SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> A new anti-DR5 antibody

<130> DSPCT-FP1141

<150> JP 2010-243549
<151> 2010-10-29

<160> 89

<170> PatentIn version 3.4

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<213> Mus musculus

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gtg ttc tct gag gtt cag ctg cag cag tct gga cct gag ctg gtg aag       96
Val Phe Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

cct ggg gct tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttt      144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

att ggc tac ttt atg aac tgg atg aag cag agc cat gga aag agc ctt      192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser His Gly Lys Ser Leu
    50                  55                  60

gag tgg att gga cgt ttt aat cca tac aat ggt gat act ttc tac aac      240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ttg act gta gac aaa tcc tct acc      288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
                85                  90                  95

aca gcc cac atg gag ctc ctg agc ctg aca tct gag gac tct gca gtc      336
Thr Ala His Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

tat ttt tgt gga aga tcg gcg tat tac ttc gat agt ggg ggc tac ttt      384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc caa ggc acc act ctc aca gtc tcc tca gcc aaa acg      432
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
    130                 135                 140
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aca ccc cca tct gtc tat cca ctg gcc cct gga tct gct gcc caa act      480
Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
145                 150                 155                 160

aac tcc atg gtg acc ctg gga tgc ctg gtc aag ggc tat ttc cct gag      528
Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
                165                 170                 175

cca gtg aca gtg acc tgg aac tct gga tcc ctg tcc agc ggt gtg cac      576
Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
            180                 185                 190

acc ttc cca gct gtc ctg cag tct gac ctc tac act ctg agc agc tca      624
Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
        195                 200                 205

gtg act gtc ccc tcc agc acc tgg ccc agc gag acc gtc acc tgc aac      672
Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
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gtt gcc cac ccg gcc agc agc acc aag gtg gac aag aaa att gtg ccc      720
Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
225                 230                 235                 240

agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa gta tca      768
Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
                245                 250                 255

tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att act      816
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
            260                 265                 270

ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag gat gat      864
Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
        275                 280                 285

ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac aca      912
Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
    290                 295                 300

gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc cgc tca      960
Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
305                 310                 315                 320

gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag gag     1008
Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
                325                 330                 335

ttc aaa tgc agg gtc aac agt gca gct ttc cct gcc ccc atc gag aaa     1056
Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
            340                 345                 350

acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac acc     1104
Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
        355                 360                 365

att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg acc     1152
Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
    370                 375                 380

tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg cag     1200
Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
385                 390                 395                 400

tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg     1248
Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
                405                 410                 415
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gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag      1296
Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
            420                 425                 430

agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat gag      1344
Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
        435                 440                 445

ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt      1392
Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
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Lys
465
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Val Phe Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

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

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
                85                  90                  95

Thr Ala His Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
145                 150                 155                 160

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
                165                 170                 175
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Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
        195                 200                 205

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
    210                 215                 220

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
225                 230                 235                 240

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
                245                 250                 255

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
            260                 265                 270

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
        275                 280                 285

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
    290                 295                 300

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
305                 310                 315                 320

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
                325                 330                 335

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
            340                 345                 350

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
        355                 360                 365

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
    370                 375                 380

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
385                 390                 395                 400

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
                405                 410                 415

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
            420                 425                 430

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
        435                 440                 445
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Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
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Lys
465


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<221>  CDS
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Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1               5                  10                  15

tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc      96
Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20                  25                  30

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt     144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
        35                  40                  45

gta cac agt aat gga aac acc tat cta cat tgg tac ctg cag aag cca     192
Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
    50                  55                  60

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct     240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65                  70                  75                  80

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca     288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95

ctc aag atc agc aga gtg gag gct gag gat ctg gga att tat ttc tgc     336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys
            100                 105                 110

tct caa agt aca cat gtt ccg tgg acg ttc ggt gga ggc acc aag ctg     384
Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125

gaa atc aaa cgg gct gat gct gca cca act gta tcc atc ttc cca cca     432
Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
    130                 135                 140

tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc ttg     480
Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145                 150                 155                 160

aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag att gat ggc     528
Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
                165                 170                 175

agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat cag gac agc     576
Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            180                 185                 190

aaa gac agc acc tac agc atg agc agc acc ctc acg ttg acc aag gac     624
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Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
        195                 200                 205

gag tat gaa cga cat aac agc tat acc tgt gag gcc act cac aag aca      672
Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
    210                 215                 220

tca act tca ccc att gtc aag agc ttc aac agg aat gag tgt            714
Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230                 235


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<213>  Mus musculus

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            20                  25                  30

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

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

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

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

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys
            100                 105                 110

Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
    130                 135                 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145                 150                 155                 160

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

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            180                 185                 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
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195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
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<210> 12
<211> 30
<212> DNA
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<223> Primer EFsmaR

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<210> 13
<211> 1704
<212> DNA
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<223> Nucleotide sequence of signal peptide, Fc region and poly A addition signal of human kappa chain

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tgttcatctc cctgctgctg tggatctccg gcgcatatgg cgatatcgtg atgattaaac 120

gtacggtggc cgcccctcc gtgttcatct tcccccctc cgacgagcag ctgaagtccg 180

gcaccgcctc cgtggtgtgc ctgctgaata acttctaccc cagagaggcc aaggtgcagt 240

ggaaggtgga caacgccctg cagtccggga actcccagga gagcgtgacc gagcaggaca 300

gcaaggacag cacctacagc ctgagcagca ccctgaccct gagcaaagcc gactacgaga 360

agcacaaggt gtacgcctgc gaggtgaccc accagggcct gagctcccc gtcaccaaga 420

gcttcaacag gggggagtgt taggggcccg tttaaacggg tggcatccct gtgacccctc 480

cccagtgcct ctcctggccc tggaagttgc cactccagtg cccaccagcc ttgtcctaat 540

aaaattaagt tgcatcattt tgtctgacta ggtgtccttc tataatatta tggggtggag 600

gggggtggta tggagcaagg ggcaagttgg gaagacaacc tgtagggcct gcggggtcta 660

ttgggaacca agctggagtg cagtggcaca atcttggctc actgcaatct ccgcctcctg 720

ggttcaagcg attctcctgc ctcagcctcc cgagttgttg ggattccagg catgcatgac 780

caggctcacc taatttttgt ttttttggta gagacggggt ttcaccatat tggccaggct 840

ggtctccaac tcctaatctc aggtgatcta cccaccttgg cctcccaaat tgctgggatt 900

acaggcgtga accactgctc cacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg 960

tggttacgcg cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt 1020

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gtgatggttc acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg 1200

agtccacgtt ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct 1260

cggtctattc ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg 1320

agctgattta acaaaaattt aacgcgaatt aattctgtgg aatgtgtgtc agttagggtg 1380

tggaaagtcc ccaggctccc cagcaggcag aagtatgcaa agcatgcatc tcaattagtc 1440

agcaaccagg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca 1500

tctcaattag tcagcaacca tagtcccgcc cctaactccg cccatcccgc ccctaactcc 1560

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cgaggccgcc tctgcctctg agctattcca gaagtagtga ggaggctttt ttggaggcct 1680

aggcttttgc aaaaagctcc cggg 1704

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<223> Nucleotide sequence of signal peptide and Fc region of human IgG1 chain

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gtcttccccc tggcaccctc ctccaagagc acctctggcg gcacagccgc cctgggctgc 180

ctggtcaagg actacttccc cgaacccgtg accgtgagct ggaactcagg cgccctgacc 240

agcggcgtgc acaccttccc cgctgtcctg cagtcctcag gactctactc cctcagcagc 300

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 360

aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 420

acatgcccac cctgcccagc acctgaactc ctgggggggac cctcagtctt cctcttcccc 480

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 540

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 600

cataatgcca agacaaagcc ccgggaggag cagtacaaca gcacgtaccg ggtggtcagc 660

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 720

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg ccagccccgg 780

gaaccacagg tgtacaccct gccccccatcc cgggaggaga tgaccaagaa ccaggtcagc 840

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ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcagggcaa cgtcttctca 1020

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cccggcaaat gagatatcgg gcccgtttaa acgggtggca 1120

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<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding the light chain of chimera B273

<220>
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<222> (1)..(717)

<400> 15

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1               5                  10                  15

ggc gca tat ggc gat gtt gtg atg acc caa act cca ctc tcc ctg cct      96
Gly Ala Tyr Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro
            20                  25                  30

gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc     144
Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctt gta cac agt aat gga aac acc tat cta cat tgg tac ctg cag aag     192
Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt     240
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc     288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

aca ctc aag atc agc aga gtg gag gct gag gat ctg gga att tat ttc     336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe
            100                 105                 110

tgc tct caa agt aca cat gtt ccg tgg acg ttc ggt gga ggc acc aag     384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125

ctg gaa atc aaa cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc     432
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg     480
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Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<223> Synthetic Construct

<400> 16

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            20                  25                  30

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

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

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

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

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe
            100                 105                 110

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

Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140
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Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 17
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer B273LF

<400> 17
aaacatatgg cgatgttgtg atgacccaaa ctccactctc c 41

<210> 18
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer B273LR

<400> 18
aaacgtacgt ttgatttcca gcttggtgcc tccaccgaac g 41

<210> 19
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding the heavy chain of chimera B273

<220>
<221> CDS
<222> (1)..(1413)

<400> 19
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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg       48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15
```

```
gtg ctg agc gag gtt cag ctg cag cag tct gga cct gag ctg gtg aag        96
Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

cct ggg gct tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttt       144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

att ggc tac ttt atg aac tgg atg aag cag agc cat gga aag agc ctt       192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser His Gly Lys Ser Leu
    50                  55                  60

gag tgg att gga cgt ttt aat cca tac aat ggt gat act ttc tac aac       240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ttg act gta gac aaa tcc tct acc       288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
                85                  90                  95

aca gcc cac atg gag ctc ctg agc ctg aca tct gag gac tct gca gtc       336
Thr Ala His Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

tat ttt tgt gga aga tcg gcg tat tac ttc gat agt ggg ggc tac ttt       384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc caa ggc acc act ctc aca gtc agc tca gcc tcc acc       432
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct       480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa       528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac       576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc       624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc       672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag       720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct       768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag       816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg       864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
```

```
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 20
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
```

```
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
                85                  90                  95

Thr Ala His Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
```

305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 21
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer B273HF

<400> 21
aaagctgagc gaggttcagc tgcagcagtc tggacctgag c 41

<210> 22
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer B273HR

<400> 22
aaagctgagc tgactgtgag agtggtgcct tggccccagt ag 42

<210> 23

<211> 130
<212> PRT
<213> Homo sapiens

<400> 23

Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala Ala Pro
1 5 10 15

Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu Cys Pro Pro Gly His
20 25 30

His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln
35 40 45

Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr
50 55 60

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

Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser
85 90 95

Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
100 105 110

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys
115 120 125

Glu Ser
130

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer DR5 Ndefw

<400> 24
gtggcatatg gctctgatca cccaacaa 28

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer DR5 Xhorv

<400> 25
cgcctcgagt gattctttgt ggacaca 27

<210> 26
<211> 139

<212> PRT
<213> Artificial Sequence

<220>
<223> rsDR5

<400> 26

Met Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala Ala
1 5 10 15

Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu Cys Pro Pro Gly
20 25 30

His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly
35 40 45

Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys
50 55 60

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

Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp
85 90 95

Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met
100 105 110

Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
115 120 125

Lys Glu Ser Leu Glu His His His His His His
130 135

<210> 27
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L1

<220>
<221> CDS
<222> (1)..(717)

<400> 27
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gca tat ggc gac atc gta atg acc cag tct ccg ctg agt ctt cct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
20 25 30

gtg act cca ggg gag ccc gca agc atc tct tgt cgc agc agt cag tca 144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser

```
        35                  40                  45

ctg gtc cat agc aat ggg aac act tac ctg cat tgg tac ctc caa aaa      192
Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggg cag tcc cca cag ctc ttg atc tac aag gtg tcc aat cgg ttc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

agt ggt gtg cct gac cgc ttc tcc gga agt ggc tcc ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

act ctt aag att tca aga gtg gag gca gaa gac gtt gga gtc tat tat      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgc tca cag agc aca cat gtc ccc tgg act ttc ggt ccc ggc aca aaa      384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc      432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 28
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

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

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30
```

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

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

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

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

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

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 29
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L2

<220>
<221> CDS
<222> (1)..(717)

<400> 29
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48

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

ggc gca tat ggc gac gtc gtc atg aca cag aca cct ctg agc ctg ccc      96
Gly Ala Tyr Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro
            20                  25                  30

gtg tct ctg ggc gaa ccc gcc agt att tct tgt agg tca tct cag tct     144
Val Ser Leu Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctg gtg cac agt aac gga aac aca tat ctc cat tgg tac ctg cag aag     192
Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggt cag tcc cca aag ctc ctg atc tat aag gtg agc aac aga ttc     240
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

tcc gga gtg cct gat cga ttc agc ggg agt ggt tca ggg acc gac ttc     288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

acc ttg aag att agc cgg gtc gag gcc gag gat gtt gga gtg tat ttc     336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe
            100                 105                 110

tgt agc cag agt aca cac gtg ccc tgg acc ttc gga cct ggg act aaa     384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag att aaa cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc     432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg     480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac     528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac     576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa     624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag     672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt         717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 30
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

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

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

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

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

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

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

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe
100 105 110

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 31
<211> 717
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence coding hB273_L3

<220>
<221> CDS
<222> (1)..(717)

<400> 31

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc       48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

ggc gca tat ggc gac gtg gtg atg acg cag act ccg ctg tca ctg ccc       96
Gly Ala Tyr Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro
            20                  25                  30

gta tct ctg gga gag cct gcc agc atc agc tgc agg agc tct caa tca      144
Val Ser Leu Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctg gtg cac tct aac ggt aat acc tac ctc cac tgg tat ctc cag aag      192
Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca gga caa tcc cca aag ttg ctc ata tat aaa gtg tcc aac cgg ttc      240
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

tca gga gtc cct gac cgg ttt agc ggt agt ggc tct ggt aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

acc ctg aaa ata tca agg gtt gaa gcg gaa gac gta gga gtg tat ttt      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe
            100                 105                 110

tgc agc cag agc acc cat gtc ccc tgg aca ttt ggg ggc ggc acc aag      384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125

gtc gaa atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc      432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 32
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

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

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

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

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

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

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

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe
            100                 105                 110

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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225 230 235

<210> 33
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H1

<220>
<221> CDS
<222> (1)..(1413)

<400> 33

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg       48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc caa gtt cag ctc gtg cag tcc ggc gcg gag gtt aag aaa       96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gca tcc gtt aaa gtg tca tgt aag gcc agc ggg tac tcc ttt      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttt atg aac tgg gtg cgg cag gcc cct ggt atg ggc ctg      192
Ile Gly Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Met Gly Leu
    50                  55                  60

gag tgg atg gga cgg ttt aat cca tat aat ggc gat act ttt tac aac      240
Glu Trp Met Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aaa ttt aaa gga agg gtc act ctc aca gtg gat aaa agc act agt      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acg gct tac atg gaa ctg tcc tcc ctc aga tca gaa gat act gcc gtc      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc cga agt gct tac tat ttc gac agc ggg ggc tac ttt      384
Tyr Tyr Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gat tat tgg ggc cag ggg acc ctg gta act gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
```

```
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 34
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

Ile Gly Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Met Gly Leu
    50                  55                  60

Glu Trp Met Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220
```

```
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 35
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2

<220>
<221> CDS
<222> (1)..(1413)

<400> 35

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtc cag ctg gtg cag agt gga gcc gag gta aaa aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggg gct agt gtc aag gtc tcc tgt aag gca tct ggt tac tct ttt       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

ata gga tac ttc atg aac tgg atg aag cag tct ccc ggt atg tct ctg       192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60

gag tgg att ggc aga ttc aac ccc tac aac ggg gac act ttt tat aat       240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aaa ggg aaa gcc act ctg acc gtg gac aag tca act tcc       288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

aca gca tac atg gaa ttg tcc tca ctg agg tcc gaa gat acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc gct cgg agt gct tat tat ttc gat agc gga ggg tat ttt       384
Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tat tgg ggg caa ggg acc ctt gta acc gtg agc tca gcc tcc acc       432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct       480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa       528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac       576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc       624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc       672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag       720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
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```
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 36
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
```

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 37
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H3

<220>
<221> CDS

<222> (1)..(1413)

<400> 37

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc gaa gtg cag ctc gtg caa agc ggc gct gaa gtg aaa aaa      96
Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca gga gcc tca gtc aaa gtg tcc tgt aag gcc tcc ggg tat agc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tat ttt atg aac tgg atg aag cag agc ccg ggc aaa agc ctc     192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Lys Ser Leu
    50                  55                  60

gaa tgg atc ggg aga ttc aat cca tac aat ggt gac acc ttt tac aat     240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aaa ttc aaa ggc aag gcc acg ctg act gta gac aaa tcc acc agc     288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

aca gcc cac atg gaa ttg tct tcc ctg agg tct gag gat acc gcg gtg     336
Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttt tgt ggc cga agt gcg tat tat ttc gat tca ggc ggg tac ttc     384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gat tac tgg ggt cag ggg acg ctc gtc acc gta agc tca gcc tcc acc     432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct     480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa     528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac     576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc     624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc     672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag     720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct     768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag     816
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```
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 38
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15
```

```
Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
```

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 39
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H1-1

<220>
<221> CDS
<222> (1)..(1413)

<400> 39
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

```
gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggc gct tct gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttc atg aac tgg atg cgg cag gcc cct ggc atg gga ctg       192
Ile Gly Tyr Phe Met Asn Trp Met Arg Gln Ala Pro Gly Met Gly Leu
    50                  55                  60

gaa tgg atg ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac       240
Glu Trp Met Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tat ttc tgc ggc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc       384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc       432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct       480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa       528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac       576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc       624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc       672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag       720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct       768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag       816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg       864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
```

```
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 40
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
```

```
        35                  40                  45

Ile Gly Tyr Phe Met Asn Trp Met Arg Gln Ala Pro Gly Met Gly Leu
    50                  55                  60

Glu Trp Met Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
```

305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 41
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2-1

<220>
<221> CDS
<222> (1)..(1413)

<400> 41
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

```
atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc atg agc ctg      192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60

gaa tgg atc ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac      240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc gcc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc      384
Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
```

```
aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 42
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60
```

```
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335
```

```
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 43
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2-2

<220>
<221> CDS
<222> (1)..(1413)

<400> 43

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa      96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc atg agc ctg     192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60

gaa tgg atc ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac     240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
```

```
65                  70                  75                  80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc cac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg      336
Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc gcc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc      384
Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
```

```
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  44
<211>  471
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  44

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15


Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30


Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45


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


Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80


Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95
```

```
Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365
```

```
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 45
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2-3

<220>
<221> CDS
<222> (1)..(1413)

<400> 45

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc gag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa      96
Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc atg agc ctg     192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60

gaa tgg atc ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac     240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc     288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc cac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg     336
```

```
Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc gcc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc      384
Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
```

```
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  46
<211>  471
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  46

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala His Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125
```

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

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

```
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  47
<211>  1413
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide sequence coding hB273_H2-4


<220>
<221>  CDS
<222>  (1)..(1413)

<400>  47
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg       48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa       96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc atg agc ctg      192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
    50                  55                  60

gaa tgg atc ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac      240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc ggc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc      384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125
```

```
gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400
```

```
atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag      1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc      1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca      1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc      1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                         1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 48
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
```

145 150 155 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 49
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2-5

<220>
<221> CDS
<222> (1)..(1413)

<400> 49

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa      96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc aag agc ctg     192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Lys Ser Leu
    50                  55                  60

gaa tgg atc ggc cgg ttc aac ccc tac aac ggc gac acc ttc tac aac     240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65                  70                  75                  80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc     288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg     336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac ttc tgc ggc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc     384
Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc     432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct     480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160
```

```
ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430
```

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca 1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc 1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

ctc tcc ctg tct ccc ggc aaa 1413
Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 50
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Gly Asp Thr Phe Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Phe Cys Gly Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
115 120 125

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

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

```
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445
```

```
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 51
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L1-NE

<220>
<221> CDS
<222> (1)..(717)

<400> 51

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc      48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggc gca tat ggc gac atc gta atg acc cag tct ccg ctg agt ctt cct      96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30

gtg act cca ggg gag ccc gca agc atc tct tgt cgc agc agt cag tca     144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctg gtc cat agc aat gag aac act tac ctg cat tgg tac ctc caa aaa     192
Leu Val His Ser Asn Glu Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggg cag tcc cca cag ctc ttg atc tac aag gtg tcc aat cgg ttc     240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

agt ggt gtg cct gac cgc ttc tcc gga agt ggc tcc ggg aca gat ttc     288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

act ctt aag att tca aga gtg gag gca gaa gac gtt gga gtc tat tat     336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgc tca cag agc aca cat gtc ccc tgg act ttc ggt ccc ggc aca aaa     384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc     432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg     480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac     528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac     576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
```

180 185 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa 624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag 672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt 717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 52
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52

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

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

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

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

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

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

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

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 53
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-F1

<400> 53
aggtaagctt gctagcgcca ccatggtgct gc 32

<210> 54
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NE-R2

<400> 54
ccaatgcagg taagtgttct cattgctatg gaccagtgac tg 42

<210> 55
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NE-F2

<400> 55
cagtcactgg tccatagcaa tgagaacact tacctgcatt gg 42

<210> 56
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-R1

<400> 56
ggatgccacc cgtttaaacg ggcccctaac ac 32

<210> 57
<211> 717
<212> DNA

<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L1-NF

<220>
<221> CDS
<222> (1)..(717)

<400> 57

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc       48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

ggc gca tat ggc gac atc gta atg acc cag tct ccg ctg agt ctt cct       96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30

gtg act cca ggg gag ccc gca agc atc tct tgt cgc agc agt cag tca      144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctg gtc cat agc aat ttc aac act tac ctg cat tgg tac ctc caa aaa      192
Leu Val His Ser Asn Phe Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggg cag tcc cca cag ctc ttg atc tac aag gtg tcc aat cgg ttc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

agt ggt gtg cct gac cgc ttc tcc gga agt ggc tcc ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

act ctt aag att tca aga gtg gag gca gaa gac gtt gga gtc tat tat      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgc tca cag agc aca cat gtc ccc tgg act ttc ggt ccc ggc aca aaa      384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc      432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
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Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 58
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58

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

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

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

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

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

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

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

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 59
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NF-R2

<400> 59
ccaatgcagg taagtgttga aattgctatg gaccagtgac tg 42

<210> 60
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NF-F2

<400> 60
cagtcactgg tccatagcaa tttcaacact tacctgcatt gg 42

<210> 61
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L1-NK

<220>
<221> CDS
<222> (1)..(717)

<400> 61
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gca tat ggc gac atc gta atg acc cag tct ccg ctg agt ctt cct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
20 25 30

gtg act cca ggg gag ccc gca agc atc tct tgt cgc agc agt cag tca 144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

ctg gtc cat agc aat aag aac act tac ctg cat tgg tac ctc caa aaa 192
Leu Val His Ser Asn Lys Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
50 55 60

cca ggg cag tcc cca cag ctc ttg atc tac aag gtg tcc aat cgg ttc 240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65 70 75 80

agt ggt gtg cct gac cgc ttc tcc gga agt ggc tcc ggg aca gat ttc 288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

```
act ctt aag att tca aga gtg gag gca gaa gac gtt gga gtc tat tat      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgc tca cag agc aca cat gtc ccc tgg act ttc ggt ccc ggc aca aaa      384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc      432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 62
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62

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

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

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

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

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

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

85 90 95

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

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 63
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NK-R2

<400> 63
ccaatgcagg taagtgttct tattgctatg gaccagtgac tg 42

<210> 64
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Priemr L-NK-F2

<400> 64
cagtcactgg tccatagcaa taagaacact tacctgcatt gg 42

<210> 65
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_L1-NL

<220>
<221> CDS
<222> (1)..(717)

<400> 65

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc        48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

ggc gca tat ggc gac atc gta atg acc cag tct ccg ctg agt ctt cct        96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30

gtg act cca ggg gag ccc gca agc atc tct tgt cgc agc agt cag tca       144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
        35                  40                  45

ctg gtc cat agc aat ctg aac act tac ctg cat tgg tac ctc caa aaa       192
Leu Val His Ser Asn Leu Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
    50                  55                  60

cca ggg cag tcc cca cag ctc ttg atc tac aag gtg tcc aat cgg ttc       240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65                  70                  75                  80

agt ggt gtg cct gac cgc ttc tcc gga agt ggc tcc ggg aca gat ttc       288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

act ctt aag att tca aga gtg gag gca gaa gac gtt gga gtc tat tat       336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

tgc tca cag agc aca cat gtc ccc tgg act ttc ggt ccc ggc aca aaa       384
Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Pro Gly Thr Lys
        115                 120                 125

gtc gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc       432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140

ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg       480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac       528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac       576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190

agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa       624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205

gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag       672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt           717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 66
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66

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

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

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

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

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

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

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

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

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 67
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NL-R2

<400> 67
ccaatgcagg taagtgttca gattgctatg gaccagtgac tg 42

<210> 68
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer L-NL-F2

<400> 68
cagtcactgg tccatagcaa tctgaacact tacctgcatt gg 42

<210> 69
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding hB273_H2-1-NE

<220>
<221> CDS
<222> (1)..(1413)

<400> 69
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct gga gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac agc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

atc ggc tac ttc atg aac tgg atg aag cag agc ccc ggc atg agc ctg 192
Ile Gly Tyr Phe Met Asn Trp Met Lys Gln Ser Pro Gly Met Ser Leu
50 55 60

gaa tgg atc ggc cgg ttc aac ccc tac aac gag gac acc ttc tac aac 240
Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Glu Asp Thr Phe Tyr Asn
65 70 75 80

cag aag ttc aag gga aag gcc acc ctg aca gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gat acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

```
                100                 105                 110

tac ttc tgc gcc aga agc gcc tac tac ttc gac agc ggc ggc tac ttc      384
Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125

gac tac tgg ggc cag ggc acc ctg gtg aca gtg agc tca gcc tcc acc      432
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct      480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
```

```
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc     1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                        1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 70
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45

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

Glu Trp Ile Gly Arg Phe Asn Pro Tyr Asn Glu Asp Thr Phe Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr Phe Asp Ser Gly Gly Tyr Phe
        115                 120                 125
```

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

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 71
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer H-F1

<400> 71
aggtaagctt gctagcgcca ccatgaaaca cc 32

<210> 72
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer H-NE-R2

<400> 72
ctggttgtag aaggtgtcct cgttgtaggg gttgaaccgg cc 42

<210> 73
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer H-NE-F2

<400> 73
ggccggttca acccctacaa cgaggacacc ttctacaacc ag 42

<210> 74
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Priemr H-R1

<400> 74
ggatgccacc cgtttaaacg ggcccgatat ctc 33

<210> 75
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding the light chain of conatumumab

<220>
<221> CDS
<222> (1)..(705)

<400> 75

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc      48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggc gca tat ggc gaa atc gtg ttg aca cag agt ccc ggc act ctt agc      96
Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20                  25                  30

ctt agc ccg ggt gaa cgc gcc acc ctg tcc tgc cgc gcc tct cag gga     144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
        35                  40                  45

atc tct cgc tct tac ctc gcg tgg tac cag cag aaa ccc ggc cag gcc     192
Ile Ser Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

ccc agt ttg ctg ata tac ggt gcc tct agc cga gca act ggc atc cca     240
Pro Ser Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65                  70                  75                  80

gac cgg ttc tca gga tct ggc tcc ggg act gac ttc act ctg acc atc     288
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

tcc aga ctg gag ccc gag gat ttc gcg gta tat tac tgc cag cag ttc     336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
            100                 105                 110

ggc agc agt cct tgg acc ttc gga cag ggt act aag gtg gag att aaa     384
Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag     432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc     480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag     528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc     576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag     624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc     672
```

```
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt                          705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  76
<211>  235
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  76

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

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
        35                  40                  45

Ile Ser Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Ser Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile 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 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
            100                 105                 110

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

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205
```

```
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 77
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding the heavy chain of conatumumab

<220>
<221> CDS
<222> (1)..(1413)

<400> 77

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctt cag gaa agc ggg ccc ggc ctc gtg aag      96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            20                  25                  30

ccc tcc cag acc ctg tct ctt act tgt aca gtg agc ggt ggc agc att     144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
        35                  40                  45

tct tca ggc gat tac ttc tgg agt tgg att cgc caa ctg cct ggt aaa     192
Ser Ser Gly Asp Tyr Phe Trp Ser Trp Ile Arg Gln Leu Pro Gly Lys
    50                  55                  60

ggg ctg gaa tgg atc ggg cat att cac aat tca gga acc aca tat tat     240
Gly Leu Glu Trp Ile Gly His Ile His Asn Ser Gly Thr Thr Tyr Tyr
65                  70                  75                  80

aac cct tca ctg aag agc cgg gta act atc tcc gtt gac act agc aag     288
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95

aaa cag ttc tcc ctc cgg ctg tct tct gtc aca gcc gct gac acc gct     336
Lys Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100                 105                 110

gtt tac tac tgt gca aga gat cgg ggt ggc gac tac tat tac ggc atg     384
Val Tyr Tyr Cys Ala Arg Asp Arg Gly Gly Asp Tyr Tyr Tyr Gly Met
        115                 120                 125

gat gtt tgg gga cag gga acc acc gta aca gtg agc tca gcc tcc acc     432
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct     480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa     528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175
```

```
ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac      960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac     1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc     1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg     1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag     1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac     1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag     1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc     1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca     1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445
```

```
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc      1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                      1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 78
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 78

```
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
        35                  40                  45

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

Gly Leu Glu Trp Ile Gly His Ile His Asn Ser Gly Thr Thr Tyr Tyr
65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95

Lys Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Asp Arg Gly Gly Asp Tyr Tyr Tyr Gly Met
        115                 120                 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
```

```
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
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465 470

<210> 79
<211> 16
<212> PRT
<213> Mus musculus

<400> 79

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 80
<211> 7
<212> PRT
<213> Mus musculus

<400> 80

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Ser Gln Ser Thr His Val Pro Trp Thr
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Gly Tyr Phe Met Asn
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Gly

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Gly