gcggcggcgg cggcagcggc ggcggcggca gcgaggtgaa gctggtggag 480

agcggcggcg gcctggtgca gcccggcggc agcctgagcc tgagctgcgc cgccagcggc 540

ttcaccttca ccgactacta catgagctgg gtgaggcagc cccccggcaa ggccctggag 600

tggctggccc tgatcaggag caaggccgac ggctacacca ccgagtacag cgccagcgtg 660

aagggcaggt tcaccctgag cagggacgac agccagagca tcctgtacct gcagatgaac 720

gccctgaggc ccgaggacag cgccacctac tactgcgcca gggacgccgc ctactacagc 780

tactacagcc ccgagggcgc catggactac tggggccagg gcaccagcgt gaccgtgagc 840

agcgccagcg gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 900

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 960

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 1020

tgtggggtcc ttctcctgtc actggttatc acccttttact gcaggagtaa gaggagcagg 1080

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1140

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1200

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1260

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1320

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1380

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1440

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1500

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1560

gccggcgacg tggaggagaa ccccggcccc atggccctgc ccgtgaccgc cctgctgctg 1620

cccctggccc tgctgctgca cgccgccagg cccatggccg actacaagga catcgtgatg 1680

acccagagcc acaagttcct gctggtgagc gtgggcgaca gggtgagcat cacctgcaag 1740

gccagccagg acgtgagcac cgccgtggcc tggtaccagc agaagcccgg ccagagcccc 1800

aagctgctga tctacagcgc cagctacagg tacaccggcg tgcccgacag gttcatcggc 1860

agcggcagcg gcaccgactt caccctgacc atcagcagcg tgcaggccga ggacctggcc 1920

gactacttct gccagcagca ctacagcacc cccctgacct tcggcgccgg caccaagctg 1980

gagatcaaga ggggcggcgg cggcagcggc ggcggcggca gcggcggcgg cggcagcagc 2040

ggcggcggca gcgaggtgca gctgaaggag agcggccccg gcctggtggc ccccagccag 2100

agcctgagca tcacctgcac cgtgagcggc ttccccctga ccagctacgg cgtgagctgg 2160

gtgaggcagc cccccggcaa gggcctggag tggctgggcg tgatctgggg cgacggcagc 2220

accaactacc acagcgccct gatcagcagg ctgagcatca gcaaggacaa cagcaagagc 2280

caggtgttcc tgaagctgaa caacctgcag accgacgaca ccgccaccta ctactgcgcc 2340

agggacacct actaccccta ctacgccatg gactactggg gccagggcac cagcgtgacc 2400

gtgagcagca ccaccacccc cgcccccagg ccccccaccc ccgcccccac catcgccagc 2460

cagcccctga gcctgaggcc cgaggcctgc aggcccgccg ccggcggcgc cgtgcacacc 2520

aggggcctgg acttcgcctg cgacatctac atctgggccc ccctggccgg cacctgcggc 2580

gtgctgctgc tgagcctggt gatcaccctg tactgcaaac ggggcagaaa gaaactcctg 2640

tatatattca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt 2700

agctgccgat ttccagaaga agaagaagga ggatgtgaac tgagggtgaa gttcagcagg 2760

agcgccgacg cccccgccta ccagcagggc cagaaccagc tgtacaacga gctgaacctg 2820

ggcaggaggg aggagtacga cgtgctggac aagaggaggg gcagggaccc cgagatgggc 2880

ggcaagcccc agaggaggaa gaacccccag gagggcctgt acaacgagct gcagaaggac 2940

aagatggccg aggcctacag cgagatcggc atgaagggcg agaggaggag gggcaagggc 3000

cacgacggcc tgtaccaggg cctgagcacc gccaccaagg acacctacga cgccctgcac 3060

atgcaggccc tgcccccag gtaa 3084

<210> 140
<211> 763
<212> PRT
<213> Artificial Sequence

<220>

<223> (BCMA-A7D-28-4-1BBL, CD269 A7D-28-4-1BBL amino acid sequence)

<400> 140

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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 Arg Ser
                325                 330                 335

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

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

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

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

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

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

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

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

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

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

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

Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro
        515                 520                 525

Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu
    530                 535                 540

Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys
545                 550                 555                 560

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
                565                 570                 575

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
            580                 585                 590

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
        595                 600                 605

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
    610                 615                 620

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys
625                 630                 635                 640
```

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
645 650 655

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
660 665 670

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

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

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

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
725 730 735

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
740 745 750

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
755 760

<210> 141
<211> 2300
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-4-1BBL, CD269 A7D-28-4-1BBL CAR nucleotide sequence)

<400> 141
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg 120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccтttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggcagc ggcgaaggcc gcggcagcct gctgacctgc 1500

ggcgatgtgg aagaaaaccc gggccccatg gaatacgcct ctgacgcttc actggacccc 1560

gaagccccgt ggcctcccgc gccccgcgct cgcgcctgcc gcgtactgcc ttgggccctg 1620

gtcgcggggc tgctgctgct gctgctgctc gctgccgcct gcgccgtctt cctcgcctgc 1680

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tttgcgcagc tggtggccca aaatgttctg ctgatcgatg ggcccctgag ctggtacagt 1860

gacccaggcc tggcaggcgt gtccctgacg gggggcctga gctacaaaga ggacacgaag 1920

gagctggtgg tggccaaggc tggagtctac tatgtcttct ttcaactaga gctgcggcgc 1980

gtggtggccg gcgagggctc aggctccgtt tcacttgcgc tgcacctgca gccactgcgc 2040

tctgctgctg gggccgccgc cctggctttg accgtggacc tgccacccgc ctcctccgag 2100

gctcggaact cggccttcgg tttccagggc cgcttgctgc acctgagtgc cggccagcgc 2160

ctgggcgtcc atcttcacac tgaggccagg gcacgccatg cctggcagct tacccagggc 2220

gccacagtct tgggactctt ccgggtgacc cccgaaatcc cagccggact cccttcaccg 2280

aggtcggaat aagtttaaac 2300

<210> 142
<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15/IL-15sushi anchor,
CD269-A7D-28-IL-15/IL-15sushi anchor CAR amino acid sequence)

<400> 142

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 Arg Ser
                325                 330                 335
```

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

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

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

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

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

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

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

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

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

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

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

Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr
        515                 520                 525

Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
    530                 535                 540

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
```

```
545                 550                 555                 560

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                565                 570                 575

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            580                 585                 590

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        595                 600                 605

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    610                 615                 620

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
625                 630                 635                 640

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                645                 650                 655

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
            660                 665                 670

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
        675                 680                 685

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
    690                 695                 700

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
705                 710                 715                 720

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
                725                 730                 735

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
            740                 745                 750

Ile Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
        755                 760                 765
```

```
Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
    770                 775                 780

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Val
785                 790                 795                 800

Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser
                805                 810                 815

Leu Leu Ala Cys Tyr
            820
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<210> 143
<211> 2474
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15/IL-15sushi anchor,
CD269-A7D-28-IL-15/IL-15sushi anchor CAR nucleotide sequence)

<400> 143

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atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg      120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag      180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc      240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag      300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccctg gaccttcggc      360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga      420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc      480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg      540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag      600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc      660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc      720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg      780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc      840
```

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccttttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1500

gccggcgacg tggaggagaa ccccggcccc atgtacagaa tgcagctgct gagctgcatc 1560

gccctgagcc tggccctggt gaccaacagc ggcatccacg tgttcatcct gggctgcttc 1620

agcgccggcc tgcccaagac cgaggccaac tgggtgaacg tgatcagcga cctgaagaag 1680

atcgaggacc tgatccagag catgcacatc gacgccaccc tgtacaccga gagcgacgtg 1740

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ctggagagcg gcgacgccag catccacgac accgtggaga acctgatcat cctggccaac 1860

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gaggagaaga acatcaagga gttcctgcag agcttcgtgc acatcgtgca gatgttcatc 1980

aacaccagct ccggcggcgg ctccggcggc ggcggctccg gcggcggcgg ctccggcggc 2040

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gccgacatct gggtgaagag ctacagcctg tacagcagag agagatacat ctgcaacagc 2160

ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt gcgtgctgaa caaggccacc 2220

aacgtggccc actggaccac ccccagcctg aagtgcatca gaaccaccac ccccgccccc 2280

aggcccccca cccccgcccc caccatcgcc agccagcccc tgagcctgag gcccgaggcc 2340

tgcaggcccg ccgccggcgg cgccgtgcac accaggggcc tggacttcgc ctgcgacgtg 2400

gctatctcca cgtccactgt cctgctgtgt gggctgagcg ctgtgtctct cctggcatgc 2460

tactaagttt aaac 2474

<210> 144
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> (BAFFR-28-2G CAR amino acid sequence)

<400> 144

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 Val Gln Leu Gln Gln Ser Gly Pro Gly Leu
20 25 30

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

Ser Val Ser Ser Asn Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro
50 55 60

Gly Arg Gly Leu Glu Trp Leu Gly Arg Ile Tyr Tyr Arg Ser Lys Trp
65 70 75 80

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

Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro
100 105 110

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Asp Trp Val Pro Lys
115 120 125

Ile Gly Val Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser
130 135 140

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

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
                165                 170                 175

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Ile Ser Ser Ser
            180                 185                 190

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

Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
225                 230                 235                 240

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Leu Tyr Ser Ser Pro
                245                 250                 255

Met Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro
            260                 265                 270

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

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

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

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

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

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

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser 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> 145
<211> 1484
<212> DNA
<213> Artificial Sequence

<220>
<223> (BAFFR-28-2G CAR nucleotide sequence)

<400> 145

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ctgatctgcg ccatttcagg cgacagcgtg agcagcaaca gcgccgcctg gggctggatc      180

aggcagagcc ccggtagggg cctggaatgg ctgggcagga tctactacag gtccaagtgg      240

tacaacagct acgccgtgag cgtgaagagc aggatcacca tcaaccctga caccagcaag      300

aaccagttct cactgcagct caacagcgtg acccccgagg acaccgccgt gtactactgc      360

gccagatacg actgggtgcc caagatcggc gtgttcgaca gctggggcca gggcaccctg      420

gtgaccgtgt caagcggagg ggggggatcc gggggaggag gctccggcgg aggcggaagc      480
```

gatatcgtgc tgacacagag ccccgccacc ctgagcctga gcccaggcga gagggccacc 540

ctgtcctgca gggccagcca gtttatcagc agcagctacc tgtcctggta tcagcagaag 600

cccggccagg cccctagact gctgatctac ggcagctcct ctcgggccac cggcgtgccc 660

gccaggttca gcggcagcgg ctccggcacc gacttcaccc tgacaatcag cagcctggag 720

cccgaggact tcgccgtgta ctactgccag cagctgtaca gctcacccat gaccttcggc 780

cagggcacca aggtggagat caagaccacc acccccgccc ccaggccccc cacccccgcc 840

cccaccatcg ccagccagcc cctgagcctg aggcccgagg cctgcaggcc cgccgccggc 900

ggcgccgtgc acaccagggg cctggacttc gcctgcgaca tctacatctg ggcccccctg 960

gccggcacct gcggcgtgct gctgctgagc ctggtgatca ccctgtactg caggagtaag 1020

aggagcaggc tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc 1080

cgcaagcatt accagcccta tgccccacca cgcgacttcg cagcctatcg ctccagggtg 1140

aagttcagca ggagcgccga cgcccccgcc taccagcagg gccagaacca gctgtacaac 1200

gagctgaacc tgggcaggag ggaggagtac gacgtgctgg acaagaggag gggcagggac 1260

cccgagatgg gcggcaagcc ccagaggagg aagaaccccc aggagggcct gtacaacgag 1320

ctgcagaagg acaagatggc cgaggcctac agcgagatcg gcatgaaggg cgagaggagg 1380

aggggcaagg gccacgacgg cctgtaccag ggcctgagca ccgccaccaa ggacacctac 1440

gacgccctgc acatgcaggc cctgcccccc aggtaagttt aaac 1484

<210> 146
<211> 1024
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD4-CD123b-2G CAR amino acid sequence)

<400> 146

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 Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

```
Ala Val Ser Leu Gly Glu Arg Val Thr Met Asn Cys Lys Ser Ser Gln
        35                  40                  45

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
145                 150                 155                 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
            180                 185                 190

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
    210                 215                 220

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
        275                 280                 285

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

Ala Leu Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile
    530                 535                 540

Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg
545                 550                 555                 560

Val Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala
                565                 570                 575

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr Ser
            580                 585                 590

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

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
    610                 615                 620

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe
625                 630                 635                 640

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
            660                 665                 670

Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
        675                 680                 685
```

```
Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met
    690                 695                 700

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

Ile Arg Ser Lys Ala Asp Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val
                725                 730                 735

Lys Gly Arg Phe Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr
            740                 745                 750

Leu Gln Met Asn Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys
        755                 760                 765

Ala Arg Asp Ala Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met
    770                 775                 780

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Gly
785                 790                 795                 800

Ala Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
                805                 810                 815

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

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

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

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

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

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

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
        915                 920                 925

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

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
945                 950                 955                 960

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
                965                 970                 975

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
            980                 985                 990

Arg Arg Gly Lys Gly His Asp Gly  Leu Tyr Gln Gly Leu  Ser Thr Ala
        995                 1000                1005

Thr Lys  Asp Thr Tyr Asp Ala  Leu His Met Gln Ala  Leu Pro Pro
    1010                1015                1020

Arg
```

<210> 147
<211> 3083
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD4-CD123b-2G CAR nucleotide sequence)

<400> 147

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cccgacatcg tgatgaccca aagccccgac agcctggccg tgagcctggg cgagagggtg      120

accatgaact gcaaaagcag ccagtccctg ctgtactcca ccaaccagaa gaactacctg      180

gcttggtatc aacagaagcc cggacagagc cccaagctgc tgatctattg ggccagcact      240

agggaaagcg gcgtgcccga taggttcagc ggcagcggga gcggcacaga cttcactctg      300
```

accattagca gcgtgcaggc tgaggatgtg gccgtctact actgccagca gtactacagc 360

tacaggacct ttgggggcgg aactaagctg gagatcaagg gaggggggag atccggggga 420

ggaggctccg gcggaggcgg aagccaagtg caactgcagc agagcggccc agaggtggtc 480

aaacctgggg caagcgtgaa gatgagctgc aaggctagcg gctatacctt caccagctat 540

gtgatccact gggtgaggca gaaaccagga cagggcctgg actggatcgg ctacatcaac 600

ccctacaatg acggcaccga ttatgacgaa aaattcaagg ggaaggccac cctgaccagc 660

gacaccagca caagcaccgc ctacatggag ctgtccagcc tgaggtccga ggacaccgcc 720

gtgtattact gtgccaggga gaaggacaat tacgccaccg gcgcttggtt cgcctactgg 780

ggccagggca cactggtgac agtgagcagc accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcc 960

cccctggccg gcacctgcgg cgtgctgctg ctgagcctgg tgatcaccct gtactgcaag 1020

aggggcagga agaagctgct gtacatcttc aagcagccct tcatgaggcc cgtgcagacc 1080

acccaggagg aggacggctg cagctgcagg ttccccgagg aggaggaggg cggctgcgag 1140

ctgagggtga agttcagcag gagcgccgac gcccccgcct accagcaggg ccagaaccag 1200

ctgtacaacg agctgaacct gggcaggagg gaggagtacg acgtgctgga caagaggagg 1260

ggcagggacc ccgagatggg cggcaagccc cagaggagga agaaccccca ggagggcctg 1320

tacaacgagc tgcagaagga caagatggcc gaggcctaca gcgagatcgg catgaagggc 1380

gagaggagga ggggcaaggg ccacgacggc ctgtaccagg gcctgagcac cgccaccaag 1440

gacacctacg acgccctgca catgcaggcc ctgccccccа ggggaagcgg agctactaac 1500

ttcagcctgc tgaagcaggc tggagacgtg gaggagaacc ctggacctat ggccttacca 1560

gtgaccgcct tgctcctgcc gctggccttg ctgctccacg ccgccaggcc gatggccgac 1620

tacaaggaca tcgtgatgac ccagagccac aagttcatga gcaccagcgt gggcgacagg 1680

gtgaacatca cctgcaaggc cagccagaac gtggacagcg ccgtggcctg gtaccagcag 1740

aagcccggcc agagccccaa ggccctgatc tacagcgcca gctacaggta cagcggcgtg 1800

cccgacaggt tcaccggcag gggcagcggc accgacttca ccctgaccat cagcagcgtg 1860

caggccgagg acctggccgt gtactactgc cagcagtact acagcacccc ctggaccttc 1920

ggcggcggca ccaagctgga gatcaagagg ggcggcggcg gcagcggcgg cggcggcagc 1980

ggcggcggcg gcagcggcgg cggcggcagc gaggtgaagc tggtggagag cggcggcggc 2040

ctggtgcagc ccggcggcag cctgagcctg agctgcgccg ccagcggctt caccttcacc 2100

gactactaca tgagctgggt gaggcagccc cccggcaagg ccctggagtg gctggccctg 2160

atcaggagca aggccgacgg ctacaccacc gagtacagcg ccagcgtgaa gggcaggttc 2220

accctgagca gggacgacag ccagagcatc ctgtacctgc agatgaacgc cctgaggccc 2280

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gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 3000

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ctgccccctc gctaagttta aac 3083

<210> 148
<211> 782
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15/IL-15sushi, CD269-A7D-28-IL-15/IL-15sushi CAR amino acid sequence)

<400> 148

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 Arg Ser
                325                 330                 335

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

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

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

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

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

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

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

```
        435                 440                 445

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

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

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

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg
            500                 505                 510

Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
        515                 520                 525

Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
    530                 535                 540

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
545                 550                 555                 560

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
                565                 570                 575

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
            580                 585                 590

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
        595                 600                 605

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
    610                 615                 620

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
625                 630                 635                 640

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
                645                 650                 655
```

Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
660 665 670

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

Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu
690 695 700

Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys
705 710 715 720

Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
725 730 735

Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
740 745 750

Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
755 760 765

Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
770 775 780

<210> 149
<211> 2357
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15/IL-15sushi, CD269-A7D-28-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 149
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg 120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccтttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggcagc ggcgaaggcc gcggcagcct gctgacctgc 1500

ggcgatgtgg aagaaaaccc gggccccatg tacagaatgc agctgctgag ctgcatcgcc 1560

ctgagcctgg ccctggtgac caacagcggc atccacgtgt tcatcctggg ctgcttcagc 1620

gccggcctgc ccaagaccga ggccaactgg gtgaacgtga tcagcgacct gaagaagatc 1680

gaggacctga tccagagcat gcacatcgac gccaccctgt acaccgagag cgacgtgcac 1740

cccagctgca aggtgaccgc catgaagtgc ttcctgctgg agctgcaggt gatcagcctg 1800

gagagcggcg acgccagcat ccacgacacc gtggagaacc tgatcatcct ggccaacaac 1860

agcctgagca gcaacggcaa cgtgaccgag agcggctgca aggagtgcga ggagctggag 1920

gagaagaaca tcaaggagtt cctgcagagc ttcgtgcaca tcgtgcagat gttcatcaac 1980

accagctccg gcggcggctc cggcggcggc ggctccggcg gcggcggctc cggcggcggc 2040

ggctccggcg gcggctccct gcaggccccc agaagagcca gaggctgcag aaccctgggc 2100

ctgcccgccc tgctgctgct gctgctgctg agacccccg ccaccagagg catcacctgc 2160

ccccccccca tgagcgtgga gcacgccgac atctgggtga agagctacag cctgtacagc 2220

agagagagat acatctgcaa cagcggcttc aagagaaagg ccggcaccag cagcctgacc 2280

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccccag cctgaagtgc 2340

atcagataag tttaaac 2357

<210> 150
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> (CLL-1-3233-28-2G CAR amino acid sequence)

<400> 150

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 Ser Pro Ser Ser Leu
20 25 30

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

Ser Val Ser Thr Ser Ser Tyr Asn Tyr Met His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

```
Cys Gln His Ser Trp Glu Ile Pro Leu Thr Phe Gly Gln Gly Thr Lys
        115                 120                 125

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
                165                 170                 175

Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
            180                 185                 190

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

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

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

Tyr Tyr Cys Ala Ile Glu Arg Gly Ala Asp Leu Glu Gly Tyr Ala Met
                245                 250                 255

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr
            260                 265                 270

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

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300

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

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

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

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

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

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

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

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

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

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

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

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

<210> 151
<211> 1487
<212> DNA
<213> Artificial Sequence

<220>
<223> (CLL-1-3233-28-2G CAR nucleotide sequence)

<400> 151
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccgacatcc agatgaccca gagccccagc agcctgagcg ccagcgtggg cgacagggtg 120

accatcacct gcagggccag ccagagcgtg agcaccagca gctacaacta catgcactgg 180

taccagcaga agcccggcaa gccccccaag ctgctgatca agtacgccag caacctggag 240

agcggcgtgc ccagcaggtt cagcggcagc ggcagcggca ccgacttcac cctgaccatc 300

agcagcctgc agcccgagga cttcgccacc tactactgcc agcacagctg ggagatcccc 360

ctgaccttcg gccagggcac caaggtggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag cgaggtgcag ctggtgcaga gcggcgccga ggtgaagaag 480

cccggcgcca gcgtgaaggt gagctgcaag gccagcggct acagcttcac cgactactac 540

atgcactggg tgaggcaggc ccccggccag ggcctggagt ggatcggcag gatcaacccc 600

tacaacggcg ccgccttcta cagccagaac ttcaaggaca gggtgaccct gaccgtggac 660

accagcacca gcaccgccta cctggagctg agcagcctga ggagcgagga caccgccgtg 720

tactactgcg ccatcgagag gggcgccgac ctggagggct acgccatgga ctactggggc 780

cagggcaccc tggtgaccgt gagcagcacc accacccccg cccccaggcc ccccacccc 840

gcccccacca tcgccagcca gcccctgagc ctgaggcccg aggcctgcag gcccgccgcc 900

ggcggcgccg tgcacaccag gggcctggac ttcgcctgcg acatctacat ctgggccccc 960

ctggccggca cctgcggcgt gctgctgctg agcctggtga tcaccctgta ctgcaggagt 1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctccccgccg ccccgggccc 1080

acccgcaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccagg 1140

gtgaagttca gcaggagcgc cgacgccccc gcctaccagc agggccagaa ccagctgtac 1200

aacgagctga acctgggcag gagggaggag tacgacgtgc tggacaagag gaggggcagg 1260

gaccccgaga tgggcggcaa gccccagagg aggaagaacc cccaggaggg cctgtacaac 1320

gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg 1380

aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc 1440

tacgacgccc tgcacatgca ggccctgccc cccaggtaag tttaaac 1487

<210> 152
<211> 486
<212> PRT
<213> Artificial Sequence

<220>

<223> (CLL-1-3738-28-2G CAR amino acid sequence)

<400> 152

```
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 Ser His Lys Phe Met
            20                  25                  30


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


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


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


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


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


Tyr Ser Thr Pro Tyr 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 Glu
    130                 135                 140


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


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


Leu Asp Trp Val Lys Gln Ser His Gly Glu Ser Phe Glu Trp Ile Gly
            180                 185                 190


Arg Val Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe Lys
        195                 200                 205
```

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

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

Arg Asp His Tyr Arg Tyr Asp Pro Leu Leu Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Thr Leu 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 Arg Ser Lys Arg
                325                 330                 335

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

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

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

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

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

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

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

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

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

Gln Ala Leu Pro Pro Arg
485

<210> 153
<211> 1469
<212> DNA
<213> Artificial Sequence

<220>
<223> (CLL-1-3738-28-2G CAR nucleotide sequence)

<400> 153
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccgacatcc agatgaccca gagccacaag ttcatgagca ccagcgtggg cgacagggtg 120

agcatcacct gcaaggccag ccaggacgtg agcaccgccg tggcctggtt ccagcagaag 180

cccggccaga gccccaagct gctgatctac agccccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcacc gacttcacct tcaccatcag cagcgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagctgtaca gcacccccta caccttcggc 360

ggcggcacca agctggagat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcg aggtgcagct gcagcagagc ggccccgagc tggtgaagcc cggcgccagc 480

gtgaagatga gctgcaaggc cagcggctac accttcaccg actactacct ggactgggtg 540

aagcagagcc acggcgagag cttcgagtgg atcggcaggg tgaaccccta caacggcggc 600

accatctaca accagaagtt caagggcaag gccaccctga ccgtggacaa gagcagcagc 660

accgcctaca tggacctgaa cagcctgacc agcgaggaca gcgccgtgta ctactgcgcc 720

agggaccact acaggtacga ccccctgctg gactactggg gccagggcac caccctgacc 780

gtgagcagca ccaccacccc cgcccccagg ccccccaccc ccgcccccac catcgccagc 840

cagcccctga gcctgaggcc cgaggcctgc aggcccgccg ccggcggcgc cgtgcacacc 900

aggggcctgg acttcgcctg cgacatctac atctgggccc ccctggccgg cacctgcggc 960

gtgctgctgc tgagcctggt gatcaccctg tactgcagga gtaagaggag caggctcctg 1020

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080

ccctatgccc caccacgcga cttcgcagcc tatcgctcca gggtgaagtt cagcaggagc 1140

gccgacgccc ccgcctacca gcagggccag aaccagctgt acaacgagct gaacctgggc 1200

aggagggagg agtacgacgt gctggacaag aggaggggca gggaccccga gatgggcggc 1260

aagccccaga ggaggaagaa cccccaggag ggcctgtaca acgagctgca gaaggacaag 1320

atggccgagg cctacagcga gatcggcatg aagggcgaga ggaggagggg caagggccac 1380

gacggcctgt accagggcct gagcaccgcc accaaggaca cctacgacgc cctgcacatg 1440

caggccctgc cccccaggta agtttaaac 1469

<210> 154
<211> 1011
<212> PRT
<213> Artificial Sequence

<220>
<223> (CLL-1-3233-CD33b-2G CAR amino acid sequence)

<400> 154

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 Ser Pro Ser Ser Leu
20 25 30

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

Ser Val Ser Thr Ser Ser Tyr Asn Tyr Met His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

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

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
                165                 170                 175

Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
            180                 185                 190

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

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

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

Tyr Tyr Cys Ala Ile Glu Arg Gly Ala Asp Leu Glu Gly Tyr Ala Met
                245                 250                 255

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr
            260                 265                 270

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

```
Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300

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

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

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

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

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

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

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

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

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

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

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

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

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

```
Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
        515                 520                 525

Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile Val Met
    530                 535                 540

Thr Gln Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser
545                 550                 555                 560

Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr
                565                 570                 575

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser
            580                 585                 590

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

Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
    610                 615                 620

Asp Tyr Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala
625                 630                 635                 640

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

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

Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
        675                 680                 685

Thr Cys Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp
    690                 695                 700

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
705                 710                 715                 720
```

```
Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser
                725                 730                 735

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn
            740                 745                 750

Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr
        755                 760                 765

Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
    770                 775                 780

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
785                 790                 795                 800

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
                805                 810                 815

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
            820                 825                 830

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
        835                 840                 845

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
    850                 855                 860

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
865                 870                 875                 880

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
                885                 890                 895

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
            900                 905                 910

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
        915                 920                 925

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
    930                 935                 940
```

```
Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
945                 950                 955                 960


Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
                965                 970                 975


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
            980                 985                 990


Ser Thr Ala Thr Lys Asp Thr Tyr  Asp Ala Leu His Met  Gln Ala Leu
        995                 1000                1005


Pro Pro  Arg
    1010
```

<210> 155
<211> 3044
<212> DNA
<213> Artificial Sequence

<220>
<223> (CLL-1-3233-CD33b-2G CAR nucleotide sequence)

<400> 155

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atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg       60

cccgacatcc agatgaccca gagccccagc agcctgagcg ccagcgtggg cgacagggtg      120

accatcacct gcagggccag ccagagcgtg agcaccagca gctacaacta catgcactgg      180

taccagcaga agcccggcaa gccccccaag ctgctgatca agtacgccag caacctggag      240

agcggcgtgc ccagcaggtt cagcggcagc ggcagcggca ccgacttcac cctgaccatc      300

agcagcctgc agcccgagga cttcgccacc tactactgcc agcacagctg ggagatcccc      360

ctgaccttcg gccagggcac caaggtggag atcaagggag gggggggatc cgggggagga      420

ggctccggcg gaggcggaag cgaggtgcag ctggtgcaga gcggcgccga ggtgaagaag      480

cccggcgcca gcgtgaaggt gagctgcaag gccagcggct acagcttcac cgactactac      540

atgcactggg tgaggcaggc ccccggccag ggcctggagt ggatcggcag gatcaacccc      600

tacaacggcg ccgccttcta cagccagaac ttcaaggaca gggtgaccct gaccgtggac      660

accagcacca gcaccgccta cctggagctg agcagcctga ggagcgagga caccgccgtg      720
```

tactactgcg ccatcgagag gggcgccgac ctggagggct acgccatgga ctactggggc 780

cagggcaccc tggtgaccgt gagcagcacc acgacgccag cgccgcgacc accaacaccg 840

gcgcccacca tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg 900

gggggcgcag tgcacacgag ggggctggac ttcgcctgtg atatctacat ctgggccccc 960

ctggccggca cctgcggcgt gctgctgctg agcctggtga tcaccctgta ctgcaggagt 1020

aagaggagca ggctcctgca cagtgactac atgaacatga ctccccgccg ccccgggccc 1080

acccgcaagc attaccagcc ctatgcccca ccacgcgact tcgcagccta tcgctccagg 1140

gtgaagttca gcaggagcgc cgacgccccc gcctaccagc agggccagaa ccagctgtac 1200

aacgagctga acctgggcag gagggaggag tacgacgtgc tggacaagag gaggggcagg 1260

gaccccgaga tgggcggcaa gccccagagg aggaagaacc cccaggaggg cctgtacaac 1320

gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagagg 1380

aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggacacc 1440

tacgacgccc tgcacatgca ggccctgccc cccaggggaa gcggagccac caacttcagc 1500

ctgctgaagc aggccggcga cgtggaggag aaccccggcc ccatggccct gcccgtgacc 1560

gccctgctgc tgcccctggc cctgctgctg cacgccgcca ggcccatggc cgactacaag 1620

gacatcgtga tgacccagag ccacaagttc ctgctggtga gcgtgggcga cagggtgagc 1680

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gaggacctgg ccgactactt ctgccagcag cactacagca ccccccctgac cttcggcgcc 1920

ggcaccaagc tggagatcaa gaggggcggc ggcggcagcg gcggcggcgg cagcggcggc 1980

ggcggcagca gcggcggcgg cagcgaggtg cagctgaagg agagcggccc cggcctggtg 2040

gcccccagcc agagcctgag catcacctgc accgtgagcg gcttcccccct gaccagctac 2100

ggcgtgagct gggtgaggca gccccccggc aagggcctgg agtggctggg cgtgatctgg 2160

ggcgacggca gcaccaacta ccacagcgcc ctgatcagca ggctgagcat cagcaaggac 2220

aacagcaaga gccaggtgtt cctgaagctg aacaacctgc agaccgacga caccgccacc 2280

tactactgcg ccagggacac ctactacccc tactacgcca tggactactg gggccagggc 2340

accagcgtga ccgtgagcag caccaccacc cccgccccca ggccccccac ccccgccccc 2400

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gccgtgcaca ccaggggcct ggacttcgcc tgcgacatct acatctgggc ccccctggcc 2520

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aagttcagca ggagcgccga cgcccccgcc taccagcagg gccagaacca gctgtacaac 2760

gagctgaacc tgggcaggag ggaggagtac gacgtgctgg acaagaggag gggcagggac 2820

cccgagatgg gcggcaagcc ccagaggagg aagaaccccc aggagggcct gtacaacgag 2880

ctgcagaagg acaagatggc cgaggcctac agcgagatcg gcatgaaggg cgagaggagg 2940

aggggcaagg gccacgacgg cctgtaccag ggcctgagca ccgccaccaa ggacacctac 3000

gacgccctgc acatgcaggc cctgcccccc aggtaagttt aaac 3044

<210> 156
<211> 1011
<212> PRT
<213> Artificial Sequence

<220>
<223> (CLL-1-3738-CD33b-2G CAR amino acid sequence)

<400> 156

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 Ser Pro Ser Ser Leu
20 25 30

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

Ser Val Ser Thr Ser Ser Tyr Asn Tyr Met His Trp Tyr Gln Gln Lys
50 55 60

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

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

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

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

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
                165                 170                 175

Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
            180                 185                 190

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

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

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

Tyr Tyr Cys Ala Ile Glu Arg Gly Ala Asp Leu Glu Gly Tyr Ala Met
                245                 250                 255

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr
            260                 265                 270

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

```
Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
    290                 295                 300

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

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

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

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

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

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

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

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

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

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

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

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

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

```
Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
        515                 520                 525

Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile Val Met
    530                 535                 540

Thr Gln Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser
545                 550                 555                 560

Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr
                565                 570                 575

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser
            580                 585                 590

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

Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
    610                 615                 620

Asp Tyr Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala
625                 630                 635                 640

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

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

Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
        675                 680                 685

Thr Cys Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp
    690                 695                 700

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
705                 710                 715                 720
```

```
Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser
                725                 730                 735

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn
            740                 745                 750

Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr
        755                 760                 765

Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
    770                 775                 780

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
785                 790                 795                 800

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
                805                 810                 815

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
            820                 825                 830

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
        835                 840                 845

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
    850                 855                 860

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
865                 870                 875                 880

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
                885                 890                 895

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
            900                 905                 910

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
        915                 920                 925

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
    930                 935                 940
```

```
Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
945                 950                 955                 960


Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
                965                 970                 975


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
            980                 985                 990


Ser Thr Ala Thr Lys Asp Thr Tyr  Asp Ala Leu His Met  Gln Ala Leu
        995                 1000                1005


Pro Pro  Arg
    1010
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<210> 157
<211> 2999
<212> DNA
<213> Artificial Sequence

<220>
<223> (CLL-1-3738-CD33b-2G CAR nucleotide sequence)

<400> 157

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gctgacccag agccccgcca tcatgagcgc cagccccggc gagaaggtga ccatcacctg      120

cagcgccagc agcagcatca gctacatgca ctggttccag cagaagcccg gcaccagccc      180

caagctgtgg atctacacca ccagcaacct ggccagcggc gtgcccgcca gattcagcgg      240

cagcggcagc ggcaccagct acagcctgac catcagcaga atggaggccg aggacgccgc      300

cacctactac tgccaccaga gaagcaccta ccccctgacc ttcggcagcg gcaccaagct      360

ggagctgaag ggaggggggg gatccggggg aggaggctcc ggcggaggcg gaagccaggt      420

gcagctgcag cagagcggcg ccgagctggc caagcccggc gccagcgtga agatgagctg      480

caaggccagc ggctacacct tcaccagcta cagaatgcac tgggtgaagc agagacccgg      540

ccagggcctg gagtggatcg gctacatcaa ccccagcacc ggctacaccg agtacaacca      600

gaagttcaag gacaaggcca ccctgaccgc cgacaagagc agcagcaccg cctacatgca      660

gctgagcagc ctgaccttcg aggacagcgc cgtgtactac tgcgccagag gcggcggcgt      720
```

gttcgactac tggggccagg gcaccaccct gaccgtgagc agcaccacga cgccagcgcc 780

gcgaccacca acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc 840

gtgccggcca gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat 900

ctacatctgg gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac 960

cctttactgc aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc 1020

ccgccgcccc gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc 1080

agcctatcgc tccagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg 1140

ccagaaccag ctctataacg agctcatcta ggacgaagag aggagtacga tgttttggac 1200

aagagacgtg gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag 1260

gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 1320

atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca 1380

gccaccaagg acacctacga cgcccttcac atgcaggccc tgcccctcg cggaagcgga 1440

gccaccaact tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggccccatg 1500

gccctgcccg tgaccgccct gctgctgccc ctggccctgc tgctgcacgc cgccaggccc 1560

atggccgact acaaggacat cgtgatgacc cagagccaca agttcctgct ggtgagcgtg 1620

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taccagcaga agcccggcca gagccccaag ctgctgatct acagcgccag ctacaggtac 1740

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agcagcgtgc aggccgagga cctggccgac tacttctgcc agcagcacta cagcaccccc 1860

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cccctgacca gctacggcgt gagctgggtg aggcagcccc ccggcaaggg cctggagtgg 2100

ctgggcgtga tctggggcga cggcagcacc aactaccaca gcgccctgat cagcaggctg 2160

agcatcagca aggacaacag caagagccag gtgttcctga agctgaacaa cctgcagacc 2220

gacgacaccg ccacctacta ctgcgccagg gacacctact acccctacta cgccatggac 2280

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tgcaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gagaccagta 2580

caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga 2640

tgtgaactga gggtgaagtt cagcaggagc gccgacgccc ccgcctacca gcagggccag 2700

aaccagctgt acaacgagct gaacctgggc aggagggagg agtacgacgt gctggacaag 2760

aggaggggca gggaccccga gatgggcggc aagccccaga ggaggaagaa cccccaggag 2820

ggcctgtaca acgagctgca gaaggacaag atggccgagg cctacagcga gatcggcatg 2880

aagggcgaga ggaggagggg caagggccac gacggcctgt accagggcct gagcaccgcc 2940

accaaggaca cctacgacgc cctgcacatg caggccctgc cccccaggta agtttaaac 2999

<210> 158
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> (extracellular domain of BAFF-receptor amino acid sequence)

<400> 158

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

Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys
20 25 30

Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala
35 40 45

Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly
50 55 60

Ala Gly Ala Gly Glu Ala Ala Leu Pro Leu Pro Gly Leu Leu
65 70 75

<210> 159
<211> 2663
<212> DNA
<213> Artificial Sequence

<220>
<223> (L8-CD7-28-52 -IL-15/IL-15sushi CAR nucleotide sequence)

<400> 159
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggcgccc agcccgccat ggccgcctac aaggacatcc agatgaccca gaccaccagc 120

agcctgagcg ccagcctggg cgacagagtg accatcagct gcagcgccag ccagggcatc 180

agcaactacc tgaactggta ccagcagaag cccgacggca ccaacaagct gctgatctac 240

tacaccagca gcctgcacag cggcgtgccc agcagattca gcggcagcgg cagcggcacc 300

gactacagcc tgcacagcaa cctggagccc gaggacatcg ccacctacta ctgccagcag 360

tacagcaagc tgccctacac cttcggcggc ggcaccaagc tggagatcaa gagaggcggc 420

ggcggcagcg gcggcggcgg cagcggcggc ggcggcagcg gcggcggcgg cagcgaggtg 480

cagctggtgg agagcggcgg cggcctggtg aagcccggcg gcagcctgaa gctgagctgc 540

gccgccagcg gcctgacctt cagcagctac gccatgagct ggaacagaca gaccccgag 600

aagagactgg agtgggtggc cagcatcagc agcggcggct tcacctacta ccccgacagc 660

aacaagggca gattcaccat cagcagagac aacgccagaa acatcctgta cctgcagatg 720

agcagcctga gaagcgagga caccgccatg tactactgcg ccagagacga ggtgagaggc 780

tacctggacg tgtggggcgc cggcaccacc gtgaccgtga gcagcaccac gacgccagcg 840

ccgcgaccac caacaccggc gcccaccatc gcgtcgcagc ccctgtccct gcgcccagag 900

gcgtgccggc cagcggcggg gggcgcagtg cacacgaggg ggctggactt cgcctgtgat 960

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gcagcctatc gctccagagt gaagttcagc aggagcgcag acgcccccgc gtaccagcag 1200

ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 1260

gacaagagac gtggccggga ccctgagatg gggggaaagc cgcagagaag gaagaaccct 1320

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acagccacca aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgcggcagc 1500

ggcgaaggcc gcggcagcct gctgacctgc ggcgatgtgg aagaaaaccc gggccccatg 1560

gccctgcccg tgaccgccct gctgctgccc ctggccctgc tgctgcacgc cgccaggccc 1620

ggccagaacg acaccagcca gaccagcagc cccagcagcc cgctgtttcc gggcccgagc 1680

aaaccgtttt gggtgctggt ggtggtgggc ggcgtgctgg cgtgctatag cctgctggtg 1740

accgtggcgt ttattatttt ttgggtggga agcggagcta ctaacttgag cctgctgaag 1800

caggctggag acgtggagga gaaccctgga cctatgtaca gaatgcagct gctgagctgc 1860

atcgccctga gcctggccct ggtgaccaac agcggcatcc acgtgttcat cctgggctgc 1920

ttcagcgccg gcctgcccaa gaccgaggcc aactgggtga acgtgatcag cgacctgaag 1980

aagatcgagg acctgatcca gagcatgcac atcgacgcca ccctgtacac cgagagcgac 2040

gtgcacccca gctgcaaggt gaccgccatg aagtgcttcc tgctggagct gcaggtgatc 2100

agcctggaga gcggcgacgc cagcatccac gacaccgtgg agaacctgat catcctggcc 2160

aacaacagcc tgagcagcaa cggcaacgtg accgagagcg gctgcaagga gtgcgaggag 2220

ctggaggaga agaacatcaa ggagttcctg cagagcttcg tgcacatcgt gcagatgttc 2280

atcaacacca gctccggcgg cggctccggc ggcggcggct ccggcggcgg cggctccggc 2340

ggcggcggct ccggcggcgg ctccctgcag gcccccagaa gagccagagg ctgcagaacc 2400

ctgggcctgc ccgccctgct gctgctgctg ctgctgagac cccccgccac cagaggcatc 2460

acctgccccc cccccatgag cgtggagcac gccgacatct gggtgaagag ctacagcctg 2520

tacagcagag agagatacat ctgcaacagc ggcttcaaga gaaaggccgg caccagcagc 2580

ctgaccgagt gcgtgctgaa caaggccacc aacgtggccc actggaccac ccccagcctg 2640

aagtgcatca gataagttta aac 2663

<210> 160
<211> 884
<212> PRT
<213> Artificial Sequence

<220>
<223> (L8-CD7-28-52 -IL-15/IL-15sushi CAR amino acid sequence)

<400> 160

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 Gly Ala Gln Pro Ala Met Ala Ala Tyr Lys Asp
20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
35 40 45

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

Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Asn Lys Leu Leu Ile Tyr
65 70 75 80

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

Gly Ser Gly Thr Asp Tyr Ser Leu His Ser Asn Leu Glu Pro Glu Asp
100 105 110

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Tyr Thr Phe
115 120 125

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

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

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

Lys Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Ser Tyr Ala Met
180 185 190

Ser Trp Asn Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala Ser
195 200 205

```
Ile Ser Ser Gly Gly Phe Thr Tyr Tyr Pro Asp Ser Asn Lys Gly Arg
    210                 215                 220

Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu Gln Met
225                 230                 235                 240

Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Asp
                245                 250                 255

Glu Val Arg Gly Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr Val Thr
            260                 265                 270

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

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

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

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

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

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
        355                 360                 365

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
    370                 375                 380

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430
```

```
Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Gln Asn Asp
    530                 535                 540

Thr Ser Gln Thr Ser Ser Pro Ser Ser Pro Leu Phe Pro Gly Pro Ser
545                 550                 555                 560

Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
                565                 570                 575

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Gly Ser Gly
            580                 585                 590

Ala Thr Asn Leu Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
        595                 600                 605

Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser
    610                 615                 620

Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys
625                 630                 635                 640
```

```
Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile
                645                 650                 655

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
            660                 665                 670

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
        675                 680                 685

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
    690                 695                 700

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
705                 710                 715                 720

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
                725                 730                 735

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
            740                 745                 750

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly
        755                 760                 765

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    770                 775                 780

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

Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala
                805                 810                 815

Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp
            820                 825                 830

Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys
        835                 840                 845

Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys
    850                 855                 860
```

```
Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu
865                 870                 875                 880


Lys Cys Ile Arg



<210>  161
<211>  201
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  (CLL-1 antigen recognition domain amino acid sequence)

<400>  161

His Val Thr Leu Lys Ile Glu Met Lys Lys Met Asn Lys Leu Gln Asn
1               5                   10                  15


Ile Ser Glu Glu Leu Gln Arg Asn Ile Ser Leu Gln Leu Met Ser Asn
            20                  25                  30


Met Asn Ile Ser Asn Lys Ile Arg Asn Leu Ser Thr Thr Leu Gln Thr
        35                  40                  45


Ile Ala Thr Lys Leu Cys Arg Glu Leu Tyr Ser Lys Glu Gln Glu His
    50                  55                  60


Lys Cys Lys Pro Cys Pro Arg Arg Trp Ile Trp His Lys Asp Ser Cys
65                  70                  75                  80


Tyr Phe Leu Ser Asp Asp Val Gln Thr Trp Gln Glu Ser Lys Met Ala
                85                  90                  95


Cys Ala Ala Gln Asn Ala Ser Leu Leu Lys Ile Asn Asn Lys Asn Ala
            100                 105                 110


Leu Glu Phe Ile Lys Ser Gln Ser Arg Ser Tyr Asp Tyr Trp Leu Gly
        115                 120                 125


Leu Ser Pro Glu Glu Asp Ser Thr Arg Gly Met Arg Val Asp Asn Ile
    130                 135                 140
```

```
Ile Asn Ser Ser Ala Trp Val Ile Arg Asn Ala Pro Asp Leu Asn Asn
145                 150                 155                 160


Met Tyr Cys Gly Tyr Ile Asn Arg Leu Tyr Val Gln Tyr Tyr His Cys
                165                 170                 175


Thr Tyr Lys Lys Arg Met Ile Cys Glu Lys Met Ala Asn Pro Val Gln
            180                 185                 190


Leu Gly Ser Thr Tyr Phe Arg Glu Ala
        195                 200


<210>  162
<211>  793
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  (L8-CD7-28-IL-15/IL-15sushi CAR amino acid sequence)

<400>  162

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 Gly Ala Gln Pro Ala Met Ala Ala Tyr Lys Asp
            20                  25                  30


Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
        35                  40                  45


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


Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Asn Lys Leu Leu Ile Tyr
65                  70                  75                  80


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


Gly Ser Gly Thr Asp Tyr Ser Leu His Ser Asn Leu Glu Pro Glu Asp
            100                 105                 110
```

```
Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Tyr Thr Phe
        115                 120                 125

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

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

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

Lys Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Ser Tyr Ala Met
            180                 185                 190

Ser Trp Asn Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala Ser
        195                 200                 205

Ile Ser Ser Gly Gly Phe Thr Tyr Tyr Pro Asp Ser Asn Lys Gly Arg
    210                 215                 220

Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu Gln Met
225                 230                 235                 240

Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Asp
                245                 250                 255

Glu Val Arg Gly Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr Val Thr
            260                 265                 270

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

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

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
305                 310                 315                 320
```

```
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
                325                 330                 335

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

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
        355                 360                 365

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
    370                 375                 380

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Ala Thr Asn Leu Ser Leu Leu Lys Gln Ala Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser
        515                 520                 525

Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val
    530                 535                 540
```

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

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
                565                 570                 575

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
            580                 585                 590

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
        595                 600                 605

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
    610                 615                 620

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
625                 630                 635                 640

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
                645                 650                 655

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
            660                 665                 670

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

Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala
    690                 695                 700

Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu
705                 710                 715                 720

Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser
                725                 730                 735

Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg
            740                 745                 750
```

Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser
        755   760   765

Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp
    770   775   780

Thr Thr Pro Ser Leu Lys Cys Ile Arg
785   790

<210> 163
<211> 2398
<212> DNA
<213> Artificial Sequence

<220>
<223> (L8-CD7-28-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 163
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg   60

ccgccaggcc gggcgcccag cccgccatgg ccgcctacaa ggacatccag atgacccaga   120

ccaccagcag cctgagcgcc agcctgggcg acagagtgac catcagctgc agcgccagcc   180

agggcatcag caactacctg aactggtacc agcagaagcc cgacggcacc aacaagctgc   240

tgatctacta caccagcagc ctgcacagcg gcgtgcccag cagattcagc ggcagcggca   300

gcggcaccga ctacagcctg cacagcaacc tggagcccga ggacatcgcc acctactact   360

gccagcagta cagcaagctg ccctacacct tcggcggcgg caccaagctg gagatcaaga   420

gaggcggcgg cggcagcggc ggcggcggca gcggcggcgg cggcagcggc ggcggcggca   480

gcgaggtgca gctggtggag agcggcggcg gcctggtgaa gcccggcggc agcctgaagc   540

tgagctgcgc cgccagcggc ctgaccttca gcagctacgc catgagctgg aacagacaga   600

cccccgagaa gagactggag tgggtggcca gcatcagcag cggcggcttc acctactacc   660

ccgacagcaa caagggcaga ttcaccatca gcagagacaa cgccagaaac atcctgtacc   720

tgcagatgag cagcctgaga agcgaggaca ccgccatgta ctactgcgcc agagacgagg   780

tgagaggcta cctggacgtg tggggcgccg gcaccaccgt gaccgtgagc agcaccacga   840

cgccagcgcc gcgaccacca acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc   900

gcccagaggc gtgccggcca gcggcggggg gcgcagtgca cacgaggggg ctggacttcg   960

cctgtgatat ctacatctgg gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac   1020

tggttatcac cctttactgc aggagtaaga ggagcaggct cctgcacagt gactacatga 1080

acatgactcc ccgccgcccc gggcccaccc gcaagcatta ccagccctat gccccaccac 1140

gcgacttcgc agcctatcgc tccagagtga agttcagcag gagcgcagac gcccccgcgt 1200

accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga gaggagtacg 1260

atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg cagagaagga 1320

agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg gaggcctaca 1380

gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc ctttaccagg 1440

gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc ctgccccctc 1500

gcggaagcgg agctactaac ttgagcctgc tgaagcaggc tggagacgtg gaggagaacc 1560

ctggacctat gtacagaatg cagctgctga gctgcatcgc cctgagcctg gccctggtga 1620

ccaacagcgg catccacgtg ttcatcctgg gctgcttcag cgccggcctg cccaagaccg 1680

aggccaactg ggtgaacgtg atcagcgacc tgaagaagat cgaggacctg atccagagca 1740

tgcacatcga cgccaccctg tacaccgaga gcgacgtgca ccccagctgc aaggtgaccg 1800

ccatgaagtg cttcctgctg gagctgcagg tgatcagcct ggagagcggc gacgccagca 1860

tccacgacac cgtggagaac ctgatcatcc tggccaacaa cagcctgagc agcaacggca 1920

acgtgaccga gagcggctgc aaggagtgcg aggagctgga ggagaagaac atcaaggagt 1980

tcctgcagag cttcgtgcac atcgtgcaga tgttcatcaa caccagctcc ggcggcggct 2040

ccggcggcgg cggctccggc ggcggcggct ccggcggcgg cggctccggc ggcggctccc 2100

tgcaggcccc cagaagagcc agaggctgca gaaccctggg cctgcccgcc ctgctgctgc 2160

tgctgctgct gagacccccc gccaccagag gcatcacctg ccccccccca atgagcgtgg 2220

agcacgccga catctgggtg aagagctaca gcctgtacag cagagagaga tacatctgca 2280

acagcggctt caagagaaag gccggcacca gcagcctgac cgagtgcgtg ctgaacaagg 2340

ccaccaacgt ggcccactgg accacccccа gcctgaagtg catcagataa gtttaaac 2398

<210> 164
<211> 767
<212> PRT
<213> Artificial Sequence

<220>

<223> (CD19b-28-4-1BBL CAR amino acid sequence)

<400> 164

```
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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30


Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45


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


Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80


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


Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110


Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125


Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160


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


Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190


Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205
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```
Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

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
        355                 360                 365

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

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

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

```
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420                 425                 430

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

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

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

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

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

Pro Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp
        515                 520                 525

Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu
    530                 535                 540

Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val
545                 550                 555                 560

Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly
                565                 570                 575

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
            580                 585                 590

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
        595                 600                 605

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

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
625                 630                 635                 640
```

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
645 650 655

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
660 665 670

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

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

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
705 710 715 720

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
725 730 735

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
740 745 750

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

<210> 165
<211> 2320
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-28-4-1BBL CAR nucleotide sequence)

<400> 165
gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60

ccgccaggcc ggaggtccag ctgcagcagt ctggacctga gctgataaag cctggggctt 120

cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg 180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg 240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca 300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg 360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc 420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg 480

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg actccccgcc 1080

gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac ttcgcagcct 1140

atcgctccag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag cagggccaga 1200

accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt ttggacaaga 1260

gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct caggaaggcc 1320

tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt gggatgaaag 1380

gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt acagccacca 1440

aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgcggcagc ggcgaaggcc 1500

gcggcagcct gctgacctgc ggcgatgtgg aagaaaaccc gggccccatg gaatacgcct 1560

ctgacgcttc actggacccc gaagccccgt ggcctcccgc gccccgcgct cgcgcctgcc 1620

gcgtactgcc ttgggccctg gtcgcggggc tgctgctgct gctgctgctc gctgccgcct 1680

gcgccgtctt cctcgcctgc ccctgggccg tgtccggggc tcgcgcctcg cccggctccg 1740

cggccagccc gagactccgc gagggtcccg agctttcgcc cgacgatccc gccggcctct 1800

tggacctgcg gcagggcatg tttgcgcagc tggtggccca aaatgttctg ctgatcgatg 1860

ggcccctgag ctggtacagt gacccaggcc tggcaggcgt gtccctgacg gggggcctga 1920

gctacaaaga ggacacgaag gagctggtgg tggccaaggc tggagtctac tatgtcttct 1980

ttcaactaga gctgcggcgc gtggtggccg gcgagggctc aggctccgtt tcacttgcgc 2040

tgcacctgca gccactgcgc tctgctgctg gggccgccgc cctggctttg accgtggacc 2100

tgccacccgc ctcctccgag gctcggaact cggccttcgg tttccagggc cgcttgctgc 2160

acctgagtgc cggccagcgc ctgggcgtcc atcttcacac tgaggccagg gcacgccatg 2220

cctggcagct tacccagggc gccacagtct tgggactctt ccgggtgacc cccgaaatcc 2280

cagccggact cccttcaccg aggtcggaat aagtttaaac 2320

<210> 166
<211> 1001
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19b-CD22b-28 amino acid sequence)

<400> 166

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65 70 75 80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
115 120 125

```
Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335
```

```
Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

Ala Leu Leu Leu His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser
    530                 535                 540

Gly Ala Glu Leu Ser Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
545                 550                 555                 560
```

```
Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Leu His Trp Ile Lys Gln
                565                 570                 575

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn
            580                 585                 590

Asp Tyr Thr Glu Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr
        595                 600                 605

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
    610                 615                 620

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr
625                 630                 635                 640

Phe Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly
                645                 650                 655

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu
            660                 665                 670

Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Asn Val Thr
        675                 680                 685

Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ala Asn His Lys
    690                 695                 700

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
705                 710                 715                 720

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
                725                 730                 735

Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Gln Val
            740                 745                 750

Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr
        755                 760                 765
```

```
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr Pro Ala
    770                 775                 780

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

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

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

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

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

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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser 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> 167
<211> 3014
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-CD22b-28 CAR nucleotide sequence)

<400> 167
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gagggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 1200

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 1260

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 1320

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1380

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1440

gacacctacg acgcccttca catgcaggcc ctgccccctc gcggaagcgg agccaccaac 1500

ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggccccat ggccctgccc 1560

gtgaccgccc tgctgctgcc cctggccctg ctgctgcacg ccgccaggcc ccaggtgcag 1620

ctgcaggaga gcggcgccga gctgagcaag cccggcgcca gcgtgaagat gagctgcaag 1680

gccagcggct acaccttcac cagctactgg ctgcactgga tcaagcagag gcccggccag 1740

ggcctggagt ggatcggcta catcaacccc aggaacgact acaccgagta caaccagaac 1800

ttcaaggaca aggccaccct gaccgccgac aagagcagca gcaccgccta catgcagctg 1860

agcagcctga ccagcgagga cagcgccgtg tactactgcg ccaggaggga catcaccacc 1920

ttctactggg gccagggcac caccctgacc gtgagcagcg gagggggggg atccgggggа 1980

ggaggctccg gcggaggcgg aagcgacatc cagctgaccc agagccccag cagcctggcc 2040

gtgagcgccg gcgagaacgt gaccatgagc tgcaagagca gccagagcgt gctgtacagc 2100

gccaaccaca agaactacct ggcctggtac cagcagaagc ccggccagag ccccaagctg 2160

ctgatctact gggccagcac cagggagagc ggcgtgcccg acaggttcac cggcagcggc 2220

accgacttca ccctgaccat cagcagggtg caggtggagg acctggccat ctactactgc 2280

caccagtacc tgagcagctg gaccttcggc ggcggcacca agctggagat caagaggacc 2340

accacccccg cccccaggcc ccccacccccc gcccccacca tcgccagcca gcccctgagc 2400

ctgaggcccg aggcctgcag gcccgccgcc ggcggcgccg tgcacaccag gggcctggac 2460

ttcgcctgcg acatctacat ctgggccccc ctggccggca cctgcggcgt gctgctgctg 2520

agcctggtga tcaccctgta ctgcaggagt aagaggagca ggctcctgca cagtgactac 2580

atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgcccca 2640

ccacgcgact tcgcagccta tcgctccagg gtgaagttca gcaggagcgc cgacgccccc 2700

gcctaccagc agggccagaa ccagctgtac aacgagctga acctgggcag gagggaggag 2760

tacgacgtgc tggacaagag gaggggcagg gaccccgaga tgggcggcaa gcccaggagg 2820

aagaaccccc aggagggcct gtacaacgag ctgcagaagg acaagatggc cgaggcctac 2880

agcgagatcg gcatgaaggg cgagaggagg aggggcaagg gccacgacgg cctgtaccag 2940

ggcctgagca ccgccaccaa ggacacctac gacgccctgc acatgcaggc cctgcccccc 3000

aggtaagttt aaac 3014

<210> 168
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> (FcER1A-28-2G CAR amino acid sequence)

<400> 168

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 Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro
20 25 30

Pro Trp Asn Arg Ile Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn
35 40 45

Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly
50 55 60

Ser Leu Ser Glu Glu Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys
65 70 75 80

Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu
85 90 95

Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln
100 105 110

Ala Ser Ala Glu Val Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys
115 120 125

His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp
130 135 140

```
Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr
145                 150                 155                 160

Asn Ala Thr Val Glu Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val
                165                 170                 175

Trp Gln Leu Asp Tyr Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys
            180                 185                 190

Ala Pro Arg Glu Lys Tyr Trp Leu Gln Ile Tyr Ile Trp Ala Pro Leu
        195                 200                 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
    210                 215                 220

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
225                 230                 235                 240

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
                245                 250                 255

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
            260                 265                 270

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        275                 280                 285

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    290                 295                 300

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
305                 310                 315                 320

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
                325                 330                 335

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
            340                 345                 350
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
        355                 360                 365


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    370                 375


<210>  169
<211>  1148
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (FcER1A-28-2G CAR nucleotide sequence)

<400>  169
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggtgcccc agaagcccaa ggtgagcctg aacccccccct ggaacaggat cttcaagggc      120

gagaacgtga ccctgacctg caacggcaac aacttcttcg aggtgagcag caccaagtgg      180

ttccacaacg gcagcctgag cgaggagacc aacagcagcc tgaacatcgt gaacgccaag      240

ttcgaggaca gcggcgagta caagtgccag caccagcagg tgaacgagag cgagcccgtg      300

tacctggagg tgttcagcga ctggctgctg ctgcaggcca gcgccgaggt ggtgatggag      360

ggccagcccc tgttcctgag gtgccacggc tggaggaact gggacgtgta caaggtgatc      420

tactacaagg acggcgaggc cctgaagtac tggtacgaga accacaacat cagcatcacc      480

aacgccaccg tggaggacag cggcacctac tactgcaccg gcaaggtgtg gcagctggac      540

tacgagagcg agcccctgaa catcaccgtg atcaaggccc ccagggagaa gtactggctg      600

cagatctaca tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt      660

atcacccttt actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg      720

actccccgcc gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac      780

ttcgcagcct atcgctccag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag      840

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt      900

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgcagag aaggaagaac      960

cctcaggaag gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagtgag     1020

attgggatga aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc     1080

agtacagcca ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgctaa     1140
```

gtttaaac 1148

<210> 170
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> (FcER1A-28-4-1BBL CAR amino acid sequence)

<400> 170

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 Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro
20 25 30

Pro Trp Asn Arg Ile Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn
35 40 45

Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly
50 55 60

Ser Leu Ser Glu Glu Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys
65 70 75 80

Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu
85 90 95

Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln
100 105 110

Ala Ser Ala Glu Val Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys
115 120 125

His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp
130 135 140

Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr
145 150 155 160

```
Asn Ala Thr Val Glu Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val
                165                 170                 175

Trp Gln Leu Asp Tyr Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys
            180                 185                 190

Ala Pro Arg Glu Lys Tyr Trp Leu Gln Ile Tyr Ile Trp Ala Pro Leu
        195                 200                 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
    210                 215                 220

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
225                 230                 235                 240

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
                245                 250                 255

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
            260                 265                 270

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        275                 280                 285

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    290                 295                 300

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
305                 310                 315                 320

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
                325                 330                 335

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
            340                 345                 350

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
        355                 360                 365

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly
    370                 375                 380
```

```
Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
385                 390                 395                 400

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
                405                 410                 415

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
            420                 425                 430

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
        435                 440                 445

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

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
465                 470                 475                 480

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
                485                 490                 495

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
            500                 505                 510

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

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
    530                 535                 540

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
545                 550                 555                 560

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
                565                 570                 575

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
            580                 585                 590
```

```
Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
        595                 600                 605


Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
    610                 615                 620


Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
625                 630                 635                 640


Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
                645                 650


<210>  171
<211>  1973
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (FcER1A-28-4-1BBL CAR nucleotide sequence)

<400>  171
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggtgcccc agaagcccaa ggtgagcctg aacccccccct ggaacaggat cttcaagggc      120

gagaacgtga ccctgacctg caacggcaac aacttcttcg aggtgagcag caccaagtgg      180

ttccacaacg gcagcctgag cgaggagacc aacagcagcc tgaacatcgt gaacgccaag      240

ttcgaggaca gcggcgagta caagtgccag caccagcagg tgaacgagag cgagcccgtg      300

tacctggagg tgttcagcga ctggctgctg ctgcaggcca gcgccgaggt ggtgatggag      360

ggccagcccc tgttcctgag gtgccacggc tggaggaact gggacgtgta caaggtgatc      420

tactacaagg acggcgaggc cctgaagtac tggtacgaga accacaacat cagcatcacc      480

aacgccaccg tggaggacag cggcacctac tactgcaccg gcaaggtgtg gcagctggac      540

tacgagagcg agcccctgaa catcaccgtg atcaaggccc ccagggagaa gtactggctg      600

cagatctaca tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt      660

atcacccttt actgcaggag taagaggagc aggctcctgc acagtgacta catgaacatg      720

actccccgcc gccccgggcc cacccgcaag cattaccagc cctatgcccc accacgcgac      780

ttcgcagcct atcgctccag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag      840

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt      900
```

ttggacaaga gacgtggccg ggaccctgag atgggggaa agccgcagag aaggaagaac 960

cctcaggaag gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagtgag 1020

attgggatga aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc 1080

agtacagcca ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgcggc 1140

agcggcgaag gccgcggcag cctgctgacc tgcggcgatg tggaagaaaa cccgggcccc 1200

atggaatacg cctctgacgc ttcactggac cccgaagccc cgtggcctcc cgcgccccgc 1260

gctcgcgcct gccgcgtact gccttgggcc ctggtcgcgg ggctgctgct gctgctgctg 1320

ctcgctgccg cctgcgccgt cttcctcgcc tgcccctggg ccgtgtccgg ggctcgcgcc 1380

tcgcccggct ccgcggccag cccgagactc cgcgagggtc ccgagctttc gcccgacgat 1440

cccgccggcc tcttggacct gcggcagggc atgtttgcgc agctggtggc ccaaaatgtt 1500

ctgctgatcg atgggcccct gagctggtac agtgacccag gcctggcagg cgtgtccctg 1560

acgggggggcc tgagctacaa agaggacacg aaggagctgg tggtggccaa ggctggagtc 1620

tactatgtct tctttcaact agagctgcgg cgcgtggtgg ccggcgaggg ctcaggctcc 1680

gtttcacttg cgctgcacct gcagccactg cgctctgctg ctggggccgc cgccctggct 1740

ttgaccgtgg acctgccacc cgcctcctcc gaggctcgga actcggcctt cggtttccag 1800

ggccgcttgc tgcacctgag tgccggccag cgcctgggcg tccatcttca cactgaggcc 1860

agggcacgcc atgcctggca gcttacccag ggcgccacag tcttgggact cttccgggtg 1920

acccccgaaa tcccagccgg actcccttca ccgaggtcgg aataagttta aac 1973

<210> 172
<211> 1007
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19b-BAFFR sequence CAR amino acid sequence)

<400> 172

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

```
Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240
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Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

Ala Leu Leu Leu His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser
    530                 535                 540

Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Ile Cys Ala
545                 550                 555                 560

Ile Ser Gly Asp Ser Val Ser Ser Asn Ser Ala Ala Trp Gly Trp Ile
                565                 570                 575

Arg Gln Ser Pro Gly Arg Gly Leu Glu Trp Leu Gly Arg Ile Tyr Tyr
            580                 585                 590

Arg Ser Lys Trp Tyr Asn Ser Tyr Ala Val Ser Val Lys Ser Arg Ile
        595                 600                 605

Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn
    610                 615                 620

Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Asp
625                 630                 635                 640

Trp Val Pro Lys Ile Gly Val Phe Asp Ser Trp Gly Gln Gly Thr Leu
                645                 650                 655

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            660                 665                 670
```

```
Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
        675                 680                 685

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe
    690                 695                 700

Ile Ser Ser Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
705                 710                 715                 720

Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly Val Pro
                725                 730                 735

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
            740                 745                 750

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Leu
        755                 760                 765

Tyr Ser Ser Pro Met Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
    770                 775                 780

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
785                 790                 795                 800

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
                805                 810                 815

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
            820                 825                 830

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
        835                 840                 845

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
    850                 855                 860

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
865                 870                 875                 880

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

```
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
            900                 905                 910

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

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

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
945                 950                 955                 960

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
                965                 970                 975

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

Lys Asp Thr Tyr Asp Ala Leu His  Met Gln Ala Leu Pro  Pro Arg
        995                 1000                1005
```

<210> 173
<211> 3040
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-BAFFR CAR nucleotide sequence)

<400> 173

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gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg       60

ccgccaggcc ggaggtccag ctgcagcagt ctggacctga gctgataaag cctggggctt      120

cagtgaagat gtcctgcaag gcttctggat acacattcac tagctatgtt atgcactggg      180

tgaagcagaa gcctgggcag ggccttgagt ggattggata tattaatcct tacaatgatg      240

gtactaagta caatgagaag ttcaaaggca aggccacact gacttcagac aaatcctcca      300

gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg      360

caagagggac ttattactac ggtagtaggg tatttgacta ctggggccaa ggcaccactc      420

tcacagtctc ctcaggtgga gggggctcag gcggaggtgg ctctgggggt ggaggctcgg      480
```

acattgtgat gactcaggct gcaccctcta tacctgtcac tcctggagag tcagtatcca 540

tctcctgcag gtctagtaag agtctcctga atagtaatgg caacacttac ttgtattggt 600

tcctgcagag gccaggccag tctcctcagc tcctgatata tcggatgtcc aaccttgcct 660

caggagtccc agacaggttc agtggcagtg ggtcaggaac tgctttcaca ctgagaatca 720

gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta gaatatccgt 780

tcacgttcgg tgctgggacc aagctggagc tgaaacggac cacgacgcca gcgccgcgac 840

caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc 900

ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt gatatctaca 960

tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt atcacccttt 1020

actgcaaacg gggcagaaag aaactcctgt atatattcaa acaaccattt atgagaccag 1080

tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa gaagaaggag 1140

gatgtgaact gagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 1200

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 1260

agagacgtgg ccgggaccct gagatggggg gaaagccgca gagaaggaag aaccctcagg 1320

aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt gagattggga 1380

tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt ctcagtacag 1440

ccaccaagga cacctacgac gcccttcaca tgcaggccct gcccccctcgc ggaagcggag 1500

ccaccaactt cagcctgctg aagcaggccg gcgacgtgga ggagaacccc ggccccatgg 1560

ccctgcccgt gaccgccctg ctgctgcccc tggccctgct gctgcacgcc gccaggcccc 1620

aggtgcagct gcagcagagc ggcccaggcc tggtcaagcc ctctcagacc ctgtcactga 1680

tctgcgccat ttcaggcgac agcgtgagca gcaacagcgc cgcctggggc tggatcaggc 1740

agagccccgg taggggcctg gaatggctgg gcaggatcta ctacaggtcc aagtggtaca 1800

acagctacgc cgtgagcgtg aagagcagga tcaccatcaa ccctgacacc agcaagaacc 1860

agttctcact gcagctcaac agcgtgaccc ccgaggacac cgccgtgtac tactgcgcca 1920

gatacgactg ggtgcccaag atcggcgtgt tcgacagctg gggccagggc accctggtga 1980

ccgtgtcaag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgata 2040

tcgtgctgac acagagcccc gccaccctga gcctgagccc aggcgagagg gccaccctgt 2100

cctgcagggc cagccagttt atcagcagca gctacctgtc ctggtatcag cagaagcccg 2160

gccaggcccc tagactgctg atctacggca gctcctctcg ggccaccggc gtgcccgcca 2220

ggttcagcgg cagcggctcc ggcaccgact tcaccctgac aatcagcagc ctggagcccg 2280

aggacttcgc cgtgtactac tgccagcagc tgtacagctc acccatgacc ttcggccagg 2340

gcaccaaggt ggagatcaag accaccaccc ccgcccccag gccccccacc cccgccccca 2400

ccatcgccag ccagcccctg agcctgaggc ccgaggcctg caggcccgcc gccggcggcg 2460

ccgtgcacac caggggcctg gacttcgcct gcgacatcta catctgggcc cccctggccg 2520

gcacctgcgg cgtgctgctg ctgagcctgg tgatcaccct gtactgcagg agtaagagga 2580

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 2640

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc agggtgaagt 2700

tcagcaggag cgccgacgcc cccgcctacc agcagggcca gaaccagctg tacaacgagc 2760

tgaacctggg caggagggag gagtacgacg tgctggacaa gaggaggggc agggaccccg 2820

agatgggcgg caagccccag aggaggaaga acccccagga gggcctgtac aacgagctgc 2880

agaaggacaa gatggccgag gcctacagcg agatcggcat gaagggcgag aggaggaggg 2940

gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggac acctacgacg 3000

ccctgcacat gcaggccctg ccccccaggt aagtttaaac 3040

<210> 174
<211> 789
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19b-BB-IL-15/IL-15sushi CAR amino acid sequence)

<400> 174

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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

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

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255
```

```
Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

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

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
    530                 535                 540

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

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

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
                645                 650                 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
            660                 665                 670

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        675                 680                 685
```

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
690 695 700

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro
705 710 715 720

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
725 730 735

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
740 745 750

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
755 760 765

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
770 775 780

Leu Lys Cys Ile Arg
785

<210> 175
<211> 2378
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-BB-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 175
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gaggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 1200

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 1260

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 1320

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1380

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1440

gacacctacg acgcccttca catgcaggcc ctgccccctc gcggaagcgg agccaccaac 1500

ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggccccat gtacagaatg 1560

cagctgctga gctgcatcgc cctgagcctg gccctggtga ccaacagcgg catccacgtg 1620

ttcatcctgg gctgcttcag cgccggcctg cccaagaccg aggccaactg ggtgaacgtg 1680

atcagcgacc tgaagaagat cgaggacctg atccagagca tgcacatcga cgccaccctg 1740

tacaccgaga gcgacgtgca ccccagctgc aaggtgaccg ccatgaagtg cttcctgctg 1800

gagctgcagg tgatcagcct ggagagcggc gacgccagca tccacgacac cgtggagaac 1860

ctgatcatcc tggccaacaa cagcctgagc agcaacggca acgtgaccga gagcggctgc 1920

aaggagtgcg aggagctgga ggagaagaac atcaaggagt tcctgcagag cttcgtgcac 1980

atcgtgcaga tgttcatcaa caccagctcc ggcggcggct ccggcggcgg cggctccggc 2040

ggcggcggct ccggcggcgg cggctccggc ggcggctccc tgcaggcccc cagaagagcc 2100

agaggctgca gaaccctggg cctgcccgcc ctgctgctgc tgctgctgct gagacccccc 2160

gccaccagag gcatcacctg ccccccccc atgagcgtgg agcacgccga catctgggtg 2220

aagagctaca gcctgtacag cagagagaga tacatctgca acagcggctt caagagaaag 2280

gccggcacca gcagcctgac cgagtgcgtg ctgaacaagg ccaccaacgt ggcccactgg 2340

accaccccca gcctgaagtg catcagataa gtttaaac 2378

<210> 176
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-2G, CD269-A7D-28-2G CAR amino acid sequence)

<400> 176

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 Arg Ser
                325                 330                 335

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

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

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

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

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

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

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

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

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

His Met Gln Ala Leu Pro Pro Arg
485

<210> 177
<211> 1475
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-2G, CD269-A7D-28-2G CAR nucleotide sequence)

<400> 177
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg 120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgctaagtt taaac 1475

<210> 178
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-28, CD269-C11D-28 CAR amino acid sequence)

<400> 178

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 Pro Ser Leu
            20                  25                  30

Ala Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
        35                  40                  45

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

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

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

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

Cys Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly 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 Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
145                 150                 155                 160

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165                 170                 175

Thr Asp Tyr Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly Leu
            180                 185                 190

Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala
        195                 200                 205

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

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

Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

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

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

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

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

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

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

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

Phe Ala Ala Tyr Arg Ser 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
485

<210> 179
<211> 1397
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-28, CD269-C11D-28 CAR nucleotide sequence)

<400> 179
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcg tgctgaccca gagcccccgc agcctggcca tgagcctggg caagagggcc 120

accatcagct gcagggccag cgagagcgtg accatcctgg gcagccacct gatccactgg 180

taccagcaga agcccggcca gccccccacc ctgctgatcc agctggccag caacgtgcag 240

accggcgtgc ccgccaggtt cagcggcagc ggcagcagga ccgacttcac cctgaccatc 300

gaccccgtgg aggaggacga cgtggccgtg tactactgcc tgcagagcag gaccatcccc 360

aggaccttcg gcggcggcac caagctggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag ccagatccag ctggtgcaga gcggccccga gctgaagaag 480

cccggcgaga ccgtgaagat cagctgcaag gccagcggct acaccttcac cgactacagc 540

atcaactggg tgaagagggc ccccggcaag ggcctgaagt ggatgggctg gatcaacacc 600

gagaccaggg agcccgccta cgcctacgac ttcaggggca ggttcgcctt cagcctggag 660

accagcgcca gcaccgccta cctgcagatc aacaacctga agtacgagga caccgccacc 720

tacttctgcg ccctggacta cagctacgcc atggactact ggggccaggg caccagcgtg 780

accgtgagca gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg 840

tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac 900

acgagggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1320

aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc tttacca 1397

<210> 180
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> (CS1-hu63-28-2G CAR amino acid sequence)

<400> 180

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 Ser Pro Ser Ser Leu
20 25 30

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

Asp Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
50 55 60

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

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

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

```
Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

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

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Phe Ser Arg Tyr Trp Met
                165                 170                 175

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

Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp
        195                 200                 205

Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
    210                 215                 220

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

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

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

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

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

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

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

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

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
355 360 365

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

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

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

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

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

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

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

Leu Pro Pro Arg

<210> 181
<211> 1463
<212> DNA
<213> Artificial Sequence

<220>
<223> (CS1-hu63-28-2G CAR nucleotide sequence)

<400> 181
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcc agatgaccca gagccccagc agcctgagcg ccagcgtggg cgacagggtg 120

accatcacct gcaaggccag ccaggacgtg ggcatcgccg tggcctggta ccagcagaag 180

cccggcaagg tgcccaagct gctgatctac tgggccagca ccaggcacac cggcgtgccc 240

gacaggttca gcggcagcgg cagcggcacc gacttcaccc tgaccatcag cagcctgcag 300

cccgaggacg tggccaccta ctactgccag cagtacagca gctaccccta caccttcggc 360

cagggcacca aggtggagat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcg aggtgcagct ggtggagagc ggcggcggcc tggtgcagcc cggcggcagc 480

ctgaggctga gctgcgccgc cagcggcttc ttcagcaggt actggatgag ctgggtgagg 540

caggcccccg gcaagggcct ggagtggatc ggcgagatca accccgacag cagcaccatc 600

aactacgccc ccagcctgaa ggacaagttc atcatcagca gggacaacgc caagaacagc 660

ctgtacctgc agatgaacag cctgagggcc gaggacaccg ccgtgtacta ctgcgccagg 720

cccgacggca actactggta cttcgacgtg tggggccagg gcaccctggt gaccgtgagc 780

agcaccacga cgccagcgcc gcgaccacca acaccggcgc ccaccatcgc gtcgcagccc 840

ctgtccctgc gcccagaggc gtgccggcca gcggcggggg gcgcagtgca cacgaggggg 900

ctggacttcg cctgtgatat ctacatctgg gcgcccttgg ccgggacttg tggggtcctt 960

ctcctgtcac tggttatcac cctttactgc aggagtaaga ggagcaggct cctgcacagt 1020

gactacatga acatgactcc ccgccgcccc gggcccaccc gcaagcatta ccagccctat 1080

gccccaccac gcgacttcgc agcctatcgc tccagagtga agttcagcag gagcgcagac 1140

gcccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 1200

gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg 1260

cagagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 1320

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 1380

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 1440

ctgccccctc gctaagttta aac 1463

<210> 182
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> (CS1-mu34-28-2G CAR amino acid sequence)

<400> 182

```
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 Ser Ser Ser Tyr Leu
            20                  25                  30


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


His Ile Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala
    50                  55                  60


Pro Arg Leu Leu Ile Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro
65                  70                  75                  80


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


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


Trp 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


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


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


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

```
Ala Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr Gln Lys Phe Lys
        195                 200                 205

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

Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Gly Lys Val Tyr Tyr Gly Ser Asn Pro Phe Ala Tyr Trp Gly Gln
                245                 250                 255

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

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

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser 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
                485
```

<210> 183
<211> 1471
<212> DNA
<213> Artificial Sequence

<220>
<223> (CS1-mu34-28-2G CAR nucleotide sequence)

<400> 183

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tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac gccgccaggc       60

cggacatcca gatgacccag agcagcagct acctgagcgt gagcctgggc ggcagggtga      120

ccatcacctg caaggccagc gaccacatca acaactggct ggcctggtac cagcagaagc      180

ccggcaacgc ccccaggctg ctgatcagcg gcgccaccag cctggagacc ggcgtgccca      240

gcaggttcag cggcagcggc agcggcaagg actacaccct gagcatcacc agcctgcaga      300

ccgaggacgt ggccacctac tactgccagc agtactggag cacccctgg accttcggcg      360

gcggcaccaa gctggagatc aagggagggg ggggatccgg gggaggaggc tccggcggag      420

gcggaagcca ggtgcagctg cagcagagcg gcgccgagct ggccaggccc ggcgccagcg      480

tgaagctgag ctgcaaggcc agcggctaca ccttcaccag ctactggatg cagtgggtga      540

agcagaggcc cggccagggc ctggagtgga tcggcgccat ctaccccggc gacggcgaca      600

ccaggtacac ccagaagttc aagggcaagg ccaccctgac cgccgacaag agcagcagca      660

ccgcctacat gcagctgagc agcctggcca gcgaggacag cgccgtgtac tactgcgcca      720
```

ggggcaaggt gtactacggc agcaacccct tcgcctactg gggccagggc accctggtga 780

ccgtgagcgc caccacgacg ccagcgccgc gaccaccaac accggcgccc accatcgcgt 840

cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc gcagtgcaca 900

cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc gggacttgtg 960

gggtccttct cctgtcactg gttatcaccc tttactgcag gagtaagagg agcaggctcc 1020

tgcacagtga ctacatgaac atgactcccc gccgccccgg gcccacccgc aagcattacc 1080

agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag ttcagcagga 1140

gcgcagacgc ccccgcgtac cagcagggcc agaaccagct ctataacgag ctcaatctag 1200

gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct gagatggggg 1260

gaaagccgca gagaaggaag aaccctcagg aaggcctgta caatgaactg cagaaagata 1320

agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg ggcaaggggc 1380

acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac gcccttcaca 1440

tgcaggccct gcccctcgc taagtttaaa c 1471

<210> 184
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> (CS1-mu90-28-2G CAR amino acid sequence)

<400> 184

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 Met Thr Gln Ser Gln Lys Ser Met
20 25 30

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln
35 40 45

Asp Val Ile Thr Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

```
Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
65                  70                  75                  80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
                85                  90                  95

Ser Asn Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
            100                 105                 110

Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    130                 135                 140

Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Thr Tyr Trp
                165                 170                 175

Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
            180                 185                 190

Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Lys Phe Lys Asp
        195                 200                 205

Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
    210                 215                 220

Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225                 230                 235                 240

Ser Thr Met Ile Ala Thr Arg Ala Met Asp Tyr Trp Gly Gln Gly Thr
                245                 250                 255

Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
            260                 265                 270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
        275                 280                 285
```

```
Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
    290                 295                 300

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
305                 310                 315                 320

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser
                325                 330                 335

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
            340                 345                 350

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
        355                 360                 365

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
    370                 375                 380

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385                 390                 395                 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
                405                 410                 415

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
            420                 425                 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
        435                 440                 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
    450                 455                 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465                 470                 475                 480

Ala Leu Pro Pro Arg
                485
```

<210> 185
<211> 1466
<212> DNA
<213> Artificial Sequence

<220>
<223> (CS1-mu90-28-2G CAR nucleotide sequence)

<400> 185
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcg tgatgaccca gagccagaag agcatgagca ccagcgtggg cgacagggtg 120

agcatcacct gcaaggccag ccaggacgtg atcaccggcg tggcctggta ccagcagaag 180

cccggccaga gccccaagct gctgatctac agcgccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcacc gacttcacct tcaccatcag caacgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccct gaccttcggc 360

gccggcacca agctggagct gaagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc aggtgcagct gcagcagccc ggcgccgagc tggtgaggcc cggcgccagc 480

gtgaagctga gctgcaaggc cagcggctac agcttcacca cctactggat gaactgggtg 540

aagcagaggc ccggccaggg cctggagtgg atcggcatga tccaccccag cgacagcgag 600

accaggctga acaagttcaa ggacaaggcc accctgaccg tggacaagag cagcagcacc 660

gcctacatgc agctgagcag ccccaccagc gaggacagcg ccgtgtacta ctgcgccagg 720

agcaccatga tcgccaccag ggccatggac tactggggcc agggcaccag cgtgaccgtg 780

agcagcacca cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgcag 840

cccctgtccc tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg 900

gggctggact tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtggggtc 960

cttctcctgt cactggttat cacccttttac tgcaggagta agaggagcag gctcctgcac 1020

agtgactaca tgaacatgac tccccgccgc cccgggccca cccgcaagca ttaccagccc 1080

tatgccccac cacgcgactt cgcagcctat cgctccagag tgaagttcag caggagcgca 1140

gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga 1200

agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat gggggggaaag 1260

ccgcagagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg 1320

gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 1380

ggcctttacc agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag 1440

gccctgcccc ctcgctaagt ttaaac 1466

<210> 186
<211> 772
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD33b-28-4-1BBL CAR amino acid sequence)

<400> 186

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
65 70 75 80

Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
100 105 110

Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Glu Val Gln Leu Lys Glu
145 150 155 160

```
Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys
                165                 170                 175

Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp
        195                 200                 205

Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser
    210                 215                 220

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn Leu Gln
225                 230                 235                 240

Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr Tyr Pro
                245                 250                 255

Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305                 310                 315                 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser
            340                 345                 350

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        355                 360                 365
```

```
Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    370                 375                 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385                 390                 395                 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                405                 410                 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            420                 425                 430

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465                 470                 475                 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490                 495

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp
        515                 520                 525

Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val
    530                 535                 540

Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala
545                 550                 555                 560

Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala
                565                 570                 575

Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
            580                 585                 590
```

```
Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
        595                 600                 605

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
    610                 615                 620

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
625                 630                 635                 640

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
                645                 650                 655

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
            660                 665                 670

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
        675                 680                 685

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
    690                 695                 700

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
705                 710                 715                 720

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
                725                 730                 735

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
            740                 745                 750

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
        755                 760                 765

Pro Arg Ser Glu
    770
```

<210> 187
<211> 2327
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD33b-28-4-1BBL CAR nucleotide sequence)

<400> 187
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cccatggccg actacaagga catcgtgatg acccagagcc acaagttcct gctggtgagc 120

gtgggcgaca gggtgagcat cacctgcaag gccagccagg acgtgagcac cgccgtggcc 180

tggtaccagc agaagcccgg ccagagcccc aagctgctga tctacagcgc cagctacagg 240

tacaccggcg tgcccgacag gttcatcggc agcggcagcg gcaccgactt caccctgacc 300

atcagcagcg tgcaggccga ggacctggcc gactacttct gccagcagca ctacagcacc 360

cccctgacct tcggcgccgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420

ggcggcggca gcggcggcgg cggcagcagc ggcggcggca gcgaggtgca gctgaaggag 480

agcggccccg gcctggtggc ccccagccag agcctgagca tcacctgcac cgtgagcggc 540

ttccccctga ccagctacgg cgtgagctgg gtgaggcagc cccccggcaa gggcctggag 600

tggctgggcg tgatctgggg cgacggcagc accaactacc acagcgccct gatcagcagg 660

ctgagcatca gcaaggacaa cagcaagagc caggtgttcc tgaagctgaa caacctgcag 720

accgacgaca ccgccaccta ctactgcgcc agggacacct actaccccta ctacgccatg 780

gactactggg gccagggcac cagcgtgacc gtgagcagca ccaccacccc cgcccccagg 840

ccccccaccc ccgcccccac catcgccagc cagccctga gcctgaggcc cgaggcctgc 900

aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg acttcgcctg cgacatctac 960

atctgggccc ccctggccgg cacctgcggc gtgctgctgc tgagcctggt gatcaccctg 1020

tactgcagga gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc 1080

cgccccgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 1140

tatcgctcca gggtgaagtt cagcaggagc gccgacgccc ccgcctacca gcagggccag 1200

aaccagctgt acaacgagct gaacctgggc aggagggagg agtacgacgt gctggacaag 1260

aggaggggca gggaccccga gatgggcggc aagccccaga ggaggaagaa cccccaggag 1320

ggcctgtaca acgagctgca gaaggacaag atggccgagg cctacagcga gatcggcatg 1380

aagggcgaga ggaggagggg caagggccac gacggcctgt accagggcct gagcaccgcc 1440

accaaggaca cctacgacgc cctgcacatg caggccctgc cccccagggg aagcggagcc 1500

accaacttca gcctgctgaa gcaggccggc gacgtggagg agaaccccgg ccccatggaa 1560

tacgcctctg acgcttcact ggaccccgaa gccccgtggc ctcccgcgcc ccgcgctcgc 1620

gcctgccgcg tactgccttg ggccctggtc gcggggctgc tgctgctgct gctgctcgct 1680

gccgcctgcg ccgtcttcct cgcctgcccc tgggccgtgt ccggggctcg cgcctcgccc 1740

ggctccgcgg ccagcccgag actccgcgag ggtcccgagc tttcgcccga cgatcccgcc 1800

ggcctcttgg acctgcggca gggcatgttt gcgcagctgg tggcccaaaa tgttctgctg 1860

atcgatgggc ccctgagctg gtacagtgac ccaggcctgg caggcgtgtc cctgacgggg 1920

ggcctgagct acaaagagga cacgaaggag ctggtggtgg ccaaggctgg agtctactat 1980

gtcttctttc aactagagct gcggcgcgtg gtggccggcg agggctcagg ctccgtttca 2040

cttgcgctgc acctgcagcc actgcgctct gctgctgggg ccgccgccct ggctttgacc 2100

gtggacctgc cacccgcctc ctccgaggct cggaactcgg ccttcggttt ccagggccgc 2160

ttgctgcacc tgagtgccgg ccagcgcctg ggcgtccatc ttcacactga ggccagggca 2220

cgccatgcct ggcagcttac ccagggcgcc acagtcttgg gactcttccg ggtgaccccc 2280

gaaatcccag ccggactccc ttcaccgagg tcggaataag tttaaac 2327

<210> 188
<211> 792
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD33b-BB-IL-15/IL-15sushi CAR amino acid sequence)

<400> 188

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
50 55 60

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Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
65                  70                  75                  80

Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
            100                 105                 110

Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr
        115                 120                 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Glu Val Gln Leu Lys Glu
145                 150                 155                 160

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys
                165                 170                 175

Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp
        195                 200                 205

Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser
    210                 215                 220

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn Leu Gln
225                 230                 235                 240

Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr Tyr Pro
                245                 250                 255

Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270
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Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305                 310                 315                 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
            340                 345                 350

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
        355                 360                 365

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            420                 425                 430

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495
```

```
Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys
        515                 520                 525

Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe
    530                 535                 540

Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp
545                 550                 555                 560

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                565                 570                 575

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            580                 585                 590

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
        595                 600                 605

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
    610                 615                 620

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
625                 630                 635                 640

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
                645                 650                 655

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            660                 665                 670

Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        675                 680                 685

Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg
    690                 695                 700
```

```
Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu
705                 710                 715                 720


Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val
                725                 730                 735


Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
            740                 745                 750


Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
        755                 760                 765


Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
    770                 775                 780


Thr Pro Ser Leu Lys Cys Ile Arg
785                 790


<210>  189
<211>  2387
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (CD33b-BB-IL-15/IL-15sushi CAR nucleotide sequence)

<400>  189
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cccatggccg actacaagga catcgtgatg acccagagcc acaagttcct gctggtgagc      120

gtgggcgaca gggtgagcat cacctgcaag gccagccagg acgtgagcac cgccgtggcc      180

tggtaccagc agaagcccgg ccagagcccc aagctgctga tctacagcgc cagctacagg      240

tacaccggcg tgcccgacag gttcatcggc agcggcagcg gcaccgactt caccctgacc      300

atcagcagcg tgcaggccga ggacctggcc gactacttct gccagcagca ctacagcacc      360

cccctgacct tcggcgccgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc      420

ggcggcggca gcggcggcgg cggcagcagc ggcggcggca gcgaggtgca gctgaaggag      480

agcggccccg gcctggtggc ccccagccag agcctgagca tcacctgcac cgtgagcggc      540

ttccccctga ccagctacgg cgtgagctgg gtgaggcagc cccccggcaa gggcctggag      600

tggctgggcg tgatctgggg cgacggcagc accaactacc acagcgccct gatcagcagg      660
```

ctgagcatca gcaaggacaa cagcaagagc caggtgttcc tgaagctgaa caacctgcag 720

accgacgaca ccgccaccta ctactgcgcc agggacacct actaccccta ctacgccatg 780

gactactggg gccagggcac cagcgtgacc gtgagcagca ccaccacccc cgcccccagg 840

ccccccaccc ccgcccccac catcgccagc cagcccctga gcctgaggcc cgaggcctgc 900

aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg acttcgcctg cgacatctac 960

atctgggccc ccctggccgg cacctgcggc gtgctgctgc tgagcctggt gatcaccctg 1020

tactgcaaac ggggcagaaa gaaactcctg tatatattca aacaaccatt tatgagacca 1080

gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga 1140

ggatgtgaac tgagggtgaa gttcagcagg agcgccgacg cccccgccta ccagcagggc 1200

cagaaccagc tgtacaacga gctgaacctg ggcaggaggg aggagtacga cgtgctggac 1260

aagaggaggg gcagggaccc cgagatgggc ggcaagcccc agaggaggaa gaacccccag 1320

gagggcctgt acaacgagct gcagaaggac aagatggccg aggcctacag cgagatcggc 1380

atgaagggcg agaggaggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1440

gccaccaagg acacctacga cgccctgcac atgcaggccc tgcccccag gggaagcgga 1500

gccaccaact tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggccccatg 1560

tacagaatgc agctgctgag ctgcatcgcc ctgagcctgg ccctggtgac caacagcggc 1620

atccacgtgt tcatcctggg ctgcttcagc gccggcctgc ccaagaccga ggccaactgg 1680

gtgaacgtga tcagcgacct gaagaagatc gaggacctga tccagagcat gcacatcgac 1740

gccaccctgt acaccgagag cgacgtgcac cccagctgca aggtgaccgc catgaagtgc 1800

ttcctgctgg agctgcaggt gatcagcctg gagagcggcg acgccagcat ccacgacacc 1860

gtggagaacc tgatcatcct ggccaacaac agcctgagca gcaacggcaa cgtgaccgag 1920

agcggctgca aggagtgcga ggagctggag gagaagaaca tcaaggagtt cctgcagagc 1980

ttcgtgcaca tcgtgcagat gttcatcaac accagctccg gcggcggctc cggcggcggc 2040

ggctccggcg gcggcggctc cggcggcggc ggctccggcg gcggctccct gcaggccccc 2100

agaagagcca gaggctgcag aaccctgggc ctgcccgccc tgctgctgct gctgctgctg 2160

agacccccg ccaccagagg catcacctgc ccccccccca tgagcgtgga gcacgccgac 2220

atctgggtga agagctacag cctgtacagc agagagagat acatctgcaa cagcggcttc 2280

aagagaaagg ccggcaccag cagcctgacc gagtgcgtgc tgaacaaggc caccaacgtg 2340

gcccactgga ccacccccag cctgaagtgc atcagataag tttaaac 2387

<210> 190
<211> 829
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD33b-28-IL-15/IL-15 anchor CAR amino acid sequence)

<400> 190

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
65 70 75 80

Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
100 105 110

Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Glu Val Gln Leu Lys Glu
145 150 155 160

```
Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys
                165                 170                 175

Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp
        195                 200                 205

Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser
    210                 215                 220

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn Leu Gln
225                 230                 235                 240

Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr Tyr Pro
                245                 250                 255

Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305                 310                 315                 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser
            340                 345                 350

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        355                 360                 365
```

```
Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    370                 375                 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385                 390                 395                 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                405                 410                 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            420                 425                 430

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465                 470                 475                 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490                 495

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile
        515                 520                 525

Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile
    530                 535                 540

Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val
545                 550                 555                 560

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
                565                 570                 575

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
            580                 585                 590
```

```
Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
        595                 600                 605

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
    610                 615                 620

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
625                 630                 635                 640

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
                645                 650                 655

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser
            660                 665                 670

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        675                 680                 685

Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile Thr Cys Pro Pro Pro Met
    690                 695                 700

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser
705                 710                 715                 720

Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr
                725                 730                 735

Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His
            740                 745                 750

Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg 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 Val Ala Ile Ser Thr Ser Thr Val Leu
805 810 815

Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys Tyr
820 825

<210> 191
<211> 2498
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD33b-28-IL-15/IL-15 anchor CAR nucleotide sequence)

<400> 191
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccatggccg actacaagga catcgtgatg acccagagcc acaagttcct gctggtgagc 120

gtgggcgaca gggtgagcat cacctgcaag gccagccagg acgtgagcac cgccgtggcc 180

tggtaccagc agaagcccgg ccagagcccc aagctgctga tctacagcgc cagctacagg 240

tacaccggcg tgcccgacag gttcatcggc agcggcagcg gcaccgactt caccctgacc 300

atcagcagcg tgcaggccga ggacctggcc gactacttct gccagcagca ctacagcacc 360

cccctgacct tcggcgccgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420

ggcggcggca gcggcggcgg cggcagcagc ggcggcggca gcgaggtgca gctgaaggag 480

agcggccccg gcctggtggc ccccagccag agcctgagca tcacctgcac cgtgagcggc 540

ttccccctga ccagctacgg cgtgagctgg gtgaggcagc cccccggcaa gggcctggag 600

tggctgggcg tgatctgggg cgacggcagc accaactacc acagcgccct gatcagcagg 660

ctgagcatca gcaaggacaa cagcaagagc caggtgttcc tgaagctgaa caacctgcag 720

accgacgaca ccgccaccta ctactgcgcc agggacacct actaccccta ctacgccatg 780

gactactggg gccagggcac cagcgtgacc gtgagcagca ccaccacccc cgcccccagg 840

ccccccaccc ccgcccccac catcgccagc cagcccctga gcctgaggcc cgaggcctgc 900

aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg acttcgcctg cgacatctac 960

atctgggccc ccctggccgg cacctgcggc gtgctgctgc tgagcctggt gatcaccctg 1020

tactgcagga gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc 1080

cgccccgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 1140

tatcgctcca gggtgaagtt cagcaggagc gccgacgccc ccgcctacca gcagggccag 1200

aaccagctgt acaacgagct gaacctgggc aggagggagg agtacgacgt gctggacaag 1260

aggaggggca gggaccccga gatgggcggc aagccccaga ggaggaagaa cccccaggag 1320

ggcctgtaca acgagctgca gaaggacaag atggccgagg cctacagcga gatcggcatg 1380

aagggcgaga ggaggagggg caagggccac gacggcctgt accagggcct gagcaccgcc 1440

accaaggaca cctacgacgc cctgcacatg caggccctgc cccccagggg aagcggagcc 1500

accaacttca gcctgctgaa gcaggccggc gacgtggagg agaaccccgg ccccatgtac 1560

agaatgcagc tgctgagctg catcgccctg agcctggccc tggtgaccaa cagcggcatc 1620

cacgtgttca tcctgggctg cttcagcgcc ggcctgccca agaccgaggc caactgggtg 1680

aacgtgatca gcgacctgaa gaagatcgag gacctgatcc agagcatgca catcgacgcc 1740

accctgtaca ccgagagcga cgtgcacccc agctgcaagg tgaccgccat gaagtgcttc 1800

ctgctggagc tgcaggtgat cagcctggag agcggcgacg ccagcatcca cgacaccgtg 1860

gagaacctga tcatcctggc caacaacagc ctgagcagca acggcaacgt gaccgagagc 1920

ggctgcaagg agtgcgagga gctggaggag aagaacatca aggagttcct gcagagcttc 1980

gtgcacatcg tgcagatgtt catcaacacc agctccggcg gcggctccgg cggcggcggc 2040

tccggcggcg gcggctccgg cggcggcggc tccggcggcg gctccctgca gatcacctgc 2100

ccccccccca tgagcgtgga gcacgccgac atctgggtga agagctacag cctgtacagc 2160

agagagagat acatctgcaa cagcggcttc aagagaaagg ccggcaccag cagcctgacc 2220

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccccag cctgaagtgc 2280

atcagaacca ccacccccgc ccccaggccc cccacccccg cccccaccat cgccagccag 2340

cccctgagcc tgaggcccga ggcctgcagg cccgccgccg gcggcgccgt gcacaccagg 2400

ggcctggact tcgcctgcga cgtggctatc tccacgtcca ctgtcctgct gtgtgggctg 2460

agcgctgtgt ctctcctggc atgctactaa gtttaaac 2498

<210> 192
<211> 827
<212> PRT
<213> Artificial Sequence

<220>

<223> (CD19b-BB-IL-15/IL-15sushi anchor CAR amino acid sequence)

<400> 192

```
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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30


Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45


Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln
    50                  55                  60


Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80


Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser
                85                  90                  95


Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110


Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125


Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160


Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val
                165                 170                 175


Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190


Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205
```

```
Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415
```

```
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
            420                 425                 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
        435                 440                 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
    450                 455                 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465                 470                 475                 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser
                485                 490                 495

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
    530                 535                 540

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
625                 630                 635                 640
```

```
Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
                645                 650                 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
            660                 665                 670

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        675                 680                 685

Ser Gly Gly Gly Ser Leu Gln Ile Thr Cys Pro Pro Pro Met Ser Val
    690                 695                 700

Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu
705                 710                 715                 720

Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser
                725                 730                 735

Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
            740                 745                 750

Thr Pro Ser Leu Lys Cys Ile Arg Thr Thr Thr Pro Ala Pro Arg Pro
        755                 760                 765

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    770                 775                 780

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
785                 790                 795                 800

Asp Phe Ala Cys Asp Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys
                805                 810                 815

Gly Leu Ser Ala Val Ser Leu Leu Ala Cys Tyr
            820                 825
```

<210> 193
<211> 2492
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-BB-IL-15/IL-15sushi anchor CAR nucleotide sequence)

<400> 193
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gaggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 1200

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 1260

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 1320

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1380

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1440

gacacctacg acgcccttca catgcaggcc ctgcccccctc gcggaagcgg agccaccaac 1500

ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggccccat gtacagaatg 1560

cagctgctga gctgcatcgc cctgagcctg gccctggtga ccaacagcgg catccacgtg 1620

ttcatcctgg gctgcttcag cgccggcctg cccaagaccg aggccaactg ggtgaacgtg 1680

atcagcgacc tgaagaagat cgaggacctg atccagagca tgcacatcga cgccaccctg 1740

tacaccgaga gcgacgtgca ccccagctgc aaggtgaccg ccatgaagtg cttcctgctg 1800

gagctgcagg tgatcagcct ggagagcggc gacgccagca tccacgacac cgtggagaac 1860

ctgatcatcc tggccaacaa cagcctgagc agcaacggca acgtgaccga gagcggctgc 1920

aaggagtgcg aggagctgga ggagaagaac atcaaggagt tcctgcagag cttcgtgcac 1980

atcgtgcaga tgttcatcaa caccagctcc ggcggcggct ccggcggcgg cggctccggc 2040

ggcggcggct ccggcggcgg cggctccggc ggcggctccc tgcagatcac ctgccccccc 2100

cccatgagcg tggagcacgc cgacatctgg gtgaagagct acagcctgta cagcagagag 2160

agatacatct gcaacagcgg cttcaagaga aaggccggca ccagcagcct gaccgagtgc 2220

gtgctgaaca aggccaccaa cgtggcccac tggaccaccc ccagcctgaa gtgcatcaga 2280

accaccaccc ccgcccccag gccccccacc cccgccccca ccatcgccag ccagcccctg 2340

agcctgaggc ccgaggcctg caggcccgcc gccggcggcg ccgtgcacac caggggcctg 2400

gacttcgcct gcgacgtggc tatctccacg tccactgtcc tgctgtgtgg gctgagcgct 2460

gtgtctctcc tggcatgcta ctaagtttaa ac 2492

<210> 194
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> (CLL-1, C-type lectin domain family 12 member A, C-type lectin-like molecule 1, extracellular domain)

<400> 194

His Val Thr Leu Lys Ile Glu Met Lys Lys Met Asn Lys Leu Gln Asn
1 5 10 15

Ile Ser Glu Glu Leu Gln Arg Asn Ile Ser Leu Gln Leu Met Ser Asn
20 25 30

```
Met Asn Ile Ser Asn Lys Ile Arg Asn Leu Ser Thr Thr Leu Gln Thr
        35                  40                  45

Ile Ala Thr Lys Leu Cys Arg Glu Leu Tyr Ser Lys Glu Gln Glu His
    50                  55                  60

Lys Cys Lys Pro Cys Pro Arg Arg Trp Ile Trp His Lys Asp Ser Cys
65                  70                  75                  80

Tyr Phe Leu Ser Asp Asp Val Gln Thr Trp Gln Glu Ser Lys Met Ala
                85                  90                  95

Cys Ala Ala Gln Asn Ala Ser Leu Leu Lys Ile Asn Asn Lys Asn Ala
            100                 105                 110

Leu Glu Phe Ile Lys Ser Gln Ser Arg Ser Tyr Asp Tyr Trp Leu Gly
        115                 120                 125

Leu Ser Pro Glu Glu Asp Ser Thr Arg Gly Met Arg Val Asp Asn Ile
    130                 135                 140

Ile Asn Ser Ser Ala Trp Val Ile Arg Asn Ala Pro Asp Leu Asn Asn
145                 150                 155                 160

Met Tyr Cys Gly Tyr Ile Asn Arg Leu Tyr Val Gln Tyr Tyr His Cys
                165                 170                 175

Thr Tyr Lys Lys Arg Met Ile Cys Glu Lys Met Ala Asn Pro Val Gln
            180                 185                 190

Leu Gly Ser Thr Tyr Phe Arg Glu Ala
        195                 200
```

<210> 195
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-CS1-hu63-2G, CD269-A7D-CS1-hu63-2G CD269-A7D-28-2G CAR amino acid sequence)

<400> 195

```
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 Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430
```

```
Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
                485                 490                 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
            500                 505                 510

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
        515                 520                 525

Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
    530                 535                 540

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
545                 550                 555                 560

Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys
                565                 570                 575

Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg
            580                 585                 590

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
        595                 600                 605

Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser
    610                 615                 620

Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly
625                 630                 635                 640
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
                645                 650                 655

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
            660                 665                 670

Leu Ser Cys Ala Ala Ser Gly Phe Phe Ser Arg Tyr Trp Met Ser Trp
        675                 680                 685

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn
    690                 695                 700

Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Lys Phe
705                 710                 715                 720

Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
                725                 730                 735

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Asp
            740                 745                 750

Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
        755                 760                 765

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
    770                 775                 780

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
785                 790                 795                 800

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
                805                 810                 815

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
            820                 825                 830

Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu
        835                 840                 845

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
    850                 855                 860
```

```
Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
865                 870                 875                 880


Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
                885                 890                 895


Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            900                 905                 910


Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        915                 920                 925


Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    930                 935                 940


Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
945                 950                 955                 960


Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                965                 970                 975


Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            980                 985                 990


Pro Arg
```

<210> 196
<211> 2993
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-CS1-hu63-2G, CD269-A7D-CS1-hu63-2G CD269-A7D-28-2G CAR nucleotide sequence)

<400> 196

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atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg      120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag      180
```

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccttttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1500

gccggcgacg tggaggagaa ccccggcccc atggccttac cagtgaccgc cttgctcctg 1560

ccgctggcct tgctgctcca cgccgccagg ccggacatcc agatgaccca gagccccagc 1620

agcctgagcg ccagcgtggg cgacagggtg accatcacct gcaaggccag ccaggacgtg 1680

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tgggccagca ccaggcacac cggcgtgccc gacaggttca gcggcagcgg cagcggcacc 1800

gacttcaccc tgaccatcag cagcctgcag cccgaggacg tggccaccta ctactgccag 1860

cagtacagca gctaccccta caccttcggc cagggcacca aggtggagat caagggaggg 1920

gggggatccg ggggaggagg ctccggcgga ggcggaagcg aggtgcagct ggtggagagc 1980

ggcggcggcc tggtgcagcc cggcggcagc ctgaggctga gctgcgccgc cagcggcttc 2040

ttcagcaggt actggatgag ctgggtgagg caggcccccg gcaagggcct ggagtggatc 2100

ggcgagatca accccgacag cagcaccatc aactacgccc ccagcctgaa ggacaagttc 2160

atcatcagca gggacaacgc caagaacagc ctgtacctgc agatgaacag cctgagggcc 2220

gaggacaccg ccgtgtacta ctgcgccagg cccgacggca actactggta cttcgacgtg 2280

tggggccagg gcaccctggt gaccgtgagc agcaccacga cgccagcgcc gcgaccacca 2340

acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca 2400

gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat ctacatctgg 2460

gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cctttactgc 2520

aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 2580

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 2640

tccagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 2700

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 2760

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 2820

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 2880

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 2940

gacacctacg acgcccttca catgcaggcc ctgccccctc gctaagttta aac 2993

<210> 197
<211> 995
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-CS1-mu90-2G, CD269-A7D-CS1-mu90-2G CAR amino acid sequence)

<400> 197

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 Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445
```

```
Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
                485                 490                 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
            500                 505                 510

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
        515                 520                 525

Ala Arg Pro Asp Ile Val Met Thr Gln Ser Gln Lys Ser Met Ser Thr
    530                 535                 540

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val
545                 550                 555                 560

Ile Thr Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
                565                 570                 575

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg
            580                 585                 590

Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Asn
        595                 600                 605

Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser
    610                 615                 620

Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly
625                 630                 635                 640

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
                645                 650                 655
```

```
Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Lys
            660                 665                 670

Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Thr Tyr Trp Met Asn
        675                 680                 685

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile
    690                 695                 700

His Pro Ser Asp Ser Glu Thr Arg Leu Asn Lys Phe Lys Asp Lys Ala
705                 710                 715                 720

Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
                725                 730                 735

Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr
            740                 745                 750

Met Ile Ala Thr Arg Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
        755                 760                 765

Thr Val Ser Ser 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

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
                965                 970                 975

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            980                 985                 990

Pro Pro Arg
        995
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<210> 198
<211> 2996
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-CS1-mu90-2G, CD269-A7D-CS1-mu90-2G CAR nucleotide sequence

<400> 198

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ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg      120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag      180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc      240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag      300
```

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccttttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1500

gccggcgacg tggaggagaa ccccggcccc atggccttac cagtgaccgc cttgctcctg 1560

ccgctggcct tgctgctcca cgccgccagg ccggacatcg tgatgaccca gagccagaag 1620

agcatgagca ccagcgtggg cgacagggtg agcatcacct gcaaggccag ccaggacgtg 1680

atcaccggcg tggcctggta ccagcagaag cccggccaga gccccaagct gctgatctac 1740

agcgccagct acaggtacac cggcgtgccc gacaggttca ccggcagcgg cagcggcacc 1800

gacttcacct tcaccatcag caacgtgcag gccgaggacc tggccgtgta ctactgccag 1860

cagcactaca gcacccccct gaccttcggc gccggcacca agctggagct gaagggaggg 1920

```
gggggatccg ggggaggagg ctccggcgga ggcggaagcc aggtgcagct gcagcagccc     1980

ggcgccgagc tggtgaggcc cggcgccagc gtgaagctga gctgcaaggc cagcggctac     2040

agcttcacca cctactggat gaactgggtg aagcagaggc ccggccaggg cctggagtgg     2100

atcggcatga tccaccccag cgacagcgag accaggctga acaagttcaa ggacaaggcc     2160

accctgaccg tggacaagag cagcagcacc gcctacatgc agctgagcag ccccaccagc     2220

gaggacagcg ccgtgtacta ctgcgccagg agcaccatga tcgccaccag ggccatggac     2280

tactggggcc agggcaccag cgtgaccgtg agcagcacca cgacgccagc gccgcgacca     2340

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg     2400

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatctacatc     2460

tgggcgccct tggccgggac ttgtggggtc cttctcctgt cactggttat cacccctttac     2520

tgcaggagta agaggagcag gctcctgcac agtgactaca tgaacatgac tccccgccgc     2580

cccgggccca cccgcaagca ttaccagccc tatgccccac cacgcgactt cgcagcctat     2640

cgctccagag tgaagttcag caggagcgca gacgcccccg cgtaccagca gggccagaac     2700

cagctctata acgagctcaa tctaggacga agagaggagt acgatgtttt ggacaagaga     2760

cgtggccggg accctgagat gggggggaaag ccgcagagaa ggaagaaccc tcaggaaggc     2820

ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa     2880

ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc     2940

aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgctaagt ttaaac         2996
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<210> 199
<211> 993
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-CS1-hu63-2G, CD269-C11D-CS1-hu63-2G CAR amino acid sequence)

<400> 199

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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 Ile Val Leu Thr Gln Ser Pro Pro Ser Leu
            20                  25                  30
```

```
Ala Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
        35                  40                  45

Ser Val Thr Ile Leu Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys
    50                  55                  60

Pro Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln
65                  70                  75                  80

Thr Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe
                85                  90                  95

Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr
            100                 105                 110

Cys Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly 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 Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
145                 150                 155                 160

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165                 170                 175

Thr Asp Tyr Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly Leu
            180                 185                 190

Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala
        195                 200                 205

Tyr Asp Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
    210                 215                 220

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr
225                 230                 235                 240
```

```
Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser 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 Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
    530                 535                 540

Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly
545                 550                 555                 560

Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu
                565                 570                 575

Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe
            580                 585                 590

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
        595                 600                 605

Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr
    610                 615                 620

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly
625                 630                 635                 640

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
                645                 650                 655

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
            660                 665                 670
```

```
Ser Cys Ala Ala Ser Gly Phe Phe Ser Arg Tyr Trp Met Ser Trp Val
        675                 680                 685

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn Pro
    690                 695                 700

Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Lys Phe Ile
705                 710                 715                 720

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
                725                 730                 735

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Asp Gly
            740                 745                 750

Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
        755                 760                 765

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
    770                 775                 780

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
785                 790                 795                 800

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
                805                 810                 815

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
            820                 825                 830

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
        835                 840                 845

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
    850                 855                 860

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
865                 870                 875                 880

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
                885                 890                 895
```

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
900 905 910

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
915 920 925

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
930 935 940

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
945 950 955 960

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
965 970 975

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
980 985 990

Arg

<210> 200
<211> 2990
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-CS1-hu63-2G, CD269-C11D-CS1-hu63-2G CAR nucleotide sequence)

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ccggacatcg tgctgaccca gagcccccgc agcctggcca tgagcctggg caagagggcc 120

accatcagct gcagggccag cgagagcgtg accatcctgg gcagccacct gatccactgg 180

taccagcaga agcccggcca gccccccacc ctgctgatcc agctggccag caacgtgcag 240

accggcgtgc ccgccaggtt cagcggcagc ggcagcagga ccgacttcac cctgaccatc 300

gaccccgtgg aggaggacga cgtggccgtg tactactgcc tgcagagcag gaccatcccc 360

aggaccttcg gcggcggcac caagctggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag ccagatccag ctggtgcaga gcggccccga gctgaagaag 480

cccggcgaga ccgtgaagat cagctgcaag gccagcggct acaccttcac cgactacagc 540

atcaactggg tgaagagggc ccccggcaag ggcctgaagt ggatgggctg gatcaacacc 600

gagaccaggg agcccgccta cgcctacgac ttcaggggca ggttcgcctt cagcctggag 660

accagcgcca gcaccgccta cctgcagatc aacaacctga agtacgagga caccgccacc 720

tacttctgcg ccctggacta cagctacgcc atggactact ggggccaggg caccagcgtg 780

accgtgagca gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg 840

tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac 900

acgagggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1320

aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac 1440

atgcaggccc tgcccctcg cggaagcgga gccaccaact tcagcctgct gaagcaggcc 1500

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atcgccgtgg cctggtacca gcagaagccc ggcaaggtgc ccaagctgct gatctactgg 1740

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ttcaccctga ccatcagcag cctgcagccc gaggacgtgg ccacctacta ctgccagcag 1860

tacagcagct acccctacac cttcggccag ggcaccaagg tggagatcaa gggaggggggg 1920

ggatccgggg gaggaggctc cggcggaggc ggaagcgagg tgcagctggt ggagagcggc 1980

ggcggcctgg tgcagcccgg cggcagcctg aggctgagct gcgccgccag cggcttcttc 2040

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gagatcaacc ccgacagcag caccatcaac tacgccccca gcctgaagga caagttcatc 2160

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cgggaccctg agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac 2820

aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 2880

cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 2940

acctacgacg cccttcacat gcaggccctg ccccctcgct aagtttaaac 2990

<210> 201
<211> 996
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-CS1-mu34-2G, CD269-C11D-CS1-mu34-2G CAR amino acid sequence)

<400> 201

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 Pro Ser Leu
20 25 30

Ala Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
35 40 45

```
Ser Val Thr Ile Leu Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys
    50                  55                  60

Pro Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln
65                  70                  75                  80

Thr Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe
                85                  90                  95

Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr
            100                 105                 110

Cys Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly 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 Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
145                 150                 155                 160

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165                 170                 175

Thr Asp Tyr Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly Leu
            180                 185                 190

Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala
        195                 200                 205

Tyr Asp Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
    210                 215                 220

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr
225                 230                 235                 240

Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255
```

```
Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser 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 Ile Gln Met Thr Gln Ser Ser Ser Tyr Leu Ser Val Ser
    530                 535                 540

Leu Gly Gly Arg Val Thr Ile Thr Cys Lys Ala Ser Asp His Ile Asn
545                 550                 555                 560

Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu
                565                 570                 575

Leu Ile Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe
            580                 585                 590

Ser Gly Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu
        595                 600                 605

Gln Thr Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr
    610                 615                 620

Pro Trp 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 Ser Gly Ala Glu Leu Ala 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 Gln Trp
        675                 680                 685
```

```
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr
    690                 695                 700

Pro Gly Asp Gly Asp Thr Arg Tyr Thr Gln Lys Phe Lys Gly Lys Ala
705                 710                 715                 720

Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
                725                 730                 735

Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Lys
            740                 745                 750

Val Tyr Tyr Gly Ser Asn Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu
        755                 760                 765

Val Thr Val Ser Ala 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 Arg Ser Lys Arg Ser Arg
        835                 840                 845

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    850                 855                 860

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
865                 870                 875                 880

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
                885                 890                 895

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            900                 905                 910
```

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
915 920 925

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
930 935 940

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
945 950 955 960

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
965 970 975

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
980 985 990

Leu Pro Pro Arg
995

<210> 202
<211> 2999
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-CS1-mu34-2G, CD269-C11D-CS1-mu34-2G CAR nucleotide sequence)

<400> 202
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcg tgctgaccca gagcccccgc agcctggcca tgagcctggg caagagggcc 120

accatcagct gcagggccag cgagagcgtg accatcctgg gcagccacct gatccactgg 180

taccagcaga agcccggcca gccccccacc ctgctgatcc agctggccag caacgtgcag 240

accggcgtgc ccgccaggtt cagcggcagc ggcagcagga ccgacttcac cctgaccatc 300

gaccccgtgg aggaggacga cgtggccgtg tactactgcc tgcagagcag gaccatcccc 360

aggaccttcg gcggcggcac caagctggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag ccagatccag ctggtgcaga gcggccccga gctgaagaag 480

cccggcgaga ccgtgaagat cagctgcaag gccagcggct acaccttcac cgactacagc 540

atcaactggg tgaagagggc ccccggcaag ggcctgaagt ggatgggctg gatcaacacc 600

gagaccaggg agcccgccta cgcctacgac ttcaggggca ggttcgcctt cagcctggag 660

accagcgcca gcaccgccta cctgcagatc aacaacctga agtacgagga caccgccacc 720

tacttctgcg ccctggacta cagctacgcc atggactact ggggccaggg caccagcgtg 780

accgtgagca gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg 840

tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac 900

acgaggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1320

aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac 1440

atgcaggccc tgcccctcg cggaagcgga gccaccaact tcagcctgct gaagcaggcc 1500

ggcgacgtgg aggagaaccc cggccccatg gccttaccag tgaccgcctt gctcctgccg 1560

ctggccttgc tgctccacgc cgccaggccg gacatccaga tgacccagag cagcagctac 1620

ctgagcgtga gcctgggcgg cagggtgacc atcacctgca aggccagcga ccacatcaac 1680

aactggctgg cctggtacca gcagaagccc ggcaacgccc ccaggctgct gatcagcggc 1740

gccaccagcc tggagaccgg cgtgcccagc aggttcagcg gcagcggcag cggcaaggac 1800

tacaccctga gcatcaccag cctgcagacc gaggacgtgg ccacctacta ctgccagcag 1860

tactggagca ccccctggac cttcggcggc ggcaccaagc tggagatcaa gggaggggg 1920

ggatccgggg gaggaggctc cggcggaggc ggaagccagg tgcagctgca gcagagcggc 1980

gccgagctgg ccaggcccgg cgccagcgtg aagctgagct gcaaggccag cggctacacc 2040

ttcaccagct actggatgca gtgggtgaag cagaggcccg gccagggcct ggagtggatc 2100

ggcgccatct accccggcga cggcgacacc aggtacaccc agaagttcaa gggcaaggcc 2160

accctgaccg ccgacaagag cagcagcacc gcctacatgc agctgagcag cctggccagc 2220

gaggacagcg ccgtgtacta ctgcgccagg ggcaaggtgt actacggcag caacccttc 2280

gcctactggg gccagggcac cctggtgacc gtgagcgcca ccacgacgcc agcgccgcga 2340

ccaccaacac cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc 2400

cggccagcgg cgggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac 2460

atctgggcgc ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt 2520

tactgcagga gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc 2580

cgccccgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 2640

tatcgctcca gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag 2700

aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag 2760

agacgtggcc gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa 2820

ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg 2880

aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc 2940

accaaggaca cctacgacgc ccttcacatg caggccctgc cccctcgcta agtttaaac 2999

<210> 203
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA-C11D-CS1-mu90-2G, CD269-C11D-CS1-mu90-2G CAR amino acid sequence)

<400> 203

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 Pro Ser Leu
20 25 30

Ala Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
35 40 45

Ser Val Thr Ile Leu Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys
50 55 60

```
Pro Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln
65                  70                  75                  80

Thr Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe
                85                  90                  95

Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr
            100                 105                 110

Cys Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly 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 Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
145                 150                 155                 160

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                165                 170                 175

Thr Asp Tyr Ser Ile Asn Trp Val Lys Arg Ala Pro Gly Lys Gly Leu
            180                 185                 190

Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala
        195                 200                 205

Tyr Asp Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
    210                 215                 220

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr
225                 230                 235                 240

Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270
```

```
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
                325                 330                 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
            340                 345                 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
        355                 360                 365

Phe Ala Ala Tyr Arg Ser 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 Ile Val Met Thr Gln Ser Gln Lys Ser Met Ser Thr Ser
    530                 535                 540

Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ile
545                 550                 555                 560

Thr Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
                565                 570                 575

Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe
            580                 585                 590

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Asn Val
        595                 600                 605

Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Thr
    610                 615                 620

Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu 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 Ser Phe Thr Thr Tyr Trp Met Asn Trp
        675                 680                 685

Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile His
    690                 695                 700
```

```
Pro Ser Asp Ser Glu Thr Arg Leu Asn Lys Phe Lys Asp Lys Ala Thr
705                 710                 715                 720

Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser
                725                 730                 735

Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Met
            740                 745                 750

Ile Ala Thr Arg Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
        755                 760                 765

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
    770                 775                 780

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
785                 790                 795                 800

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
                805                 810                 815

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
            820                 825                 830

Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu
        835                 840                 845

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
    850                 855                 860

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
865                 870                 875                 880

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
                885                 890                 895

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            900                 905                 910

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        915                 920                 925
```

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
930 935 940

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
945 950 955 960

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
965 970 975

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
980 985 990

Pro Arg

<210> 204
<211> 2993
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-C11D-CS1-mu90-2G, CD269-C11D-CS1-mu90-2G CAR nucleotide sequence)

<400> 204
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcg tgctgaccca gagcccccgc agcctggcca tgagcctggg caagagggcc 120

accatcagct gcagggccag cgagagcgtg accatcctgg gcagccacct gatccactgg 180

taccagcaga agcccggcca gccccccacc ctgctgatcc agctggccag caacgtgcag 240

accggcgtgc ccgccaggtt cagcggcagc ggcagcagga ccgacttcac cctgaccatc 300

gaccccgtgg aggaggacga cgtggccgtg tactactgcc tgcagagcag gaccatcccc 360

aggaccttcg gcggcggcac caagctggag atcaagggag gggggggatc cgggggagga 420

ggctccggcg gaggcggaag ccagatccag ctggtgcaga gcggccccga gctgaagaag 480

cccggcgaga ccgtgaagat cagctgcaag gccagcggct acaccttcac cgactacagc 540

atcaactggg tgaagagggc ccccggcaag ggcctgaagt ggatgggctg gatcaacacc 600

gagaccaggg agcccgccta cgcctacgac ttcaggggca ggttcgcctt cagcctggag 660

accagcgcca gcaccgccta cctgcagatc aacaacctga agtacgagga caccgccacc 720

tacttctgcg ccctggacta cagctacgcc atggactact ggggccaggg caccagcgtg 780

accgtgagca gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg 840

tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgcac 900

acgagggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt 960

ggggtccttc tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc 1020

ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 1080

cagccctatg ccccaccacg cgacttcgca gcctatcgct ccagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1320

aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380

cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac 1440

atgcaggccc tgcccccctcg cggaagcgga gccaccaact tcagcctgct gaagcaggcc 1500

ggcgacgtgg aggagaaccc cggccccatg gccttaccag tgaccgcctt gctcctgccg 1560

ctggccttgc tgctccacgc cgccaggccg gacatcgtga tgacccagag ccagaagagc 1620

atgagcacca gcgtgggcga cagggtgagc atcacctgca aggccagcca ggacgtgatc 1680

accggcgtgg cctggtacca gcagaagccc ggccagagcc ccaagctgct gatctacagc 1740

gccagctaca ggtacaccgg cgtgcccgac aggttcaccg gcagcggcag cggcaccgac 1800

ttcaccttca ccatcagcaa cgtgcaggcc gaggacctgg ccgtgtacta ctgccagcag 1860

cactacagca ccccccctgac cttcggcgcc ggcaccaagc tggagctgaa gggaggggggg 1920

ggatccgggg gaggaggctc cggcggaggc ggaagccagg tgcagctgca gcagcccggc 1980

gccgagctgg tgaggcccgg cgccagcgtg aagctgagct gcaaggccag cggctacagc 2040

ttcaccacct actggatgaa ctgggtgaag cagaggcccg gccagggcct ggagtggatc 2100

ggcatgatcc accccagcga cagcgagacc aggctgaaca agttcaagga caaggccacc 2160

ctgaccgtgg acaagagcag cagcaccgcc tacatgcagc tgagcagccc caccagcgag 2220

gacagcgccg tgtactactg cgccaggagc accatgatcg ccaccagggc catggactac 2280

tggggccagg gcaccagcgt gaccgtgagc agcaccacga cgccagcgcc gcgaccacca 2340

acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca 2400

gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat ctacatctgg 2460

gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cctttactgc 2520

aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 2580

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 2640

tccagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 2700

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 2760

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 2820

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 2880

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 2940

gacacctacg acgcccttca catgcaggcc ctgccccctc gctaagttta aac 2993

<210> 205
<211> 1293
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-CS1-BB-IL-15/IL-15sushi, CD269-CS1-BB-IL-15/IL-15sushi CAR amino acid sequence)

<400> 205

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 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

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 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
        515                 520                 525

Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    530                 535                 540

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
545                 550                 555                 560

Gln Asp Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                565                 570                 575

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
            580                 585                 590

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        595                 600                 605

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln
    610                 615                 620

Tyr Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
625                 630                 635                 640

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
            660                 665                 670

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
        675                 680                 685

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
    690                 695                 700

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu
705                 710                 715                 720
```

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Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
                725                 730                 735

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
            740                 745                 750

Ala Arg Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
        755                 760                 765

Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
    770                 775                 780

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
785                 790                 795                 800

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
                805                 810                 815

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
            820                 825                 830

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
        835                 840                 845

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
    850                 855                 860

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
865                 870                 875                 880

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
                885                 890                 895

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
            900                 905                 910

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
        915                 920                 925

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
    930                 935                 940
```

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Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
945                 950                 955                 960


Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
                965                 970                 975


Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
            980                 985                 990


Met Gln Ala Leu Pro Pro Arg Gly  Ser Gly Glu Gly Arg  Gly Ser Leu
        995                 1000                1005


Leu Thr  Cys Gly Asp Val Glu  Glu Asn Pro Gly Pro  Met Tyr Arg
    1010                1015                1020


Met Gln  Leu Leu Ser Cys Ile  Ala Leu Ser Leu Ala  Leu Val Thr
    1025                1030                1035


Asn Ser  Gly Ile His Val Phe  Ile Leu Gly Cys Phe  Ser Ala Gly
    1040                1045                1050


Leu Pro  Lys Thr Glu Ala Asn  Trp Val Asn Val Ile  Ser Asp Leu
    1055                1060                1065


Lys Lys  Ile Glu Asp Leu Ile  Gln Ser Met His Ile  Asp Ala Thr
    1070                1075                1080


Leu Tyr  Thr Glu Ser Asp Val  His Pro Ser Cys Lys  Val Thr Ala
    1085                1090                1095


Met Lys  Cys Phe Leu Leu Glu  Leu Gln Val Ile Ser  Leu Glu Ser
    1100                1105                1110


Gly Asp  Ala Ser Ile His Asp  Thr Val Glu Asn Leu  Ile Ile Leu
    1115                1120                1125


Ala Asn  Asn Ser Leu Ser Ser  Asn Gly Asn Val Thr  Glu Ser Gly
    1130                1135                1140
```

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
1145 1150 1155

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
1160 1165 1170

Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1175 1180 1185

Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg
1190 1195 1200

Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu
1205 1210 1215

Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro
1220 1225 1230

Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
1235 1240 1245

Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
1250 1255 1260

Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
1265 1270 1275

Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
1280 1285 1290

<210> 206
<211> 3879
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-CS1-BB-IL-15/IL-15sushi, CD269-CS1-BB-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 206
agtgaccgcc ttgctcctgc cgctggcctt gctgctccac gccgccaggc cggatgtggt 60

gatgacccag agccatcgct ttatgagcac cagcgtgggc gaccgagtga gcattacctg 120

ccgcgcgagc caggatgtga acaccgcggt gagctggtat cagcagaaac cgggccagag 180

cccgaaactg ctgattttta gcgcgagcta tcgctatacc ggcgtgccgg atcgctttac 240

cggcagcggc agcggcgcgg attttaccct gaccattagc agcgtgcagg cggaagatct 300

ggcggtgtat tattgccagc agcattatag caccccgtgg acctttggcg gcggcaccaa 360

actggacatt aaaggagggg ggggatccgg gggaggaggc tccggcggag gcggaagcca 420

gattcagctg gtgcagagcg gcccggatct gaaaaaaccg ggcgaaaccg tgaaactgag 480

ctgcaaagcg agcggctata cctttaccaa ctttggcatg aactgggtga aacaggcgcc 540

gggcaaaggc tttaaatgga tggcgtggat taacaccacc cgctataccg gcgaaagcta 600

ttttgcggat gattttaaag gccgctttgc gtttagcgtg gaaaccagcg cgaccaccgc 660

gtatctgcag attaacaacc tgaaaaccga agataccgcg acctattttt gcgcgcgcgg 720

cgaaatttat tatggctatg atggcggctt tgcgtattgg ggccagggca ccctggtgac 780

cgtgagcgcg accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc 840

gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg cagtgcacac 900

gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg 960

ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa cggggcagaa agaaactcct 1020

gtatatattc aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg 1080

tagctgccga tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag 1140

gagcgcagac gcccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct 1200

aggacgaaga gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg 1260

gggaaagccg cagagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga 1320

taagatggcg gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg 1380

gcacgatggc ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca 1440

catgcaggcc ctgccccctc gcggaagcgg agccaccaac ttcagcctgc tgaagcaggc 1500

cggcgacgtg gaggagaacc ccggccccat ggccctgccc gtgaccgccc tgctgctgcc 1560

cctggccctg ctgctgcacg ccgccaggcc cgatattcag atgacccaga gcccgagcag 1620

cctgagcgcg agcgtgggcg accgggtgac cattacctgc aaagcgagcc aggatgtggg 1680

cattgcggtg gcgtggtatc agcagaaacc gggcaaagtg ccgaaactgc tgatttattg 1740

ggcgagcacc cgccataccg gcgtgccgga tcgctttagc ggcagcggca gcggcaccga 1800

ttttaccctg accattagca gcctgcagcc ggaagatgtg gcgacctatt attgccagca 1860

gtatagcagc tatccgtata cctttggcca gggcaccaaa gtggaaatta aaggaggggg 1920

gggatccggg ggaggaggct ccggcggagg cggaagcgaa gtgcagctgg tggaaagcgg 1980

cggcggcctg gtgcagccgg gcggcagcct gcgcctgagc tgcgcggcga gcggctttga 2040

ttttagccgc tattggatga gctgggtgcg ccaggcgccg ggcaaaggcc tggaatggat 2100

tggcgaaatt aacccggata gcagcaccat taactatgcg ccgagcctga aagataaatt 2160

tattattagc cgcgataacg cgaaaaacag cctgtatctg cagatgaaca gcctgcgcgc 2220

ggaagatacc gcggtgtatt attgcgcgcg cccggatggc aactattggt attttgatgt 2280

gtggggccag ggcaccctgg tgaccgtgag cagcaccacc acccccgccc ccaggccccc 2340

cacccccgcc cccaccatcg ccagccagcc cctgagcctg aggcccgagg cctgcaggcc 2400

cgccgccggc ggcgccgtgc acaccagggg cctggacttc gcctgcgaca tctacatctg 2460

ggcccccctg gccggcacct gcggcgtgct gctgctgagc ctggtgatca ccctgtactg 2520

caagaggggc aggaagaagc tgctgtacat cttcaagcag cccttcatga ggcccgtgca 2580

gaccacccag gaggaggacg gctgcagctg caggttcccc gaggaggagg agggcggctg 2640

cgagctgagg gtgaagttca gcaggagcgc cgacgccccc gcctaccagc agggccagaa 2700

ccagctgtac aacgagctga acctgggcag gagggaggag tacgacgtgc tggacaagag 2760

gaggggcagg gaccccgaga tgggcggcaa gccccagagg aggaagaacc cccaggaggg 2820

cctgtacaac gagctgcaga aggacaagat ggccgaggcc tacagcgaga tcggcatgaa 2880

gggcgagagg aggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac 2940

caaggacacc tacgacgccc tgcacatgca ggccctgccc cccaggggca gcggcgaagg 3000

ccgcggcagc ctgctgacct gcggcgatgt ggaagaaaac ccgggcccca tgtacagaat 3060

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gatcagcgac ctgaagaaga tcgaggacct gatccagagc atgcacatcg acgccaccct 3240

gtacaccgag agcgacgtgc accccagctg caaggtgacc gccatgaagt gcttcctgct 3300

ggagctgcag gtgatcagcc tggagagcgg cgacgccagc atccacgaca ccgtggagaa 3360

cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg agagcggctg 3420

caaggagtgc gaggagctgg aggagaagaa catcaaggag ttcctgcaga gcttcgtgca 3480

catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg gcggctccgg 3540

cggcggcggc tccggcggcg gcggctccgg cggcggctcc ctgcaggccc ccagaagagc 3600

cagaggctgc agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc tgagaccccc 3660

cgccaccaga ggcatcacct gccccccccc catgagcgtg gagcacgccg acatctgggt 3720

gaagagctac agcctgtaca gcagagagag atacatctgc aacagcggct tcaagagaaa 3780

ggccggcacc agcagcctga ccgagtgcgt gctgaacaag gccaccaacg tggcccactg 3840

gaccaccccc agcctgaagt gcatcagata agtttaaac 3879

<210> 207
<211> 663
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15, CD269-A7D-28-IL-15 CAR amino acid sequence)

<400> 207

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

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            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
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Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
                485                 490                 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr
            500                 505                 510

Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr
        515                 520                 525

Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
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    530                 535                 540

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
545                 550                 555                 560

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                565                 570                 575

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            580                 585                 590

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        595                 600                 605

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    610                 615                 620

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
625                 630                 635                 640

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                645                 650                 655

Gln Met Phe Ile Asn Thr Ser
            660
```

<210> 208
<211> 2000
<212> DNA
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-28-IL-15, CD269-A7D-28-IL-15 CAR nucleotide sequence)

<400> 208

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atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg       60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg      120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag      180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc      240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag      300
```

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

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ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1500

gccggcgacg tggaggagaa ccccggcccc atgtacagaa tgcagctgct gagctgcatc 1560

gccctgagcc tggccctggt gaccaacagc ggcatccacg tgttcatcct gggctgcttc 1620

agcgccggcc tgcccaagac cgaggccaac tgggtgaacg tgatcagcga cctgaagaag 1680

atcgaggacc tgatccagag catgcacatc gacgccaccc tgtacaccga gagcgacgtg 1740

caccccagct gcaaggtgac cgccatgaag tgcttcctgc tggagctgca ggtgatcagc 1800

ctggagagcg gcgacgccag catccacgac accgtggaga acctgatcat cctggccaac 1860

aacagcctga gcagcaacgg caacgtgacc gagagcggct gcaaggagtg cgaggagctg 1920

gaggagaaga acatcaagga gttcctgcag agcttcgtgc acatcgtgca gatgttcatc 1980

aacaccagct aagtttaaac 2000

<210> 209
<211> 672
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD33b-28-IL-15 CAR amino acid sequence)

<400> 209

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 Met Ala Asp Tyr Lys Asp Ile Val Met Thr Gln
20 25 30

Ser His Lys Phe Leu Leu Val Ser Val Gly Asp Arg Val Ser Ile Thr
35 40 45

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
65 70 75 80

Tyr Thr Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
100 105 110

Phe Cys Gln Gln His Tyr Ser Thr Pro Leu Thr Phe Gly Ala Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Glu Val Gln Leu Lys Glu
145 150 155 160

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Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys
                165                 170                 175

Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly Val Ser Trp Val Arg
            180                 185                 190

Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp
        195                 200                 205

Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser
    210                 215                 220

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Asn Leu Gln
225                 230                 235                 240

Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr Tyr Tyr Pro
                245                 250                 255

Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
        275                 280                 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
    290                 295                 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305                 310                 315                 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
                325                 330                 335

Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
            340                 345                 350

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
        355                 360                 365

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
```

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    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            420                 425                 430

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys
        515                 520                 525

Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe
    530                 535                 540

Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp
545                 550                 555                 560

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                565                 570                 575

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            580                 585                 590
```

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
595 600 605

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
610 615 620

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
625 630 635 640

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
645 650 655

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
660 665 670

<210> 210
<211> 2027
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD33b-28-IL-15 , CD33b-BB-IL15xp-2G CAR nucleotide sequence)

<400> 210
atggccctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccagg 60

cccatggccg actacaagga catcgtgatg acccagagcc acaagttcct gctggtgagc 120

gtgggcgaca gggtgagcat cacctgcaag gccagccagg acgtgagcac cgccgtggcc 180

tggtaccagc agaagcccgg ccagagcccc aagctgctga tctacagcgc cagctacagg 240

tacaccggcg tgcccgacag gttcatcggc agcggcagcg gcaccgactt caccctgacc 300

atcagcagcg tgcaggccga ggacctggcc gactacttct gccagcagca ctacagcacc 360

cccctgacct tcggcgccgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420

ggcggcggca gcggcggcgg cggcagcagc ggcggcggca gcgaggtgca gctgaaggag 480

agcggccccg gcctggtggc ccccagccag agcctgagca tcacctgcac cgtgagcggc 540

ttccccctga ccagctacgg cgtgagctgg gtgaggcagc cccccggcaa gggcctggag 600

tggctgggcg tgatctgggg cgacggcagc accaactacc acagcgccct gatcagcagg 660

ctgagcatca gcaaggacaa cagcaagagc caggtgttcc tgaagctgaa caacctgcag 720

accgacgaca ccgccaccta ctactgcgcc agggacacct actaccccta ctacgccatg 780

gactactggg gccagggcac cagcgtgacc gtgagcagca ccaccacccc cgcccccagg 840

ccccccaccc ccgcccccac catcgccagc cagcccctga gcctgaggcc cgaggcctgc 900

aggcccgccg ccggcggcgc cgtgcacacc aggggcctgg acttcgcctg cgacatctac 960

atctgggccc ccctggccgg cacctgcggc gtgctgctgc tgagcctggt gatcaccctg 1020

tactgcaaac ggggcagaaa gaaactcctg tatatattca aacaaccatt tatgagacca 1080

gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga 1140

ggatgtgaac tgagggtgaa gttcagcagg agcgccgacg cccccgccta ccagcagggc 1200

cagaaccagc tgtacaacga gctgaacctg ggcaggaggg aggagtacga cgtgctggac 1260

aagaggaggg gcagggaccc cgagatgggc ggcaagcccc agaggaggaa gaacccccag 1320

gagggcctgt acaacgagct gcagaaggac aagatggccg aggcctacag cgagatcggc 1380

atgaagggcg agaggaggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1440

gccaccaagg acacctacga cgccctgcac atgcaggccc tgcccccag gggaagcgga 1500

gccaccaact tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggccccatg 1560

tacagaatgc agctgctgag ctgcatcgcc ctgagcctgg ccctggtgac caacagcggc 1620

atccacgtgt tcatcctggg ctgcttcagc gccggcctgc ccaagaccga ggccaactgg 1680

gtgaacgtga tcagcgacct gaagaagatc gaggacctga tccagagcat gcacatcgac 1740

gccaccctgt acaccgagag cgacgtgcac cccagctgca aggtgaccgc catgaagtgc 1800

ttcctgctgg agctgcaggt gatcagcctg gagagcggcg acgccagcat ccacgacacc 1860

gtggagaacc tgatcatcct ggccaacaac agcctgagca gcaacggcaa cgtgaccgag 1920

agcggctgca aggagtgcga ggagctggag gagaagaaca tcaaggagtt cctgcagagc 1980

ttcgtgcaca tcgtgcagat gttcatcaac accagctaag tttaaac 2027

<210> 211
<211> 669
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD19bb-BB-IL-15 CAR amino acid sequence)

<400> 211

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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 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
            20                  25                  30

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
        35                  40                  45

Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln
    50                  55                  60

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65                  70                  75                  80

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser
                85                  90                  95

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
145                 150                 155                 160

Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val
                165                 170                 175

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
            180                 185                 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
        195                 200                 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
```

```
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
225                 230                 235                 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
                245                 250                 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

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
                325                 330                 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
            420                 425                 430
```

```
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
        435                 440                 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
    450                 455                 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465                 470                 475                 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser
                485                 490                 495

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
        515                 520                 525

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
    530                 535                 540

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
        595                 600                 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
    610                 615                 620

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
625                 630                 635                 640

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
```

645 650 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
660 665

<210> 212
<211> 2018
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD19b-BB-IL-15 CAR nucleotide sequence)

<400> 212
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggaggtcc agctgcagca gtctggacct gagctgataa agcctggggc ttcagtgaag 120

atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240

tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300

tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360

acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420

tcctcaggtg gaggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480

atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540

aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600

aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc 660

ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720

gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780

ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840

ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900

gcgggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 960

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 1020

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 1080

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1140

ctgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 1200

ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 1260

ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 1320

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1380

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1440

gacacctacg acgcccttca catgcaggcc ctgccccctc gcggaagcgg agccaccaac 1500

ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggccccat gtacagaatg 1560

cagctgctga gctgcatcgc cctgagcctg gccctggtga ccaacagcgg catccacgtg 1620

ttcatcctgg gctgcttcag cgccggcctg cccaagaccg aggccaactg ggtgaacgtg 1680

atcagcgacc tgaagaagat cgaggacctg atccagagca tgcacatcga cgccaccctg 1740

tacaccgaga gcgacgtgca ccccagctgc aaggtgaccg ccatgaagtg cttcctgctg 1800

gagctgcagg tgatcagcct ggagagcggc gacgccagca tccacgacac cgtggagaac 1860

ctgatcatcc tggccaacaa cagcctgagc agcaacggca acgtgaccga gagcggctgc 1920

aaggagtgcg aggagctgga ggagaagaac atcaaggagt tcctgcagag cttcgtgcac 1980

atcgtgcaga tgttcatcaa caccagctaa gtttaaac 2018

<210> 213
<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD269-A7D-28-IL-15/IL-15sushi anchor CAR nucleotide sequence)

<400> 213

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 Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
```

```
                485                 490                 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr
            500                 505                 510

Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr
        515                 520                 525

Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
    530                 535                 540

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
545                 550                 555                 560

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                565                 570                 575

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            580                 585                 590

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        595                 600                 605

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    610                 615                 620

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
625                 630                 635                 640

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                645                 650                 655

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
            660                 665                 670

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
        675                 680                 685

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
    690                 695                 700
```

```
Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
705                 710                 715                 720


Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
                725                 730                 735


Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
            740                 745                 750


Ile Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
        755                 760                 765


Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
    770                 775                 780


Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Val
785                 790                 795                 800


Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser
                805                 810                 815


Leu Leu Ala Cys Tyr
            820
```

<210> 214
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD269-A7D-28-IL-15/IL-15sushi anchor CAR nucleotide sequence)

<400> 214

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ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg      120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag      180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc      240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag      300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccctg gaccttcggc      360
```

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc 660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

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cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccctttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

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gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggaagc ggagccacca acttcagcct gctgaagcag 1500

gccggcgacg tggaggagaa ccccggcccc atgtacagaa tgcagctgct gagctgcatc 1560

gccctgagcc tggccctggt gaccaacagc ggcatccacg tgttcatcct gggctgcttc 1620

agcgccggcc tgcccaagac cgaggccaac tgggtgaacg tgatcagcga cctgaagaag 1680

atcgaggacc tgatccagag catgcacatc gacgccaccc tgtacaccga gagcgacgtg 1740

caccccagct gcaaggtgac cgccatgaag tgcttcctgc tggagctgca ggtgatcagc 1800

ctggagagcg gcgacgccag catccacgac accgtggaga acctgatcat cctggccaac 1860

aacagcctga gcagcaacgg caacgtgacc gagagcggct gcaaggagtg cgaggagctg 1920

gaggagaaga acatcaagga gttcctgcag agcttcgtgc acatcgtgca gatgttcatc 1980

aacaccagct ccggcggcgg ctccggcggc ggcggctccg gcggcggcgg ctccggcggc 2040

ggcggctccg gcggcggctc cctgcagatc acctgccccc cccccatgag cgtggagcac 2100

gccgacatct gggtgaagag ctacagcctg tacagcagag agagatacat ctgcaacagc 2160

ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt gcgtgctgaa caaggccacc 2220

aacgtggccc actggaccac ccccagcctg aagtgcatca gaaccaccac ccccgccccc 2280

aggcccccca cccccgcccc caccatcgcc agccagcccc tgagcctgag gcccgaggcc 2340

tgcaggcccg ccgccggcgg cgccgtgcac accaggggcc tggacttcgc ctgcgacgtg 2400

gctatctcca cgtccactgt cctgctgtgt gggctgagcg ctgtgtctct cctggcatgc 2460

tactaa 2466

<210> 215
<211> 785
<212> PRT
<213> Artificial Sequence

<220>
<223> (CD269-A7D-28-IL-15/IL-15sushi-2G CAR amino acid sequence)

<400> 215

Asp Arg Thr Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala
1 5 10 15

Leu Leu Leu His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser His
20 25 30

Arg Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg
35 40 45

Ala Ser Gln Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr
85 90 95

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys

```
            100                 105                 110

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125

Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro
145                 150                 155                 160

Gly Glu Thr Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
                165                 170                 175

Asn Phe Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys
            180                 185                 190

Trp Met Ala Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp
        195                 200                 205

Asp Phe Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr
    210                 215                 220

Ala Tyr Leu Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr
225                 230                 235                 240

Phe Cys Ala Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala
                245                 250                 255

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320
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```
Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
            340                 345                 350

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
        355                 360                 365

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser 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 Gly Ser Gly Glu Gly
                485                 490                 495

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
            500                 505                 510

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
        515                 520                 525

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
```

```
    530                 535                 540

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
545                 550                 555                 560

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
                565                 570                 575

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
            580                 585                 590

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
        595                 600                 605

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
    610                 615                 620

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
625                 630                 635                 640

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
                645                 650                 655

Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly
            660                 665                 670

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        675                 680                 685

Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu
    690                 695                 700

Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly
705                 710                 715                 720

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
                725                 730                 735

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
            740                 745                 750
```

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
        755   760   765

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
    770   775   780

Arg
785

<210> 216
<211> 2357
<212> DNA
<213> Artificial Sequence

<220>
<223> (CD269-A7D-28-IL-15/IL-15sushi-2G CAR nucleotide sequence)

<400> 216
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg   60

ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg   120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag   180

cccggccaga gccccaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc   240

gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag   300

gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccccctg gaccttcggc   360

ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga   420

ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc   480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg   540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag   600

agctacttcg ccgacgactt caagggcagg ttcgccttca gcgtggagac cagcgccacc   660

accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc   720

aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg   780

gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc   840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg   900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact   960

tgtggggtcc ttctcctgtc actggttatc acccttttact gcaggagtaa gaggagcagg 1020

ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080

taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140

aggagcgcag acgcccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260

gggggaaagc cgcagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgcggcagc ggcgaaggcc gcggcagcct gctgacctgc 1500

ggcgatgtgg aagaaaaccc gggccccatg tacagaatgc agctgctgag ctgcatcgcc 1560

ctgagcctgg ccctggtgac caacagcggc atccacgtgt tcatcctggg ctgcttcagc 1620

gccggcctgc ccaagaccga ggccaactgg gtgaacgtga tcagcgacct gaagaagatc 1680

gaggacctga tccagagcat gcacatcgac gccaccctgt acaccgagag cgacgtgcac 1740

cccagctgca aggtgaccgc catgaagtgc ttcctgctgg agctgcaggt gatcagcctg 1800

gagagcggcg acgccagcat ccacgacacc gtggagaacc tgatcatcct ggccaacaac 1860

agcctgagca gcaacggcaa cgtgaccgag agcggctgca aggagtgcga ggagctggag 1920

gagaagaaca tcaaggagtt cctgcagagc ttcgtgcaca tcgtgcagat gttcatcaac 1980

accagctccg gcggcggctc cggcggcggc ggctccggcg gcggcggctc cggcggcggc 2040

ggctccggcg gcggctccct gcaggccccc agaagagcca gaggctgcag aaccctgggc 2100

ctgcccgccc tgctgctgct gctgctgctg agacccccg ccaccagagg catcacctgc 2160

ccccccccca tgagcgtgga gcacgccgac atctgggtga agagctacag cctgtacagc 2220

agagagagat acatctgcaa cagcggcttc aagagaaagg ccggcaccag cagcctgacc 2280

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccccag cctgaagtgc 2340

atcagataag tttaaac 2357

<210> 217
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-3F8-BB-2G CAR amino acid sequence)

<400> 217

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 Val Gln Leu Lys Glu Ser Gly Pro Gly Leu
            20   25   30

Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
        35   40   45

Ser Val Thr Asn Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Leu Gly Val Ile Trp Ala Gly Gly Ile Thr Asn Tyr
65   70   75   80

Asn Ser Ala Phe Met Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys
                85   90   95

Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Ile Asp Asp Thr Ala
            100   105   110

Met Tyr Tyr Cys Ala Ser Arg Gly Gly His Tyr Gly Tyr Ala Leu Asp
        115   120   125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly
    130   135   140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ile Val Met Thr
145   150   155   160

Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile
                165   170   175

Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Thr Trp Tyr Gln
            180   185   190

Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Asn

```
        195                 200                 205

Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr
    210                 215                 220

Ala Phe Thr Phe Thr Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val
225                 230                 235                 240

Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Phe Gly Gly Gly Thr Lys Leu
                245                 250                 255

Glu Ile Lys Arg Thr Val Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
            260                 265                 270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
        275                 280                 285

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
    290                 295                 300

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
305                 310                 315                 320

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
                325                 330                 335

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
            340                 345                 350

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
        355                 360                 365

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415
```

```
Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg
                485
```

<210> 218
<211> 1480
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-3F8-BB-2G CAR nucleotide sequence)

<400> 218

```
gcgatcgcac catggccctg cccgtgaccg ccctgctgct gcccctggcc ctgctgctgc       60

acgccgccag gccccaggtg cagctgaagg agagcggccc cggcctggtg gccccagcc      120

agagcctgag catcacctgc accgtgagcg gcttcagcgt gaccaactac ggcgtgcact      180

gggtgaggca gccccccggc aagggcctgg agtggctggg cgtgatctgg gccggcggca      240

tcaccaacta caacagcgcc ttcatgagca ggctgagcat cagcaaggac aacagcaaga      300

gccaggtgtt cctgaagatg aacagcctgc agatcgacga caccgccatg tactactgcg      360

ccagcagggg cggccactac ggctacgccc tggactactg gggccagggc accagcgtga      420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcagca      480

tcgtgatgac ccagaccccc aagttcctgc tggtgagcgc cggcgacagg gtgaccatca      540

cctgcaaggc cagccagagc gtgagcaacg acgtgacctg gtaccagcag aaggccggcc      600

agagccccaa gctgctgatc tacagcgcca gcaacaggta cagcggcgtg cccgacaggt      660

tcaccggcag cggctacggc accgccttca ccttcaccat cagcaccgtg caggccgagg      720
```

acctggccgt gtacttctgc cagcaggact acagcagctt cggcggcggc accaagctgg 780

agatcaagag gaccgtgacc accacccccg cccccaggcc ccccaccccc gcccccacca 840

tcgccagcca gcccctgagc ctgaggcccg aggcctgcag gcccgccgcc ggcggcgccg 900

tgcacaccag gggcctggac ttcgcctgcg acatctacat ctgggccccc ctggccggca 960

cctgcggcgt gctgctgctg agcctggtga tcaccctgta ctgcaaacgg ggcagaaaga 1020

aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag 1080

atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agggtgaagt 1140

tcagcaggag cgccgacgcc cccgcctacc agcagggcca gaaccagctg tacaacgagc 1200

tgaacctggg caggagggag gagtacgacg tgctggacaa gaggaggggc agggaccccg 1260

agatgggcgg caagccccag aggaggaaga acccccagga gggcctgtac aacgagctgc 1320

agaaggacaa gatggccgag gcctacagcg agatcggcat gaagggcgag aggaggaggg 1380

gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggac acctacgacg 1440

ccctgcacat gcaggccctg ccccccaggt aagtttaaac 1480

<210> 219
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-3G6-BB-2G CAR amino acid sequence)

<400> 219

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 Ile Val Met Thr Gln Thr Pro Lys Phe Leu
20 25 30

Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
35 40 45

Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro

```
65                  70                  75                  80

Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile
                85                  90                  95

Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp
            100                 105                 110

Tyr Ser Ser Leu Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Val
    130                 135                 140

Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
145                 150                 155                 160

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp
                165                 170                 175

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
            180                 185                 190

Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu Ser
        195                 200                 205

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
    210                 215                 220

Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Ser Arg Gly Gly
225                 230                 235                 240

Asn Tyr Gly Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            260                 265                 270

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        275                 280                 285
```

```
Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    290                 295                 300

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
305                 310                 315                 320

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
                325                 330                 335

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
            340                 345                 350

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
        355                 360                 365

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
    370                 375                 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385                 390                 395                 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
                405                 410                 415

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
            420                 425                 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
        435                 440                 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
    450                 455                 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465                 470                 475                 480

Pro Pro Arg
```

<210> 220

<211> 1471
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-3G6-BB-2G CAR nucleotide sequence)

<400> 220
gcgatcgcac catggccctg cccgtgaccg ccctgctgct gcccctggcc ctgctgctgc 60

acgccgccag gcccagtatt gtgatgaccc agactcccaa attcctgctt gtatcagcag 120

gagacagggt taccataacc tgcaaggcca gtcagagtgt gagtaatgat gtggcttggt 180

accaacagaa gccagggcag tctccgaaac tgctgatata ctctgcatcc aatcgctaca 240

ctggagtccc tgatcgcttc actggcagtg gatatgggac ggatttcact ttcaccatca 300

gcactgtgca ggctgaagac ctggcagttt atttctgtca gcaggattat agctcgctcg 360

gaggggggac caagctggaa ataaaaggtg gaggcggttc aggcggaggt ggctctggcg 420

gtggcggatc gcaggtgcag gtgaaggagt caggacctgg cctggtggcg ccctcacaga 480

gcctgtccat cacttgcact gtctctgggt tttcattaac caattatggt gtacactggg 540

ttcgccagcc tccaggaaag ggtctggagt ggctgggagt aatatgggct ggtggaagca 600

caaattataa ttcggctctt atgtccagac tgagcatcag caaggacaac tccaagagcc 660

aagttttctt aaaaatgaac agtctgcaaa ctgatgacac agccatgtac tactgtgcca 720

gtcgggggggg taactacggc tatgctttgg actactgggg tcaaggaacc tcagtcaccg 780

tctcctcaac caccaccccc gcccccaggc cccccacccc cgcccccacc atcgccagcc 840

agcccctgag cctgaggccc gaggcctgca ggcccgccgc cggcggcgcc gtgcacacca 900

ggggcctgga cttcgcctgc gacatctaca tctgggcccc cctggccggc acctgcggcg 960

tgctgctgct gagcctggtg atcaccctgt actgcaaacg gggcagaaag aaactcctgt 1020

atatattcaa acaaccattt atgagaccag tacaaactac tcaagaggaa gatggctgta 1080

gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagggtgaag ttcagcagga 1140

gcgccgacgc ccccgcctac cagcagggcc agaaccagct gtacaacgag ctgaacctgg 1200

gcaggaggga ggagtacgac gtgctggaca agaggagggg cagggacccc gagatgggcg 1260

gcaagcccca gaggaggaag aacccccagg agggcctgta caacgagctg cagaaggaca 1320

agatggccga ggcctacagc gagatcggca tgaagggcga gaggaggagg ggcaagggcc 1380

acgacggcct gtaccagggc ctgagcaccg ccaccaagga cacctacgac gccctgcaca 1440

tgcaggccct gccccccagg taagtttaaa c 1471

<210> 221
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-8H9-BB-2G CAR amino acid sequence)

<400> 221

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 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu
20 25 30

Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Asn Tyr Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln
50 55 60

Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln
65 70 75 80

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser
85 90 95

Ser Ser Thr Ala Tyr Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser
100 105 110

Ala Val Tyr Phe Cys Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln
145 150 155 160

```
Ser Pro Thr Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser
                165                 170                 175

Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln
            180                 185                 190

Lys Ser His Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser
        195                 200                 205

Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp
    210                 215                 220

Phe Thr Leu Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr
225                 230                 235                 240

Tyr Cys Gln Asn Gly His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr
                245                 250                 255

Lys Leu Glu Leu Lys Gln Ala Ala Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        275                 280                 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
    290                 295                 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
305                 310                 315                 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
                325                 330                 335

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
            340                 345                 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
        355                 360                 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
```

```
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg
                485
```

<210> 222
<211> 1486
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-8H9-BB-2G CAR nucleotide sequence)

<400> 222

```
gcgatcgcac catggccctg cccgtgaccg ccctgctgct gcccctggcc ctgctgctgc       60

acgccgccag gccccaggtc aaactgcagc agtctggggc tgaactggta aagcctgggg      120

cttcagtgaa attgtcctgc aaggcttctg gctacacctt cacaaactat gatataaact      180

gggtgaggca gaggcctgaa cagggacttg agtggattgg atggatcttc cccggcgacg      240

gcagcaccca gtacaacgag aagttcaagg gcaaggccac cctgaccacc gacaccagca      300

gcagcaccgc ctacatgcag ctgagcaggc tgaccagcga ggactctgct gtctatttct      360

gtgcaagaca gactacggct acctggtttg cttactgggg ccaagggacc acggtcaccg      420
```

tctcctcaga tggaggcggt tcaggcggag gtggctctgg cggtggcgga tcggacatcg 480

agctcactca gtctccaacc accctgtctg tgactccagg agatagagtc tctctttcct 540

gcagggccag ccagagtatt agcgactact tacactggta ccaacaaaaa tcacatgagt 600

ctccaaggct tctcatcaaa tatgcttccc aatccatctc tgggatcccc tccaggttca 660

gtggcagtgg atcagggtca gatttcactc tcagtatcaa cagtgtggaa cctgaagatg 720

ttggagtgta ttactgtcaa aatggtcaca gctttccgct cacgttcggt gctgggacca 780

agctggagct gaaacaggcg gccaccacca cccccgcccc caggcccccc acccccgccc 840

ccaccatcgc cagccagccc ctgagcctga ggcccgaggc ctgcaggccc gccgccggcg 900

gcgccgtgca caccaggggc ctggacttcg cctgcgacat ctacatctgg gccccccctgg 960

ccggcacctg cggcgtgctg ctgctgagcc tggtgatcac cctgtactgc aaacggggca 1020

gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa actactcaag 1080

aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt gaactgaggg 1140

tgaagttcag caggagcgcc gacgcccccg cctaccagca gggccagaac cagctgtaca 1200

acgagctgaa cctgggcagg agggaggagt acgacgtgct ggacaagagg aggggcaggg 1260

accccgagat gggcggcaag ccccagagga ggaagaaccc ccaggagggc ctgtacaacg 1320

agctgcagaa ggacaagatg gccgaggcct acagcgagat cggcatgaag ggcgagagga 1380

ggaggggcaa gggccacgac ggcctgtacc agggcctgag caccgccacc aaggacacct 1440

acgacgccct gcacatgcag gccctgcccc ccaggtaagt ttaaac 1486

<210> 223
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-2G CAR amino acid sequence)

<400> 223

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

```
Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
        35                  40                  45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
    50                  55                  60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65                  70                  75                  80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460
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Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465 470 475 480

Gln Ala Leu Pro Pro Arg
485

<210> 224
<211> 1480
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-2G CAR nucleotide sequence)

<400> 224
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 ccccctcgct aagtttaaac 1480

<210> 225
<211> 1057
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-2G-41BBL-IL15/IL-15sushi CAR amino acid sequence)

<400> 225

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly

```
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335
```

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Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser
            500                 505                 510

Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala
        515                 520                 525

Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu
    530                 535                 540

Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp
```

```
545                 550                 555                 560

Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg
                565                 570                 575

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
            580                 585                 590

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
        595                 600                 605

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
    610                 615                 620

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
625                 630                 635                 640

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
                645                 650                 655

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
            660                 665                 670

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
        675                 680                 685

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
    690                 695                 700

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
705                 710                 715                 720

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
                725                 730                 735

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
            740                 745                 750

Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Ser Gly Ala Thr Asn Phe
        755                 760                 765
```

```
Leu Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
    770                 775                 780

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
785                 790                 795                 800

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
                805                 810                 815

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
            820                 825                 830

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
        835                 840                 845

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
    850                 855                 860

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
865                 870                 875                 880

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
                885                 890                 895

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
            900                 905                 910

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
        915                 920                 925

Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly
    930                 935                 940

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
945                 950                 955                 960

Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu
                965                 970                 975

Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly
```

980 985 990

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
995 1000 1005

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
1010 1015 1020

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val
1025 1030 1035

Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu
1040 1045 1050

Lys Cys Ile Arg
1055

<210> 226
<211> 3193
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-2G-41BBL-IL15/IL-15sushi CAR nucleotide sequence)

<400> 226
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatggaata cgcctctgac gcttcactgg 1560

accccgaagc cccgtggcct cccgcgcccc gcgctcgcgc ctgccgcgta ctgccttggg 1620

ccctggtcgc ggggctgctg ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg 1680

cctgcccctg ggccgtgtcc ggggctcgcg cctcgcccgg ctccgcggcc agcccgagac 1740

tccgcgaggg tcccgagctt tcgcccgacg atcccgccgg cctcttggac ctgcggcagg 1800

gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc ctgagctggt 1860

acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac aaagaggaca 1920

cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa ctagagctgc 1980

ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac ctgcagccac 2040

tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca cccgcctcct 2100

ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg agtgccggcc 2160

agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg cagcttaccc 2220

agggcgccac agtcttggga ctcttccggg tgacccccga aatcccagcc ggactccctt 2280

caccgaggtc ggaaggaagc ggagctacta acttcttgag cctgctgaag caggctggag 2340

acgtggagga gaaccctgga cctatgtaca gaatgcagct gctgagctgc atcgccctga 2400

gcctggccct ggtgaccaac agcggcatcc acgtgttcat cctgggctgc ttcagcgccg 2460

gcctgcccaa gaccgaggcc aactgggtga acgtgatcag cgacctgaag aagatcgagg 2520

acctgatcca gagcatgcac atcgacgcca ccctgtacac cgagagcgac gtgcacccca 2580

gctgcaaggt gaccgccatg aagtgcttcc tgctggagct gcaggtgatc agcctggaga 2640

gcggcgacgc cagcatccac gacaccgtgg agaacctgat catcctggcc aacaacagcc 2700

tgagcagcaa cggcaacgtg accgagagcg gctgcaagga gtgcgaggag ctggaggaga 2760

agaacatcaa ggagttcctg cagagcttcg tgcacatcgt gcagatgttc atcaacacca 2820

gctccggcgg cggctccggc ggcggcggct ccggcggcgg cggctccggc ggcggcggct 2880

ccggcggcgg ctccctgcag gcccccagaa gagccagagg ctgcagaacc ctgggcctgc 2940

ccgccctgct gctgctgctg ctgctgagac cccccgccac cagaggcatc acctgccccc 3000

cccccatgag cgtggagcac gccgacatct gggtgaagag ctacagcctg tacagcagag 3060

agagatacat ctgcaacagc ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt 3120

gcgtgctgaa caaggccacc aacgtggccc actggaccac ccccagcctg aagtgcatca 3180

gataagttta aac 3193

<210> 227
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-2G-IL15xp CAR amino acid sequence)

<400> 227

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
35 40 45

```
Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
    50                  55                  60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65                  70                  75                  80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
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            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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480
```

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Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
                485                 490                 495

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met
            500                 505                 510

Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
        515                 520                 525

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
    530                 535                 540

Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser
            660
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<210> 228
<211> 2005
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-2G-IL15xp CAR nucleotide sequence)

<400> 228
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gccccatgta cagaatgcag ctgctgagct 1560

gcatcgccct gagcctggcc ctggtgacca acagcggcat ccacgtgttc atcctgggct 1620

gcttcagcgc cggcctgccc aagaccgagg ccaactgggt gaacgtgatc agcgacctga 1680

agaagatcga ggacctgatc cagagcatgc acatcgacgc caccctgtac accgagagcg 1740

acgtgcaccc cagctgcaag gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga 1800

tcagcctgga gagcggcgac gccagcatcc acgacaccgt ggagaacctg atcatcctgg 1860

ccaacaacag cctgagcagc aacggcaacg tgaccgagag cggctgcaag gagtgcgagg 1920

agctggagga gaagaacatc aaggagttcc tgcagagctt cgtgcacatc gtgcagatgt 1980

tcatcaacac cagctaagtt taaac 2005

<210> 229
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-41BBL CAR amino acid sequence)

<400> 229

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr

```
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser
            500                 505                 510

Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala
        515                 520                 525

Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu
```

```
    530                 535                 540

Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp
545                 550                 555                 560

Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg
                565                 570                 575

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
            580                 585                 590

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
        595                 600                 605

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
    610                 615                 620

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
625                 630                 635                 640

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
                645                 650                 655

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
            660                 665                 670

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
        675                 680                 685

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
    690                 695                 700

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
705                 710                 715                 720

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
                725                 730                 735

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
            740                 745                 750
```

Ala Gly Leu Pro Ser Pro Arg Ser Glu
755 760

<210> 230
<211> 2305
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-41BBL CAR nucleotide sequence)

<400> 230
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatggaata cgcctctgac gcttcactgg 1560

accccgaagc cccgtggcct cccgcgcccc gcgctcgcgc ctgccgcgta ctgccttggg 1620

ccctggtcgc ggggctgctg ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg 1680

cctgcccctg ggccgtgtcc ggggctcgcg cctcgcccgg ctccgcggcc agcccgagac 1740

tccgcgaggg tcccgagctt tcgcccgacg atcccgccgg cctcttggac ctgcggcagg 1800

gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc ctgagctggt 1860

acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac aaagaggaca 1920

cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa ctagagctgc 1980

ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac ctgcagccac 2040

tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca cccgcctcct 2100

ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg agtgccggcc 2160

agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg cagcttaccc 2220

agggcgccac agtcttggga ctcttccggg tgacccccga aatcccagcc ggactccctt 2280

caccgaggtc ggaataagtt taaac 2305

<210> 231
<211> 819
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-IL-15/IL-15sushi anchor CAR amino acid sequence)

<400> 231

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu

```
            20                  25                  30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
        35                  40                  45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
    50                  55                  60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65                  70                  75                  80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240
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Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
```

```
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
                485                 490                 495

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met
            500                 505                 510

Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
        515                 520                 525

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
    530                 535                 540

Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            660                 665                 670
```

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile
675 680 685

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
690 695 700

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
705 710 715 720

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
725 730 735

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
740 745 750

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
755 760 765

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
770 775 780

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Val Ala Ile
785 790 795 800

Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu
805 810 815

Ala Cys Tyr

<210> 232
<211> 2479
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-IL-15/IL-15sushi anchor CAR nucleotide sequence)

<400> 232
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gccccatgta cagaatgcag ctgctgagct 1560

gcatcgccct gagcctggcc ctggtgacca acagcggcat ccacgtgttc atcctgggct 1620

gcttcagcgc cggcctgccc aagaccgagg ccaactgggt gaacgtgatc agcgacctga 1680

agaagatcga ggacctgatc cagagcatgc acatcgacgc caccctgtac accgagagcg 1740

acgtgcaccc cagctgcaag gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga 1800

tcagcctgga gagcggcgac gccagcatcc acgacaccgt ggagaacctg atcatcctgg 1860

ccaacaacag cctgagcagc aacggcaacg tgaccgagag cggctgcaag gagtgcgagg 1920

agctggagga gaagaacatc aaggagttcc tgcagagctt cgtgcacatc gtgcagatgt 1980

tcatcaacac cagctccggc ggcggctccg gcggcggcgg ctccggcggc ggcggctccg 2040

gcggcggcgg ctccggcggc ggctccctgc agatcacctg ccccccccccc atgagcgtgg 2100

agcacgccga catctgggtg aagagctaca gcctgtacag cagagagaga tacatctgca 2160

acagcggctt caagagaaag gccggcacca gcagcctgac cgagtgcgtg ctgaacaagg 2220

ccaccaacgt ggcccactgg accacccccа gcctgaagtg catcagaacc accacccccg 2280

cccccaggcc ccccacccccc gcccccacca tcgccagcca gcccctgagc ctgaggcccg 2340

aggcctgcag gcccgccgcc ggcggcgccg tgcacaccag gggcctggac ttcgcctgcg 2400

acgtggctat ctccacgtcc actgtcctgc tgtgtgggct gagcgctgtg tctctcctgg 2460

catgctacta agtttaaac 2479

<210> 233
<211> 780
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-28-IL-15/IL-15sushi CAR amino acid sequence)

<400> 233

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg

```
65                  70                  75                  80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115                 120                 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145                 150                 155                 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165                 170                 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln
```

```
            500                 505                 510

Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly
        515                 520                 525

Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr
    530                 535                 540

Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
545                 550                 555                 560

Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp
                565                 570                 575

Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu
            580                 585                 590

Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr
        595                 600                 605

Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly
    610                 615                 620

Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
625                 630                 635                 640

Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe
                645                 650                 655

Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            660                 665                 670

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro
        675                 680                 685

Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu
    690                 695                 700

Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro
705                 710                 715                 720
```

```
Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu
                725                 730                 735

Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala
            740                 745                 750

Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val
        755                 760                 765

Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
    770                 775                 780
```

<210> 234
<211> 2362
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-28-IL-15/IL-15sushi CAR nucleotide sequence)

<400> 234

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gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc       60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg      120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca      180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg      240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact      300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga      360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg      420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga      480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca      540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt      600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca      660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga      720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca      780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca      840
```

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatgtacag aatgcagctg ctgagctgca 1560

tcgccctgag cctggccctg gtgaccaaca gcggcatcca cgtgttcatc ctgggctgct 1620

tcagcgccgg cctgcccaag accgaggcca actgggtgaa cgtgatcagc gacctgaaga 1680

agatcgagga cctgatccag agcatgcaca tcgacgccac cctgtacacc gagagcgacg 1740

tgcaccccag ctgcaaggtg accgccatga agtgcttcct gctggagctg caggtgatca 1800

gcctggagag cggcgacgcc agcatccacg acaccgtgga gaacctgatc atcctggcca 1860

acaacagcct gagcagcaac ggcaacgtga ccgagagcgg ctgcaaggag tgcgaggagc 1920

tggaggagaa gaacatcaag gagttcctgc agagcttcgt gcacatcgtg cagatgttca 1980

tcaacaccag ctccggcggc ggctccggcg gcggcggctc cggcggcggc ggctccggcg 2040

gcggcggctc cggcggcggc tccctgcagg cccccagaag agccagaggc tgcagaaccc 2100

tgggcctgcc cgccctgctg ctgctgctgc tgctgagacc ccccgccacc agaggcatca 2160

cctgcccccc ccccatgagc gtggagcacg ccgacatctg ggtgaagagc tacagcctgt 2220

acagcagaga gagatacatc tgcaacagcg gcttcaagag aaaggccggc accagcagcc 2280

tgaccgagtg cgtgctgaac aaggccacca acgtggccca ctggaccacc cccagcctga 2340

agtgcatcag ataagtttaa ac 2362

<210> 235

<211> 993
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-BB-GD3-28-2G cCAR amino acid sequence)

<400> 235

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
115 120 125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145 150 155 160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
165 170 175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly

```
            180                 185                 190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400
```

```
Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val
            500                 505                 510

Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro
        515                 520                 525

Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe Val Lys Pro Gly Gly
    530                 535                 540

Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr
545                 550                 555                 560

Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys Arg Leu Glu Trp Val
                565                 570                 575

Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser Asp Ser Val
            580                 585                 590

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
        595                 600                 605

Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser Ala Met Tyr Phe Cys
```

```
    610                 615                 620

Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp Ser Trp Gly Gln Gly
625                 630                 635                 640

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                645                 650                 655

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Ala Ser Ser
            660                 665                 670

Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Ser Ala Ser
        675                 680                 685

Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
    690                 695                 700

Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val
705                 710                 715                 720

Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Tyr Ser Leu Thr
                725                 730                 735

Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Phe Cys His Gln
            740                 745                 750

Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        755                 760                 765

Lys Arg Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
    770                 775                 780

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
785                 790                 795                 800

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
                805                 810                 815

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
            820                 825                 830
```

```
Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
        835                 840                 845

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
    850                 855                 860

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
865                 870                 875                 880

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
                885                 890                 895

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            900                 905                 910

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        915                 920                 925

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    930                 935                 940

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
945                 950                 955                 960

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                965                 970                 975

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            980                 985                 990

Arg
```

<210> 236
<211> 3001
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-BB-GD3-28-2G cCAR nucleotide sequence)

<400> 236

gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg 240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact 300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 cccccctcgcg gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatggcctt accagtgacc gccttgctcc 1560

tgccgctggc cttgctgctc cacgccgcca ggccggaggt gaccctggtg gagagcggcg 1620

gcgacttcgt gaagcccggc ggcagcctga aggtgagctg cgccgccagc ggcttcgcct 1680

tcagccacta cgccatgagc tgggtgaggc agacccccgc caagaggctg gagtgggtgg 1740

cctacatcag cagcggcggc agcggcacct actacagcga cagcgtgaag ggcaggttca 1800

ccatcagcag ggacaacgcc aagaacaccc tgtacctgca gatgaggagc ctgaggagcg 1860

aggacagcgc catgtacttc tgcaccaggg tgaagctggg cacctactac ttcgacagct 1920

ggggccaggg caccaccctg accgtgagca gcggaggggg gggatccggg ggaggaggct 1980

ccggcggagg cggaagcgac atccagatga cccagaccgc cagcagcctg cccgccagcc 2040

tgggcgacag ggtgaccatc agctgcagcg ccagccagga catcagcaac tacctgaact 2100

ggtaccagca gaagcccgac ggcaccgtga agctgctgat cttctacagc agcaacctgc 2160

acagcggcgt gcccagcagg ttcagcggcg gcggcagcgg caccgactac agcctgacca 2220

tcagcaacct ggagcccgag gacatcgcca cctacttctg ccaccagtac agcaagctgc 2280

cctggacctt cggcggcggc accaagctgg agatcaagag gaccacgacg ccagcgccgc 2340

gaccaccaac accggcgccc accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt 2400

gccggccagc ggcgggggggc gcagtgcaca cgagggggct ggacttcgcc tgtgatatct 2460

acatctgggc gcccttggcc gggacttgtg gggtccttct cctgtcactg gttatcaccc 2520

tttactgcag gagtaagagg agcaggctcc tgcacagtga ctacatgaac atgactcccc 2580

gccgccccgg gcccacccgc aagcattacc agccctatgc cccaccacgc gacttcgcag 2640

cctatcgctc cagagtgaag ttcagcagga gcgcagacgc ccccgcgtac cagcagggcc 2700

agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat gttttggaca 2760

agagacgtgg ccgggaccct gagatggggg gaaagccgca gagaaggaag aaccctcagg 2820

aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt gagattggga 2880

tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt ctcagtacag 2940

ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctcgc taagtttaaa 3000

c 3001

<210> 237
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD2-BBpre-2G CAR amino acid sequence)

<400> 237

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
            20   25   30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln
        35   40   45

Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
    50   55   60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg
65   70   75   80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85   90   95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100   105   110

Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly
        115   120   125

Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130   135   140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
145   150   155   160

Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys Ala Ser Gly
                165   170   175

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
            180   185   190

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr

```
        195                 200                 205

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
    210                 215                 220

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
225                 230                 235                 240

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu 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
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```
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
                485
```

<210> 238
<211> 1483
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD2-BBpre-2G CAR nucleotide sequence)

<400> 238

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gcgatcgcac catggccctg cccgtgaccg ccctgctgct gcccctggcc ctgctgctgc       60

acgccgccag gcccgagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg      120

gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca      180

cctacctgca ctggtacctg cagaagcccg gccagagccc caagctgctg atccacaagg      240

tgagcaacag gttcagcggc gtgcccgaca ggttcagcgg cagcggcagc ggcaccgact      300

tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga      360

gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg      420

gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cgaggtgcag ctgctgcaga      480

gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca      540

gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt      600

ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca      660

gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga      720
```

ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780

ccagcgtgac cgtgagcagc accaccaccc ccgcccccag gccccccacc cccgccccca 840

ccatcgccag ccagcccctg agcctgaggc ccgaggcctg caggcccgcc gccggcggcg 900

ccgtgcacac caggggcctg gacttcgcct gcgacatcta catctgggcc cccctggccg 960

gcacctgcgg cgtgctgctg ctgagcctgg tgatcaccct gtactgcaaa cggggcagaa 1020

agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact actcaagagg 1080

aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa ctgagggtga 1140

agttcagcag gagcgccgac gcccccgcct accagcaggg ccagaaccag ctgtacaacg 1200

agctgaacct gggcaggagg gaggagtacg acgtgctgga caagaggagg ggcagggacc 1260

ccgagatggg cggcaagccc cagaggagga agaaccccca ggagggcctg tacaacgagc 1320

tgcagaagga caagatggcc gaggcctaca gcgagatcgg catgaagggc gagaggagga 1380

ggggcaaggg ccacgacggc ctgtaccagg gcctgagcac cgccaccaag gacacctacg 1440

acgccctgca catgcaggcc ctgcccccca ggtaagttta aac 1483

<210> 239
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-2G CAR amino acid sequence)

<400> 239

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr

```
65                  70                  75                  80

Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser
            100                 105                 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
        115                 120                 125

Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145                 150                 155                 160

Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165                 170                 175

Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465                 470                 475
```

<210> 240
<211> 1480
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD3-28-2G CAR nucleotide sequence)

<400> 240
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg 120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct 180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca 240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca 300

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct 360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga 420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca 480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca 540

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

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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 ccccctcgct aagtttaaac 1480

<210> 241
<211> 1057
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-2G-4-1BBL-IL15/IL-15sushi CAR amino acid sequence)

<400> 241

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr
65 70 75 80

Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser
100 105 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
115 120 125

Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145 150 155 160

Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
165 170 175

```
Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
```

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385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser
            500                 505                 510

Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala
        515                 520                 525

Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu
    530                 535                 540

Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp
545                 550                 555                 560

Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg
                565                 570                 575

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
            580                 585                 590

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
        595                 600                 605
```

```
Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
    610                 615                 620

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
625                 630                 635                 640

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
                645                 650                 655

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
            660                 665                 670

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
        675                 680                 685

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
    690                 695                 700

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
705                 710                 715                 720

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
                725                 730                 735

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
            740                 745                 750

Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Ser Gly Ala Thr Asn Phe
        755                 760                 765

Leu Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
    770                 775                 780

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
785                 790                 795                 800

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
                805                 810                 815

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
```

```
            820                 825                 830

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
        835                 840                 845

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
    850                 855                 860

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
865                 870                 875                 880

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
                885                 890                 895

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
            900                 905                 910

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
        915                 920                 925

Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly
    930                 935                 940

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
945                 950                 955                 960

Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu
                965                 970                 975

Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly
            980                 985                 990

Ile Thr Cys Pro Pro Pro Met Ser  Val Glu His Ala Asp  Ile Trp Val
        995                 1000                1005

Lys Ser  Tyr Ser Leu Tyr Ser  Arg Glu Arg Tyr Ile  Cys Asn Ser
    1010                1015                1020

Gly Phe  Lys Arg Lys Ala Gly  Thr Ser Ser Leu Thr  Glu Cys Val
    1025                1030                1035
```

Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu
    1040   1045   1050

Lys Cys Ile Arg
    1055

<210> 242
<211> 3193
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD3-28-2G-4-1BBL-IL15/IL-15sushi nucleotide sequence)

<400> 242
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg 120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct 180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca 240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca 300

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct 360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga 420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca 480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca 540

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatggaata cgcctctgac gcttcactgg 1560

accccgaagc cccgtggcct cccgcgcccc gcgctcgcgc ctgccgcgta ctgccttggg 1620

ccctggtcgc ggggctgctg ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg 1680

cctgcccctg ggccgtgtcc ggggctcgcg cctcgcccgg ctccgcggcc agcccgagac 1740

tccgcgaggg tcccgagctt tcgcccgacg atcccgccgg cctcttggac ctgcggcagg 1800

gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc ctgagctggt 1860

acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac aaagaggaca 1920

cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa ctagagctgc 1980

ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac ctgcagccac 2040

tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca cccgcctcct 2100

ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg agtgccggcc 2160

agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg cagcttaccc 2220

agggcgccac agtcttggga ctcttccggg tgacccccga aatcccagcc ggactccctt 2280

caccgaggtc ggaaggaagc ggagctacta acttcttgag cctgctgaag caggctggag 2340

acgtggagga gaaccctgga cctatgtaca gaatgcagct gctgagctgc atcgccctga 2400

gcctggccct ggtgaccaac agcggcatcc acgtgttcat cctgggctgc ttcagcgccg 2460

gcctgcccaa gaccgaggcc aactgggtga acgtgatcag cgacctgaag aagatcgagg 2520

acctgatcca gagcatgcac atcgacgcca ccctgtacac cgagagcgac gtgcacccca 2580

gctgcaaggt gaccgccatg aagtgcttcc tgctggagct gcaggtgatc agcctggaga 2640

gcggcgacgc cagcatccac gacaccgtgg agaacctgat catcctggcc aacaacagcc 2700

tgagcagcaa cggcaacgtg accgagagcg gctgcaagga gtgcgaggag ctggaggaga 2760

agaacatcaa ggagttcctg cagagcttcg tgcacatcgt gcagatgttc atcaacacca 2820

gctccggcgg cggctccggc ggcggcggct ccggcggcgg cggctccggc ggcggcggct 2880

ccggcggcgg ctccctgcag gcccccagaa gagccagagg ctgcagaacc ctgggcctgc 2940

ccgccctgct gctgctgctg ctgctgagac cccccgccac cagaggcatc acctgccccc 3000

cccccatgag cgtggagcac gccgacatct gggtgaagag ctacagcctg tacagcagag 3060

agagatacat ctgcaacagc ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt 3120

gcgtgctgaa caaggccacc aacgtggccc actggaccac ccccagcctg aagtgcatca 3180

gataagttta aac 3193

<210> 243
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-2G-IL15xp CAR amino acid sequence)

<400> 243

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr
65 70 75 80

Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser

```
            100                 105                 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
        115                 120                 125

Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145                 150                 155                 160

Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165                 170                 175

Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
                485                 490                 495

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met
            500                 505                 510

Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
        515                 520                 525

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
```

```
    530                 535                 540

Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser
            660
```

<210> 244
<211> 2005
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD3-28-2G-IL15xp nucleotide sequence)

<400> 244

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gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc       60

acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg      120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct      180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca      240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca      300
```

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct 360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga 420

ccgtgagcag cggaggggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca 480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca 540

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gccccatgta cagaatgcag ctgctgagct 1560

gcatcgccct gagcctggcc ctggtgacca acagcggcat ccacgtgttc atcctgggct 1620

gcttcagcgc cggcctgccc aagaccgagg ccaactgggt gaacgtgatc agcgacctga 1680

agaagatcga ggacctgatc cagagcatgc acatcgacgc caccctgtac accgagagcg 1740

acgtgcaccc cagctgcaag gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga 1800

tcagcctgga gagcggcgac gccagcatcc acgacaccgt ggagaacctg atcatcctgg 1860

ccaacaacag cctgagcagc aacggcaacg tgaccgagag cggctgcaag gagtgcgagg 1920

agctggagga gaagaacatc aaggagttcc tgcagagctt cgtgcacatc gtgcagatgt 1980

tcatcaacac cagctaagtt taaac 2005

<210> 245
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-41BBL CAR amino acid sequence)

<400> 245

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr
65 70 75 80

Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser
100 105 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
115 120 125

Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145 150 155 160

```
Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165                 170                 175

Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
```

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    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser
            500                 505                 510

Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala
        515                 520                 525

Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu
    530                 535                 540

Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp
545                 550                 555                 560

Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg
                565                 570                 575

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
            580                 585                 590
```

```
Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
        595                 600                 605

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
    610                 615                 620

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu
625                 630                 635                 640

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
                645                 650                 655

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
            660                 665                 670

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
        675                 680                 685

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
    690                 695                 700

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
705                 710                 715                 720

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
                725                 730                 735

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
            740                 745                 750

Ala Gly Leu Pro Ser Pro Arg Ser Glu
        755                 760


<210>  246
<211>  2305
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (GD3-28-41BBL nucleotide sequence)

<400>  246
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gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg 120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct 180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca 240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca 300

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct 360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga 420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca 480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca 540

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatggaata cgcctctgac gcttcactgg 1560

accccgaagc cccgtggcct cccgcgcccc gcgctcgcgc ctgccgcgta ctgccttggg 1620

ccctggtcgc ggggctgctg ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg 1680

cctgcccctg ggccgtgtcc ggggctcgcg cctcgcccgg ctccgcggcc agcccgagac 1740

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gcatgtttgc gcagctggtg gcccaaaatg ttctgctgat cgatgggccc ctgagctggt 1860

acagtgaccc aggcctggca ggcgtgtccc tgacgggggg cctgagctac aaagaggaca 1920

cgaaggagct ggtggtggcc aaggctggag tctactatgt cttctttcaa ctagagctgc 1980

ggcgcgtggt ggccggcgag ggctcaggct ccgtttcact tgcgctgcac ctgcagccac 2040

tgcgctctgc tgctggggcc gccgccctgg ctttgaccgt ggacctgcca cccgcctcct 2100

ccgaggctcg gaactcggcc ttcggtttcc agggccgctt gctgcacctg agtgccggcc 2160

agcgcctggg cgtccatctt cacactgagg ccagggcacg ccatgcctgg cagcttaccc 2220

agggcgccac agtcttggga ctcttccggg tgacccccga aatcccagcc ggactccctt 2280

caccgaggtc ggaataagtt taaac 2305

<210> 247
<211> 819
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-IL15/IL-15sushi anchor CAR amino acid sequence)

<400> 247

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr
65 70 75 80

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Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser
            100                 105                 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
        115                 120                 125

Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145                 150                 155                 160

Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165                 170                 175

Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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
```

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    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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
                485                 490                 495

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met
            500                 505                 510
```

```
Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
        515                 520                 525

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
    530                 535                 540

Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            660                 665                 670

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile
        675                 680                 685

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
    690                 695                 700

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
705                 710                 715                 720

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
```

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                725                 730                 735

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
            740                 745                 750

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        755                 760                 765

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    770                 775                 780

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Val Ala Ile
785                 790                 795                 800

Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu
                805                 810                 815

Ala Cys Tyr
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<210> 248
<211> 2479
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD3-28-IL15/IL-15sushi anchor nucleotide sequence)

<400> 248

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acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg      120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct      180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca      240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca      300

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct      360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga      420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca      480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca      540
```

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg 900

cagtgcacac gaggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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

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gcatcgccct gagcctggcc ctggtgacca acagcggcat ccacgtgttc atcctgggct 1620

gcttcagcgc cggcctgccc aagaccgagg ccaactgggt gaacgtgatc agcgacctga 1680

agaagatcga ggacctgatc cagagcatgc acatcgacgc caccctgtac accgagagcg 1740

acgtgcaccc cagctgcaag gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga 1800

tcagcctgga gagcggcgac gccagcatcc acgacaccgt ggagaacctg atcatcctgg 1860

ccaacaacag cctgagcagc aacggcaacg tgaccgagag cggctgcaag gagtgcgagg 1920

agctggagga gaagaacatc aaggagttcc tgcagagctt cgtgcacatc gtgcagatgt 1980

tcatcaacac cagctccggc ggcggctccg gcggcggcgg ctccggcggc ggcggctccg 2040

gcggcggcgg ctccggcggc ggctccctgc agatcacctg ccccccccccc atgagcgtgg 2100

agcacgccga catctgggtg aagagctaca gcctgtacag cagagagaga tacatctgca 2160

acagcggctt caagagaaag gccggcacca gcagcctgac cgagtgcgtg ctgaacaagg 2220

ccaccaacgt ggcccactgg accaccccca gcctgaagtg catcagaacc accacccccg 2280

cccccaggcc ccccaccccc gcccccacca tcgccagcca gcccctgagc ctgaggcccg 2340

aggcctgcag gcccgccgcc ggcggcgccg tgcacaccag gggcctggac ttcgcctgcg 2400

acgtggctat ctccacgtcc actgtcctgc tgtgtgggct gagcgctgtg tctctcctgg 2460

catgctacta agtttaaac 2479

<210> 249
<211> 780
<212> PRT
<213> Artificial Sequence

<220>
<223> (GD3-28-IL15/IL-15sushi CAR amino acid sequence)

<400> 249

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 Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe
20 25 30

Val Lys Pro Gly Gly Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe
35 40 45

Ala Phe Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys
50 55 60

Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr
65 70 75 80

Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser
100 105 110

Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp
115 120 125

```
Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
145                 150                 155                 160

Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val Thr Ile
                165                 170                 175

Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            180                 185                 190

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Phe Tyr Ser Ser Asn
        195                 200                 205

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    210                 215                 220

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr
225                 230                 235                 240

Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp Thr Phe Gly Gly Gly
                245                 250                 255

Thr Lys Leu Glu Ile Lys Arg 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 Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
```

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            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415

Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu
            420                 425                 430

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
        435                 440                 445

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
    450                 455                 460

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
465                 470                 475                 480

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
                485                 490                 495

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln
            500                 505                 510

Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly
        515                 520                 525

Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr
    530                 535                 540

Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
545                 550                 555                 560
```

```
Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp
                565                 570                 575

Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu
            580                 585                 590

Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr
        595                 600                 605

Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly
    610                 615                 620

Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
625                 630                 635                 640

Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe
                645                 650                 655

Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            660                 665                 670

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro
        675                 680                 685

Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu
    690                 695                 700

Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro
705                 710                 715                 720

Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu
                725                 730                 735

Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala
            740                 745                 750

Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val
        755                 760                 765

Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
```

770 775 780

<210> 250
<211> 2362
<212> DNA
<213> Artificial Sequence

<220>
<223> (GD3-28-IL15/IL-15sushi CAR nucleotide sequence)

<400> 250
gcgatcgcac catggcctta ccagtgaccg ccttgctcct gccgctggcc ttgctgctcc 60

acgccgccag gccggaggtg accctggtgg agagcggcgg cgacttcgtg aagcccggcg 120

gcagcctgaa ggtgagctgc gccgccagcg gcttcgcctt cagccactac gccatgagct 180

gggtgaggca gacccccgcc aagaggctgg agtgggtggc ctacatcagc agcggcggca 240

gcggcaccta ctacagcgac agcgtgaagg gcaggttcac catcagcagg gacaacgcca 300

agaacaccct gtacctgcag atgaggagcc tgaggagcga ggacagcgcc atgtacttct 360

gcaccagggt gaagctgggc acctactact tcgacagctg gggccagggc accaccctga 420

ccgtgagcag cggagggggg ggatccgggg gaggaggctc cggcggaggc ggaagcgaca 480

tccagatgac ccagaccgcc agcagcctgc ccgccagcct gggcgacagg gtgaccatca 540

gctgcagcgc cagccaggac atcagcaact acctgaactg gtaccagcag aagcccgacg 600

gcaccgtgaa gctgctgatc ttctacagca gcaacctgca cagcggcgtg cccagcaggt 660

tcagcggcgg cggcagcggc accgactaca gcctgaccat cagcaacctg gagcccgagg 720

acatcgccac ctacttctgc caccagtaca gcaagctgcc ctggaccttc ggcggcggca 780

ccaagctgga gatcaagagg accacgacgc cagcgccgcg accaccaaca ccggcgccca 840

ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg 900

cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg cccttggccg 960

ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcagg agtaagagga 1020

gcaggctcct gcacagtgac tacatgaaca tgactccccg ccgccccggg cccacccgca 1080

agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 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 gcagcggcga aggccgcggc agcctgctga 1500

cctgcggcga tgtggaagaa aacccgggcc ccatgtacag aatgcagctg ctgagctgca 1560

tcgccctgag cctggccctg gtgaccaaca gcggcatcca cgtgttcatc ctgggctgct 1620

tcagcgccgg cctgcccaag accgaggcca actgggtgaa cgtgatcagc gacctgaaga 1680

agatcgagga cctgatccag agcatgcaca tcgacgccac cctgtacacc gagagcgacg 1740

tgcaccccag ctgcaaggtg accgccatga agtgcttcct gctggagctg caggtgatca 1800

gcctggagag cggcgacgcc agcatccacg acaccgtgga gaacctgatc atcctggcca 1860

acaacagcct gagcagcaac ggcaacgtga ccgagagcgg ctgcaaggag tgcgaggagc 1920

tggaggagaa gaacatcaag gagttcctgc agagcttcgt gcacatcgtg cagatgttca 1980

tcaacaccag ctccggcggc ggctccggcg gcggcggctc cggcggcggc ggctccggcg 2040

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tgggcctgcc cgccctgctg ctgctgctgc tgctgagacc ccccgccacc agaggcatca 2160

cctgcccccc ccccatgagc gtggagcacg ccgacatctg ggtgaagagc tacagcctgt 2220

acagcagaga gagatacatc tgcaacagcg gcttcaagag aaaggccggc accagcagcc 2280

tgaccgagtg cgtgctgaac aaggccacca acgtggccca ctggaccacc cccagcctga 2340

agtgcatcag ataagtttaa ac 2362

<210> 251
<211> 1004
<212> PRT
<213> Artificial Sequence

<220>
<223> (BCMA-A7D-CD19b-BBpre-2G CAR amino acid sequence)

<400> 251

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
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Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
225                 230                 235                 240
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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 Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
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    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
                485                 490                 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
            500                 505                 510

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
        515                 520                 525

Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile Lys
    530                 535                 540

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
545                 550                 555                 560

Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
                565                 570                 575

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
            580                 585                 590

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
        595                 600                 605

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
    610                 615                 620

Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe Asp
625                 630                 635                 640

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly
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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
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Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val Ser Ile
        675                 680                 685

Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn Thr Tyr
    690                 695                 700

Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu Leu Ile
705                 710                 715                 720

Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
                725                 730                 735

Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val Glu Ala
            740                 745                 750

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr Pro Phe
        755                 760                 765

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr Thr Pro
    770                 775                 780

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
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Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
                805                 810                 815

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
            820                 825                 830

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
        835                 840                 845

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
    850                 855                 860

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
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Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
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Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
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Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys
930 935 940

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
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Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
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Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
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Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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