SEQUENCE LISTING

<110> Heat Biologics, Inc.
SCHREIBER, Taylor
FROMM, George

<120> VECTOR CO-EXPRESSING GP96-IG AND COSTIMULATORY MOLECULES

<130> HTB-021PC

<150> US 62/113,153
<151> 2015-02-06

<150> US 62/174,942
<151> 2015-06-12

<160> 49

<170> PatentIn version 3.5

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<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 2

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35 40 45

Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
50 55 60

Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
65 70 75 80

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Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
                85                  90                  95

Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
            100                 105                 110

Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly
        115                 120                 125

Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
    130                 135                 140

Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val
145                 150                 155                 160

Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn
                165                 170                 175

Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile
            180                 185                 190

Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys
        195                 200                 205

Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu
    210                 215                 220

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

Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser
                245                 250                 255

Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser
            260                 265                 270

Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr
        275                 280                 285

Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu
    290                 295                 300

Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys Lys
305                 310                 315                 320

Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met
                325                 330                 335

Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu
            340                 345                 350
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Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp
        355                 360                 365

Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys
    370                 375                 380

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

Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val
                405                 410                 415

Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe
            420                 425                 430

Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg
        435                 440                 445

Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu
    450                 455                 460

Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr
465                 470                 475                 480

Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val
                485                 490                 495

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

Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val
        515                 520                 525

Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser
    530                 535                 540

Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys
545                 550                 555                 560

Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys
                565                 570                 575

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala
            580                 585                 590

Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg
        595                 600                 605

Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp
    610                 615                 620
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Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu
625 630 635 640

Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly
645 650 655

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp
660 665 670

Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn
675 680 685

Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp
690 695 700

Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr
705 710 715 720

Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly
725 730 735

Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp
740 745 750

Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu
755 760 765

Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val
770 775 780

Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys
785 790 795 800

Asp Glu Leu

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<213> Homo sapiens

<400> 3

Lys Asp Glu Leu
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<212> DNA
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<223> Synthetic sequence

<400> 4

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gagggcagca gattcgacct gaacgacgtg tacgtgtact ggcagaccag cgagagcaag 180

accgtcgtga cctaccacat cccccagaac agctccctgg aaaacgtgga cagccggtac 240

agaaaccggg ccctgatgtc tcctgccggc atgctgagag gcgacttcag cctgcggctg 300

ttcaacgtga ccccccagga cgagcagaaa ttccactgcc tggtgctgag ccagagcctg 360

ggcttccagg aagtgctgag cgtggaagtg accctgcacg tggccgccaa tttcagcgtg 420

ccagtggtgt ctgcccccca cagcccttct caggatgagc tgaccttcac ctgtaccagc 480

atcaacggct accccagacc caatgtgtac tggatcaaca agaccgacaa cagcctgctg 540

gaccaggccc tgcagaacga taccgtgttc ctgaacatgc ggggcctgta cgacgtggtg 600

tccgtgctga gaatcgccag aacccccagc gtgaacatcg gctgctgcat cgagaacgtg 660

ctgctgcagc agaacctgac cgtgggcagc cagaccggca acgacatcgg cgagagagac 720

aagatcaccg agaaccccgt gtccaccggc gagaagaatg ccgccacctc taagtacggc 780

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tccctgacct gtctcgtgaa gggcttctac ccctccgata tcgccgtgga atgggagagc 1260

aacggccagc cagagaacaa ctacaagacc acccccccag tgctggacag cgacggctca 1320

ttcttcctgt actcccggct gacagtggac aagagcagct ggcaggaagg caacgtgttc 1380

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tccctgggca aatga 1455

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<212> PRT
<213> Artificial Sequence

<220>
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Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
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Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
        35                  40                  45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
    50                  55                  60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65                  70                  75                  80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
                85                  90                  95

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

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
        115                 120                 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
    130                 135                 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145                 150                 155                 160

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

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
            180                 185                 190

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

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
    210                 215                 220

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

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
                245                 250                 255

Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu
            260                 265                 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
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Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
325 330 335

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys Gly Leu Pro Ser Ser
355 360 365

Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln Pro Arg Glu Pro Gln
370 375 380

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

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
420 425 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
435 440 445

Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
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Ser Leu Gly Lys

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<212> DNA
<213> Artificial Sequence

<220>
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<211> 434
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<213> Artificial Sequence

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20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys Gly Leu Pro Ser
            100                 105                 110

Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln Pro Arg Glu Pro
        115                 120                 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210                 215                 220

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

Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu
                245                 250                 255

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
            260                 265                 270

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
        275                 280                 285

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
    290                 295                 300

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

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
                325                 330                 335

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

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
        355                 360                 365
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Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu
370 375 380

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
385 390 395 400

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
405 410 415

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
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Ser Glu

<210> 8
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

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gaaggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 660

aagtccctgt ctctgagcct gggcaagatc gagggccgga tggatagagc ccagggcgaa 720

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<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 9

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Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95

Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys Gly Leu Pro Ser
            100                 105                 110

Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln Pro Arg Glu Pro
        115                 120                 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205
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Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys Ile Glu Gly Arg Met Asp Arg Ala Gln Gly Glu
225 230 235 240

Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
245 250 255

His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
260 265 270

Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
275 280 285

Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
290 295 300

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

Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
325 330 335

Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
340 345 350

Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
355 360 365

Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
370 375 380

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

Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
405 410 415

Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
420 425

<210> 10
<211> 1107
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 10
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gtgacctgcg tggtggtgga tgtgtcccag gaagatcccg aggtgcagtt caattggtac 180

gtggacggcg tggaagtgca caacgccaag accaagccca gagaggaaca gttcaacagc 240

acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg attggctgag cggcaaagag 300

tacaagtgca aggtgtccag caagggcctg cccagcagca tcgagaaaac catcagcaac 360

gccaccggcc agcccaggga accccaggtg tacacactgc cccctagcca ggaagagatg 420

accaagaacc aggtgtccct gacctgtctc gtgaagggct tctacccctc cgatatcgcc 480

gtggaatggg agagcaacgg ccagcctgag aacaactaca agaccacccc cccagtgctg 540

gacagcgacg gctcattctt cctgtacagc agactgaccg tggacaagag cagctggcag 600

gaaggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 660

aagtccctgt ctctgagcct gggcaagatc gagggccgga tggatcaggt gtcacacaga 720

tacccccgga tccagagcat caaagtgcag tttaccgagt acaagaaaga gaagggcttt 780

atcctgacca gccagaaaga ggacgagatc atgaaggtgc agaacaacag cgtgatcatc 840

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agcctgcact accagaagga cgaggaaccc ctgttccagc tgaagaaagt gcggagcgtg 960

aacagcctga tggtggcctc tctgacctac aaggacaagg tgtacctgaa cgtgaccacc 1020

gacaacacca gcctggacga cttccacgtg aacggcggcg agctgatcct gattcaccag 1080

aaccccggcg agttctgcgt gctctga 1107

<210> 11
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 11

Met Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

85 90 95

Ser Gly Lys Glu Tyr Lys Cys Lys Val Ser Ser Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Asn Ala Thr Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Ser Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys Ile Glu Gly Arg Met Asp Gln Val Ser His Arg
225 230 235 240

Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys
245 250 255

Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys
260 265 270

Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile
275 280 285

Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr
290 295 300

Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val
305 310 315 320

Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu
325 330 335

Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly
340 345 350

Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu

355 360 365

<210> 12
<211> 1588
<212> DNA
<213> Homo sapiens

<400> 12
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cacccgcctt ggcctcccaa agtgctggga ttacaggcat gagccaccgc gcccggcctc 180

cattcaagtc tttattgaat atctgctatg ttctacacac tgttctaggt gctggggatg 240

caacagggga caaaataggc aaaatccctg tccttttggg gttgacattc tagtgactct 300

tcatgtagtc tagaagaagc tcagtgaata gtgtctgtgg ttgttaccag ggacacaatg 360

acaggaacat tcttgggtag agtgagaggc ctggggaggg aagggtctct aggatggagc 420

agatgctggg cagtcttagg gagcccctcc tggcatgcac cccctcatcc ctcaggccac 480

ccccgtccct tgcaggagca ccctggggag ctgtccagag cgctgtgccg ctgtctgtgg 540

ctggaggcag agtaggtggt gtgctgggaa tgcgagtggg agaactggga tggaccgagg 600

ggaggcgggt gaggaggggg gcaaccaccc aacacccacc agctgctttc agtgttctgg 660

gtccaggtgc tcctggctgg ccttgtggtc cccctcctgc ttggggccac cctgacctac 720

acataccgcc actgctggcc tcacaagccc ctggttactg cagatgaagc tgggatggag 780

gctctgaccc caccaccggc cacccatctg tcacccttgg acagcgccca cacccttcta 840

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cctggctacc ccgagaccca ggaggcgctc tgcccgcagg tgacatggtc ctgggaccag 960

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cgccagcagc agcccgcggg cctcggagcc gtttacgcgg ccctggagcg catggggctg 1260

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tagacatttt atgtcactta ttaagccgct ggcacggccc tgcgtagcag caccagccgg 1440

ccccacccct gctcgcccct atcgctccag ccaaggcgaa gaagcacgaa cgaatgtcga 1500

gagggggtga agacatttct caacttctcg gccggagttt ggctgagatc gcggtattaa 1560

atctgtgaaa gaaaacaaaa caaaacaa 1588

<210> 13
<211> 426
<212> PRT
<213> Homo sapiens

<400> 13

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Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
1               5                  10                  15

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

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
        35                  40                  45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
    50                  55                  60

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

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
                85                  90                  95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
            100                 105                 110

Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
        115                 120                 125

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
    130                 135                 140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
145                 150                 155                 160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
                165                 170                 175

Val Ser Cys Pro Thr Pro Pro Pro Ser Leu Ala Gly Ala Pro Trp Gly
            180                 185                 190

Ala Val Gln Ser Ala Val Pro Leu Ser Val Ala Gly Gly Arg Val Gly
        195                 200                 205

Val Phe Trp Val Gln Val Leu Leu Ala Gly Leu Val Val Pro Leu Leu
    210                 215                 220

Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg His Cys Trp Pro His Lys
225                 230                 235                 240

Pro Leu Val Thr Ala Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro
                245                 250                 255

Pro Ala Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu Ala
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260 265 270

Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln Leu Val Gly Asn
275 280 285

Ser Trp Thr Pro Gly Tyr Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln
290 295 300

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

Ala Ala Pro Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
325 330 335

Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro
340 345 350

Ala Arg Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala
355 360 365

Glu Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
370 375 380

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly
385 390 395 400

Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys Val Glu
405 410 415

Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
420 425

<210> 14
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 14
ctgccacggc acagtcattg 20

<210> 15
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 15
gccagttcct ccagatatcc 20

<210> 16

<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 16
ccacgctctt ctgtctactg 20

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

<220>
<223> Synthetic sequence

<400> 17
gccatagaac tgatgagagg g 21

<210> 18
<211> 21
<212> DNA
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<220>
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<400> 18
ctactgctga ccttgtctct g 21

<210> 19
<211> 20
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<220>
<223> Synthetic sequence

<400> 19
agtaaggcca tgtagggtcg 20

<210> 20
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 20
ctgcggcatg ttctggattt gact 24

<210> 21
<211> 24
<212> DNA
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<220>
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<400> 21

agtccaccac agttgctgac tcat 24

<210> 22
<211> 21
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<400> 22
gacacagtag agtgtcgcat g 21

<210> 23
<211> 20
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<220>
<223> Synthetic sequence

<400> 23
aagcatgctc tgtggagctg 20

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 24
aaggccaacc gtgaaaagat 20

<210> 25
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 25
gtggtacgac cagaggcata c 21

<210> 26
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 26

Gly Gly Gly Gly Ser
1 5

<210> 27
<211> 5
<212> PRT

<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 27

Gly Gly Gly Gly Ser
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 28

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 29

Gly Gly Gly Gly Gly Gly
1 5

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

<220>
<223> Synthetic sequence

<400> 30

Glu Ala Ala Ala Lys
1 5

<210> 31
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 31

Ala Glu Ala Ala Ala Lys Ala
1 5

<210> 32

<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 32

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 33
<211> 46
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 33

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 34
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 34

Pro Ala Pro Ala Pro
1 5

<210> 35
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 35

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

Leu Asp

<210> 36

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

<220>
<223> Synthetic sequence

<400> 36

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 37
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence

<400> 37

Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 38
<211> 852
<212> DNA
<213> Homo sapiens

<400> 38
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tcctgcaagg aggacgagta cccagtgggc tccgagtgct gccccaagtg cagtccaggt 180

tatcgtgtga aggaggcctg cggggagctg acgggcacag tgtgtgaacc ctgccctcca 240

ggcacctaca ttgcccacct caatggccta agcaagtgtc tgcagtgcca aatgtgtgac 300

ccagccatgg gcctgcgcgc gagccggaac tgctccagga cagagaacgc cgtgtgtggc 360

tgcagcccag gccacttctg catcgtccag gacggggacc actgcgccgc gtgccgcgct 420

tacgccacct ccagcccggg ccagagggtg cagaagggag gcaccgagag tcaggacacc 480

ctgtgtcaga actgcccccc ggggaccttc tctcccaatg ggaccctgga ggaatgtcag 540

caccagacca agtgcagctg gctggtgacg aaggccggag ctgggaccag cagctcccac 600

tgggtatggt ggtttctctc agggagcctc gtcatcgtca ttgtttgctc cacagttggc 660

ctaatcatat gtgtgaaaag aagaaagcca aggggtgatg tagtcaaggt gatcgtctcc 720

gtccagcgga aaagacagga ggcagaaggt gaggccacag tcattgaggc cctgcaggcc 780

cctccggacg tcaccacggt ggccgtggag gagacaatac cctcattcac ggggaggagc 840

ccaaaccatt aa 852

<210> 39
<211> 283
<212> PRT
<213> Homo sapiens

<400> 39

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Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1               5                  10                  15

Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
            20                  25                  30

Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
        35                  40                  45

Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
    50                  55                  60

Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65                  70                  75                  80

Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
                85                  90                  95

Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
            100                 105                 110

Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
        115                 120                 125

Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
    130                 135                 140

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

Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
                165                 170                 175

Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
            180                 185                 190

Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
        195                 200                 205

Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
    210                 215                 220

Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
225                 230                 235                 240

Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
                245                 250                 255

Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
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260 265 270

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
275 280

<210> 40
<211> 4900
<212> DNA
<213> Homo sapiens

<400> 40
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cggagactct caggccttgg caggtgcgtc tttcagttcc cctcacactt cgggttcctc 180

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cccatgcttg tagcgtacga caatgcggtc aaccttagct gcaagtattc ctacaatctc 360

ttctcaaggg agttccgggc atcccttcac aaaggactgg atagtgctgt ggaagtctgt 420

gttgtatatg ggaattactc ccagcagctt caggtttact caaaaacggg gttcaactgt 480

gatgggaaat tgggcaatga atcagtgaca ttctacctcc agaatttgta tgttaaccaa 540

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ctgtgacagg ccaagtctta cagtgccatg gcccacattc caacttacca tgtacttagt 1140

gacttgactg agaagttagg gtagaaaaca aaaagggagt ggattctggg agcctcttcc 1200

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gaaagaataa aatagttctc ctacatgaag aaagaatatg tcaggaaata aggtcacttt 1680

atgtcaaaat tatttgagta ctatgggacc tggcgcagtg gctcatgctt gtaatcccag 1740

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tgaaactccg tctgtactaa aaatacaaaa tttagcttgg cctggtggca ggcacctgta 1860

atcccagctg cccaagaggc tgaggcatga gaatcgcttg aacctggcag gcggaggttg 1920

cagtgagccg agatagtgcc acagctctcc agcctgggcg acagagtgag actccatctc 1980

aaacaacaac aacaacaaca acaacaacaa caaaccacaa aattatttga gtactgtgaa 2040

ggattatttg tctaacagtt cattccaatc agaccaggta ggagctttcc tgtttcatat 2100

gtttcagggt tgcacagttg gtctctttaa tgtcggtgtg gagatccaaa gtgggttgtg 2160

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taagaagggg ggaatattgt aacacaaatt taaacccact acgcagggat gaggtgctat 3000

aatatgagga ccttttaact tccatcattt tcctgtttct tgaaatagtt tatcttgtaa 3060

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gacttgatct atggtaataa atgattttgt tttctgactg gaaaaatagg cctactaaag 3480

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acagggaagt ccgttttcac tattagtatg aaccaagaaa tggttcaaaa acagtggtag 3600

gagcaatgct ttcatagttt cagatatggt agttatgaag aaaacaatgt catttgctgc 3660

tattattgta agagtcttat aattaatggt actcctataa tttttgattg tgagctcacc 3720

tatttgggtt aagcatgcca atttaaagag accaagtgta tgtacattat gttctacata 3780

ttcagtgata aaattactaa actactatat gtctgcttta aatttgtact ttaatattgt 3840

cttttggtat taagaaagat atgctttcag aatagatatg cttcgctttg gcaaggaatt 3900

tggatagaac ttgctattta aaagaggtgt ggggtaaatc cttgtataaa tctccagttt 3960

agccttttt gaaaaagcta gactttcaaa tactaatttc acttcaagca gggtacgttt 4020

ctggtttgtt tgcttgactt cagtcacaat ttcttatcag accaatggct gacctctttg 4080

agatgtcagg ctaggcttac ctatgtgttc tgtgtcatgt gaatgctgag aagtttgaca 4140

gagatccaac ttcagccttg accccatcag tccctcgggt taactaactg agccaccggt 4200

cctcatggct attttaatga gggtattgat ggttaaatgc atgtctgatc ccttatccca 4260

gccatttgca ctgccagctg ggaactatac cagacctgga tactgatccc aaagtgttaa 4320

attcaactac atgctggaga ttagagatgg tgccaataaa ggacccagaa ccaggatctt 4380

gattgctata gacttattaa taatccaggt caaagagagt gacacacact ctctcaagac 4440

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cctatagata tatgcatact ttctgacata taggaatgta tcaggaatac tcaaccatca 4560

caggcatgtt cctacctcag ggcctttaca tgtcctgttt actctgtcta gaatgtcctt 4620

ctgtagatga cctggcttgc ctcgtcaccc ttcaggtcct tgctcaagtg tcatcttctc 4680

ccctagttaa actaccccac accctgtctg ctttccttgc ttatttttct ccatagcatt 4740

ttaccatctc ttacattaga cattttctt atttatttgt agtttataag cttcatgagg 4800

caagtaactt tgctttgttt cttgctgtat ctccagtgcc cagagcagtg cctggtatat 4860

aataaatatt tattgactga gtgaaaaaaa aaaaaaaaaa 4900

<210> 41
<211> 220
<212> PRT
<213> Homo sapiens

<400> 41

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

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

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

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Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
                85                  90                  95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125

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

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145                 150                 155                 160

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

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            180                 185                 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        195                 200                 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    210                 215                 220
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<210> 42
<211> 1906
<212> DNA
<213> Homo sapiens

<400> 42

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ccaagtcaca tgattcagga ttcaggggga gaatccttct tggaacagag atgggcccag       60

aactgaatca gatgaagaga gataaggtgt gatgtgggga agactatata aagaatggac      120

ccagggctgc agcaagcact caacggaatg gcccctcctg gagacacagc catgcatgtg      180

ccggcgggct ccgtggccag ccacctgggg accacgagcc gcagctattt ctatttgacc      240

acagccactc tggctctgtg ccttgtcttc acggtggcca ctattatggt gttggtcgtt      300

cagaggacgg actccattcc caactcacct gacaacgtcc ccctcaaagg aggaaattgc      360

tcagaagacc tcttatgtat cctgaaaaga gctccattca agaagtcatg ggcctacctc      420

caagtggcaa agcatctaaa caaaaccaag ttgtcttgga acaaagatgg cattctccat      480

ggagtcagat atcaggatgg gaatctggtg atccaattcc ctggtttgta cttcatcatt      540

tgccaactgc agtttcttgt acaatgccca aataattctg tcgatctgaa gttggagctt      600

ctcatcaaca agcatatcaa aaaacaggcc ctggtgacag tgtgtgagtc tggaatgcaa      660

acgaaacacg tataccagaa tctctctcaa ttcttgctgg attacctgca ggtcaacacc      720

accatatcag tcaatgtgga tacattccag tacatagata caagcacctt tcctcttgag      780
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aatgtgttgt ccatcttctt atacagtaat tcagactgaa cagtttctct tggccttcag 840

gaagaaagcg cctctctacc atacagtatt tcatccctcc aaacacttgg gcaaaaagaa 900

aactttagac caagacaaac tacacagggt attaaatagt atacttctcc ttctgtctct 960

tggaaagata cagctccagg gttaaaaaga gagtttttag tgaagtatct ttcagatagc 1020

aggcagggaa gcaatgtagt gtggtgggca gagccccaca cagaatcaga agggatgaat 1080

ggatgtccca gcccaaccac taattcactg tatggtcttg atctatttct tctgttttga 1140

gagcctccag ttaaaatggg gcttcagtac cagagcagct agcaactctg ccctaatggg 1200

aaatgaaggg gagctgggtg tgagtgttta cactgtgccc ttcacgggat acttctttta 1260

tctgcagatg gcctaatgct tagttgtcca agtcgcgatc aaggactctc tcacacagga 1320

aacttcccta tactggcaga tacacttgtg actgaaccat gcccagttta tgcctgtctg 1380

actgtcactc tggcactagg aggctgatct tgtactccat atgaccccac ccctaggaac 1440

ccccagggaa aaccaggctc ggacagcccc ctgttcctga gatggaaagc acaaatttaa 1500

tacaccacca caatggaaaa caagttcaaa gacttttact tacagatcct ggacagaaag 1560

ggcataatga gtctgaaggg cagtcctcct tctccaggtt acatgaggca ggaataagaa 1620

gtcagacaga gacagcaaga cagttaacaa cgtaggtaaa gaaatagggt gtggtcactc 1680

tcaattcact ggcaaatgcc tgaatggtct gtctgaagga agcaacagag aagtggggaa 1740

tccagtctgc taggcaggaa agatgcctct aagttcttgt ctctggccag aggtgtggta 1800

tagaaccaga aacccatatc aagggtgact aagcccggct tccggtatga gaaattaaac 1860

ttgtatacaa aatggttgcc aaggcaacat aaaattataa gaattc 1906

<210> 43
<211> 234
<212> PRT
<213> Homo sapiens

<400> 43

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly
20 25 30

Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu
35 40 45

Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
50 55 60

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

Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys

85 90 95

Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
100 105 110

Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
115 120 125

Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln
130 135 140

Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu
145 150 155 160

Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val
165 170 175

Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln
180 185 190

Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val
195 200 205

Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val
210 215 220

Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
225 230

<210> 44
<211> 1629
<212> DNA
<213> Homo sapiens

<400> 44
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agtggtcctg ccgcctggtc tcacctcgct atggttcgtc tgcctctgca gtgcgtcctc 120

tggggctgct tgctgaccgc tgtccatcca gaaccaccca ctgcatgcag agaaaaacag 180

tacctaataa acagtcagtg ctgttctttg tgccagccag gacagaaact ggtgagtgac 240

tgcacagagt tcactgaaac ggaatgcctt ccttgcggtg aaagcgaatt cctagacacc 300

tggaacagag agacacactg ccaccagcac aaatactgcg accccaacct agggcttcgg 360

gtccagcaga agggcacctc agaaacagac accatctgca cctgtgaaga aggctggcac 420

tgtacgagtg aggcctgtga gagctgtgtc ctgcaccgct catgctcgcc cggctttggg 480

gtcaagcaga ttgctacagg ggtttctgat accatctgcg agccctgccc agtcggcttc 540

ttctccaatg tgtcatctgc tttcgaaaaa tgtcaccctt ggacaagctg tgagaccaaa 600

gacctggttg tgcaacaggc aggcacaaac aagactgatg ttgtctgtgg tccccaggat 660

cggctgagag ccctggtggt gatccccatc atcttcggga tcctgtttgc catcctcttg 720

gtgctggtct ttatcaaaaa ggtggccaag aagccaacca ataaggcccc ccaccccaag 780

caggaacccc aggagatcaa ttttcccgac gatcttcctg gctccaacac tgctgctcca 840

gtgcaggaga ctttacatgg atgccaaccg gtcacccagg aggatggcaa agagagtcgc 900

atctcagtgc aggagagaca gtgaggctgc acccacccag gagtgtggcc acgtgggcaa 960

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ctggcactgg atgcagaaac agttcacctt gaagaacctc tcacttcacc ctggagccca 1140

tccagtctcc caacttgtat taaagacaga ggcagaagtt tggtggtggt ggtgttgggg 1200

tatggtttag taatatccac cagaccttcc gatccagcag tttggtgccc agagaggcat 1260

catggtggct tccctgcgcc caggaagcca tatacacaga tgcccattgc agcattgttt 1320

gtgatagtga acaactggaa gctgcttaac tgtccatcag caggagactg gctaaataaa 1380

attagaatat atttatacaa cagaatctca aaaacactgt tgagtaagga aaaaaaggca 1440

tgctgctgaa tgatgggtat ggaacttttt aaaaaagtac atgcttttat gtatgtatat 1500

tgcctatgga tatatgtata aatacaatat gcatcatata ttgatataac aagggttctg 1560

gaagggtaca cagaaaaccc acagctcgaa gagtggtgac gtctggggtg gggaagaagg 1620

gtctggggg 1629

<210> 45
<211> 277
<212> PRT
<213> Homo sapiens

<400> 45

Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr
1 5 10 15

Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
20 25 30

Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
35 40 45

Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
50 55 60

Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
85 90 95

Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
100 105 110

Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
115 120 125

Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
180 185 190

Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
195 200 205

Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
210 215 220

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
225 230 235 240

Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
245 250 255

Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser
260 265 270

Val Gln Glu Arg Gln
275

<210> 46
<211> 913
<212> DNA
<213> Homo sapiens

<400> 46
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ggaggggggct gcagtttcct tccttccttc tcggcagcgc tccgcgcccc catcgccccct 120

cctgcgctag cggaggtgat cgccgcggcg atgccggagg agggttcggg ctgctcggtg 180

cggcgcaggc cctatgggtg cgtcctgcgg gctgctttgg tcccattggt cgcgggcttg 240

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gagtcacttg ggtgggacgt agctgagctg cagctgaatc acacaggacc tcagcaggac 360

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ctggacaagg ggcagctacg tatccatcgt gatggcatct acatggtaca catccaggtg 480

acgctggcca tctgctcctc cacgacggcc tccaggcacc accccaccac cctggccgtg 540

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tgtaccattg cctcccagcg cctgacgccc ctggcccgag gggacacact ctgcaccaac 660

ctcactggga cactttgcc ttcccgaaac actgatgaga ccttctttgg agtgcagtgg 720

gtgcgcccct gaccactgct gctgattagg gtttttaaa ttttatttta ttttatttaa 780

gttcaagaga aaaagtgtac acacaggggc cacccggggt tggggtggga gtgtggtggg 840

gggtagtggt ggcaggacaa gagaaggcat tgagcttttt ctttcatttt cctattaaaa 900

aatacaaaaa tca 913

<210> 47
<211> 193
<212> PRT
<213> Homo sapiens

<400> 47

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu
35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His
50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala
65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu
85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu
115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg
130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro
145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu
165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro

<210> 48
<211> 723
<212> DNA
<213> Homo sapiens

<400> 48
atggaggaga gtgtcgtacg gccctcagtg tttgtggtgg atggacagac cgacatccca 60

ttcacgaggc tgggacgaag ccaccggaga cagtcgtgca gtgtggcccg ggtgggtctg 120

ggtctcttgc tgttgctgat gggggccggg ctggccgtcc aaggctggtt cctcctgcag 180

ctgcactggc gtctaggaga gatggtcacc cgcctgcctg acggacctgc aggctcctgg 240

gagcagctga tacaagagcg aaggtctcac gaggtcaacc cagcagcgca tctcacaggg 300

gccaactcca gcttgaccgg cagcgggggg ccgctgttat gggagactca gctgggcctg 360

gccttcctga ggggcctcag ctaccacgat ggggcccttg tggtcaccaa agctggctac 420

tactacatct actccaaggt gcagctgggc ggtgtgggct gcccgctggg cctggccagc 480

accatcaccc acggcctcta caagcgcaca ccccgctacc ccgaggagct ggagctgttg 540

gtcagccagc agtcaccctg cggacgggcc accagcagct cccgggtctg gtgggacagc 600

agcttcctgg gtggtgtggt acacctggag gctggggagg aggtggtcgt ccgtgtgctg 660

gatgaacgcc tggttcgact gcgtgatggt acccggtctt acttcggggc tttcatggtg 720

tga 723

<210> 49
<211> 240
<212> PRT
<213> Homo sapiens

<400> 49

Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
1 5 10 15

Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
20 25 30

Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
35 40 45

Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
50 55 60

Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
65 70 75 80

Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala

```
                85                  90                  95

His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
            100                 105                 110

Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
        115                 120                 125

His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
    130                 135                 140

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

Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
                165                 170                 175

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

Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
        195                 200                 205

Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu
    210                 215                 220

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