SEQUENCE LISTING

<110> Celldex Therapeutics Inc.

<120> ANTIBODIES THAT BIND HUMAN DENDRITIC AND EPITHELIAL CELL 205 (DEC-205)

<130> SG1723A

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> 61/002,253
<151> 2007-11-07

<150> 61/191,551
<151> 2008-09-10

<160> 106

<170> PatentIn version 3.5

<210> 1
<211> 1722
<212> PRT
<213> Homo sapiens

<400> 1

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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
        35                  40                  45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
    50                  55                  60

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
65                  70                  75                  80

Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
                85                  90                  95

Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
            100                 105                 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
        115                 120                 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
    130                 135                 140

Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
145                 150                 155                 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
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                165                 170                 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
            180                 185                 190

Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
        195                 200                 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
    210                 215                 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
225                 230                 235                 240

Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
                245                 250                 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
            260                 265                 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
        275                 280                 285

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

Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
305                 310                 315                 320

Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
                325                 330                 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
            340                 345                 350

Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
        355                 360                 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
    370                 375                 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
385                 390                 395                 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
                405                 410                 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
            420                 425                 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
        435                 440                 445
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Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
    450                 455                 460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
465                 470                 475                 480

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

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
            500                 505                 510

Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
        515                 520                 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu
    530                 535                 540

Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
545                 550                 555                 560

Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly
                565                 570                 575

Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
            580                 585                 590

Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
        595                 600                 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys
    610                 615                 620

Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp
625                 630                 635                 640

Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
                645                 650                 655

Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
            660                 665                 670

Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
        675                 680                 685

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

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
705                 710                 715                 720
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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
                725                 730                 735

Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
            740                 745                 750

Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
        755                 760                 765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
    770                 775                 780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
785                 790                 795                 800

Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
                805                 810                 815

Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
            820                 825                 830

Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
        835                 840                 845

Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala
    850                 855                 860

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
865                 870                 875                 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe
                885                 890                 895

Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
            900                 905                 910

Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
        915                 920                 925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
    930                 935                 940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
945                 950                 955                 960

Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
                965                 970                 975

Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
            980                 985                 990
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Gln Ile Glu Gln Asp Phe Ile Thr  Ser Leu Leu Pro Asp  Met Glu Ala
        995                 1000                1005

Thr Leu  Trp Ile Gly Leu Arg  Trp Thr Ala Tyr Glu  Lys Ile Asn
    1010                 1015                 1020

Lys Trp  Thr Asp Asn Arg Glu  Leu Thr Tyr Ser Asn  Phe His Pro
    1025                 1030                 1035

Leu Leu  Val Ser Gly Arg Leu  Arg Ile Pro Glu Asn  Phe Phe Glu
    1040                 1045                 1050

Glu Glu  Ser Arg Tyr His Cys  Ala Leu Ile Leu Asn  Leu Gln Lys
    1055                 1060                 1065

Ser Pro  Phe Thr Gly Thr Trp  Asn Phe Thr Ser Cys  Ser Glu Arg
    1070                 1075                 1080

His Phe  Val Ser Leu Cys Gln  Lys Tyr Ser Glu Val  Lys Ser Arg
    1085                 1090                 1095

Gln Thr  Leu Gln Asn Ala Ser  Glu Thr Val Lys Tyr  Leu Asn Asn
    1100                 1105                 1110

Leu Tyr  Lys Ile Ile Pro Lys  Thr Leu Thr Trp His  Ser Ala Lys
    1115                 1120                 1125

Arg Glu  Cys Leu Lys Ser Asn  Met Gln Leu Val Ser  Ile Thr Asp
    1130                 1135                 1140

Pro Tyr  Gln Gln Ala Phe Leu  Ser Val Gln Ala Leu  Leu His Asn
    1145                 1150                 1155

Ser Ser  Leu Trp Ile Gly Leu  Phe Ser Gln Asp Asp  Glu Leu Asn
    1160                 1165                 1170

Phe Gly  Trp Ser Asp Gly Lys  Arg Leu His Phe Ser  Arg Trp Ala
    1175                 1180                 1185

Glu Thr  Asn Gly Gln Leu Glu  Asp Cys Val Val Leu  Asp Thr Asp
    1190                 1195                 1200

Gly Phe  Trp Lys Thr Val Asp  Cys Asn Asp Asn Gln  Pro Gly Ala
    1205                 1210                 1215

Ile Cys  Tyr Tyr Ser Gly Asn  Glu Thr Glu Lys Glu  Val Lys Pro
    1220                 1225                 1230

Val Asp  Ser Val Lys Cys Pro  Ser Pro Val Leu Asn  Thr Pro Trp
    1235                 1240                 1245

Ile Pro  Phe Gln Asn Cys Cys  Tyr Asn Phe Ile Ile  Thr Lys Asn
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    1250                1255                1260

Arg His  Met Ala Thr Thr Gln  Asp Glu Val His Thr  Lys Cys Gln
    1265                1270                1275

Lys Leu  Asn Pro Lys Ser His  Ile Leu Ser Ile Arg  Asp Glu Lys
    1280                1285                1290

Glu Asn  Asn Phe Val Leu Glu  Gln Leu Leu Tyr Phe  Asn Tyr Met
    1295                1300                1305

Ala Ser  Trp Val Met Leu Gly  Ile Thr Tyr Arg Asn  Asn Ser Leu
    1310                1315                1320

Met Trp  Phe Asp Lys Thr Pro  Leu Ser Tyr Thr His  Trp Arg Ala
    1325                1330                1335

Gly Arg  Pro Thr Ile Lys Asn  Glu Lys Phe Leu Ala  Gly Leu Ser
    1340                1345                1350

Thr Asp  Gly Phe Trp Asp Ile  Gln Thr Phe Lys Val  Ile Glu Glu
    1355                1360                1365

Ala Val  Tyr Phe His Gln His  Ser Ile Leu Ala Cys  Lys Ile Glu
    1370                1375                1380

Met Val  Asp Tyr Lys Glu Glu  His Asn Thr Thr Leu  Pro Gln Phe
    1385                1390                1395

Met Pro  Tyr Glu Asp Gly Ile  Tyr Ser Val Ile Gln  Lys Lys Val
    1400                1405                1410

Thr Trp  Tyr Glu Ala Leu Asn  Met Cys Ser Gln Ser  Gly Gly His
    1415                1420                1425

Leu Ala  Ser Val His Asn Gln  Asn Gly Gln Leu Phe  Leu Glu Asp
    1430                1435                1440

Ile Val  Lys Arg Asp Gly Phe  Pro Leu Trp Val Gly  Leu Ser Ser
    1445                1450                1455

His Asp  Gly Ser Glu Ser Ser  Phe Glu Trp Ser Asp  Gly Ser Thr
    1460                1465                1470

Phe Asp  Tyr Ile Pro Trp Lys  Gly Gln Thr Ser Pro  Gly Asn Cys
    1475                1480                1485

Val Leu  Leu Asp Pro Lys Gly  Thr Trp Lys His Glu  Lys Cys Asn
    1490                1495                1500

Ser Val  Lys Asp Gly Ala Ile  Cys Tyr Lys Pro Thr  Lys Ser Lys
    1505                1510                1515
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Lys Leu  Ser Arg Leu Thr Tyr  Ser Ser Arg Cys Pro  Ala Ala Lys
    1520                1525                1530

Glu Asn  Gly Ser Arg Trp Ile  Gln Tyr Lys Gly His  Cys Tyr Lys
    1535                1540                1545

Ser Asp  Gln Ala Leu His Ser  Phe Ser Glu Ala Lys  Lys Leu Cys
    1550                1555                1560

Ser Lys  His Asp His Ser Ala  Thr Ile Val Ser Ile  Lys Asp Glu
    1565                1570                1575

Asp Glu  Asn Lys Phe Val Ser  Arg Leu Met Arg Glu  Asn Asn Asn
    1580                1585                1590

Ile Thr  Met Arg Val Trp Leu  Gly Leu Ser Gln His  Ser Val Asp
    1595                1600                1605

Gln Ser  Trp Ser Trp Leu Asp  Gly Ser Glu Val Thr  Phe Val Lys
    1610                1615                1620

Trp Glu  Asn Lys Ser Lys Ser  Gly Val Gly Arg Cys  Ser Met Leu
    1625                1630                1635

Ile Ala  Ser Asn Glu Thr Trp  Lys Lys Val Glu Cys  Glu His Gly
    1640                1645                1650

Phe Gly  Arg Val Val Cys Lys  Val Pro Leu Gly Pro  Asp Tyr Thr
    1655                1660                1665

Ala Ile  Ala Ile Ile Val Ala  Thr Leu Ser Ile Leu  Val Leu Met
    1670                1675                1680

Gly Gly  Leu Ile Trp Phe Leu  Phe Gln Arg His Arg  Leu His Leu
    1685                1690                1695

Ala Gly  Phe Ser Ser Val Arg  Tyr Ala Gln Gly Val  Asn Glu Asp
    1700                1705                1710

Glu Ile  Met Leu Pro Ser Phe  His Asp
    1715                1720
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<213> Homo sapiens

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tgtgcagcgt ctggattcat cttcagtatc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agctcctcac 360

tttgactact ggggccaggg aaccctggtc accgtctcct cagctagc 408

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<212> PRT
<213> Homo sapiens

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

Ser Ile Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ser
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<210> 4
<211> 115
<212> PRT
<213> Homo sapiens

<400> 4
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ile Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

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

<400> 5
Ile Tyr Gly Met His
1 5

<210> 6
<211> 17
<212> PRT
<213> Homo sapiens

<400> 6
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 7
<211> 6
<212> PRT
<213> Homo sapiens

<400> 7
Ala Pro His Phe Asp Tyr
1 5

<210> 8
<211> 384
<212> DNA
<213> Homo sapiens

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acttgtcggg cgagtcaggg tattagcagc tggttagcct ggtatcagca gaaaccagag 180

aaagccccta agtccctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 240

ttcagcggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa 300

gattttgcaa cttattactg ccaacagtat aatagttacc cgtacacttt tggccagggg 360

accaagctgg agatcaaacg tacg 384

<210> 9
<211> 129
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<400> 9
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1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys
50 55 60

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

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

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

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

Lys

<210> 10
<211> 107
<212> PRT
<213> Homo sapiens

<400> 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

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

<400> 11
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 12
<211> 7
<212> PRT
<213> Homo sapiens

<400> 12
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
1 5

<210> 14
<211> 439
<212> DNA
<213> Homo sapiens

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ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agctcctcac 360

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tcggtcttcc ccctggcac 439

<210> 15
<211> 134

<212> PRT
<213> Homo sapiens

<400> 15
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1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe
35 40 45

Ser Ile Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ser
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<210> 16
<211> 115
<212> PRT
<213> Homo sapiens

<400> 16
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ile Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Ala Pro His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 17
<211> 5
<212> PRT
<213> Homo sapiens

<400> 17
Ile Tyr Gly Met His
1 5

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

<400> 18
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 19
<211> 6
<212> PRT
<213> Homo sapiens

<400> 19
Ala Pro His Phe Asp Tyr
1 5

<210> 20
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<212> DNA
<213> Homo sapiens

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gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180

aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tctcactttc 360

ggcggaggga ccaaggtgga gatcaaa 387

<210> 21
<211> 129
<212> PRT
<213> Homo sapiens

<400> 21
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65 70 75 80

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

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

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

Lys

<210> 22
<211> 107
<212> PRT
<213> Homo sapiens

<400> 22
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 23
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<212> PRT
<213> Homo sapiens

<400> 23
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 24
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<400> 24
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 25
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<400> 25
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 26
<211> 417
<212> DNA
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tgtgcagcgt ctggattcac cttcagtaat tatggcatgt actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatctctgg 360

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<210> 27
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<212> PRT
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<400> 27
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

```
Ser Asn Tyr Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Leu Trp Gly Trp Tyr Phe Asp Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala
145
```

<210> 28
<211> 130
<212> PRT
<213> Homo sapiens

<400> 28

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Leu Trp Gly Trp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

Leu Ala
```

130

<210> 29
<211> 5
<212> PRT
<213> Homo sapiens

<400> 29
Asn Tyr Gly Met Tyr
1 5

<210> 30
<211> 17
<212> PRT
<213> Homo sapiens

<400> 30
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 31
<211> 9
<212> PRT
<213> Homo sapiens

<400> 31
Asp Leu Trp Gly Trp Tyr Phe Asp Tyr
1 5

<210> 32
<211> 384
<212> DNA
<213> Homo sapiens

<400> 32
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attgtgttga cacagtctcc agccaccctg tctttgtctc caggggaaag agccaccctc 120

tcctgcaggg ccagtcagag tgttagcagc tacttagcct ggtaccaaca gaaacctggc 180

caggctccca ggctcctcat ctatgatgca tccaacaggg ccactggcat cccagccagg 240

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagcct agagcctgaa 300

gattttgcag tttattactg tcagcagcgt cgcaactggc cgctcacttt cggcggaggg 360

accaaggtgg agatcaaacg tacg 384

<210> 33
<211> 127
<212> PRT
<213> Homo sapiens

<400> 33
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser

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            20                  25                  30

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

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

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

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


<210> 34
<211> 107
<212> PRT
<213> Homo sapiens

<400> 34
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Arg Asn Trp Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 35
<211> 11
<212> PRT
<213> Homo sapiens

<400> 35
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10
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<210> 36
<211> 7
<212> PRT
<213> Homo sapiens

<400> 36
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 37
<211> 9
<212> PRT
<213> Homo sapiens

<400> 37
Gln Gln Arg Arg Asn Trp Pro Leu Thr
1 5

<210> 38
<211> 447
<212> DNA
<213> Homo sapiens

<400> 38
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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtacc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcaattata tggtatgatg gaggtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacttctac 360

tggtacttcg atctctgggg ccgtggcacc ctggtcactg tctcctcagc ctccaccaag 420

ggcccatcgg tcttccccct ggcaagg 447

<210> 39
<211> 148
<212> PRT
<213> Homo sapiens

<400> 39
Met Glu Phe Gly Leu Thr Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala
65 70 75 80

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

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

Tyr Tyr Cys Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
        115                 120                 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

Phe Pro Leu Ala
145
```

<210> 40
<211> 129
<212> PRT
<213> Homo sapiens

<400> 40

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

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

Ala
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<210> 41
<211> 5
<212> PRT
<213> Homo sapiens

<400> 41
Thr Tyr Gly Met His
1 5

<210> 42
<211> 17
<212> PRT
<213> Homo sapiens

<400> 42
Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 43
<211> 8
<212> PRT
<213> Homo sapiens

<400> 43
Asp Phe Tyr Trp Tyr Phe Asp Leu
1 5

<210> 44
<211> 372
<212> DNA
<213> Homo sapiens

<400> 44
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 180

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcagcag cgtaggacgt tcggccaagg gaccaaggtg 360

gaaatcaaac ga 372

<210> 45
<211> 123
<212> PRT
<213> Homo sapiens

<400> 45
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

```
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120


<210> 46
<211> 103
<212> PRT
<213> Homo sapiens

<400> 46
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

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

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

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

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

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

Gly Thr Lys Val Glu Ile Lys
            100


<210> 47
<211> 11
<212> PRT
<213> Homo sapiens

<400> 47
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1               5                   10


<210> 48
<211> 7
<212> PRT
<213> Homo sapiens

<400> 48
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Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 49
<211> 5
<212> PRT
<213> Homo sapiens

<400> 49
Gln Gln Arg Arg Thr
1 5

<210> 50
<211> 454
<212> DNA
<213> Homo sapiens

<400> 50
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tataacatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcatttata tggtatgatg gaagtaataa atactatgga 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaaaaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agaagagctg 360

gggatcgggt ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctcagcc 420

tccaccaagg gcccatcggt cttccccctg gcac 454

<210> 51
<211> 151
<212> PRT
<213> Homo sapiens

<400> 51
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

```
Tyr Tyr Cys Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
        115                 120                 125


Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140


Pro Ser Val Phe Pro Leu Ala
145                 150


<210> 52
<211> 132
<212> PRT
<213> Homo sapiens

<400> 52
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
    50                  55                  60


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


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


Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


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


Phe Pro Leu Ala
    130


<210> 53
<211> 5
<212> PRT
<213> Homo sapiens

<400> 53
Ser Tyr Asn Met His
1               5


<210> 54
<211> 17
<212> PRT
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<213> Homo sapiens

<400> 54
Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys
1               5                   10                  15

Gly

<210> 55
<211> 11
<212> PRT
<213> Homo sapiens

<400> 55
Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
1               5                   10

<210> 56
<211> 454
<212> DNA
<213> Homo sapiens

<400> 56
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 180

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcagcag cgtaggacgt tcggccaagg gaccaaggtg 360

gaaatcaaac gaactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 420

ttgaaatctg gaactgcctc tgttgtgtgc ctgc 454

<210> 57
<211> 123
<212> PRT
<213> Homo sapiens

<400> 57
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                   10                  15

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

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

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65                  70                  75                  80

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120
```

<210> 58
<211> 103
<212> PRT
<213> Homo sapiens

<400> 58

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

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

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

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

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

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

Gly Thr Lys Val Glu Ile Lys
            100
```

<210> 59
<211> 11
<212> PRT
<213> Homo sapiens

<400> 59

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

<210> 60
<211> 7
<212> PRT
<213> Homo sapiens

<400> 60

```
Asp Ala Ser Asn Arg Ala Thr
1               5
```

<210> 61
<211> 5

<212> PRT
<213> Homo sapiens

<400> 61
Gln Gln Arg Arg Thr
1 5

<210> 62
<211> 433
<212> DNA
<213> Homo sapiens

<400> 62
atggagtttg tgctgagctg ggttctcctt gttgctatat taaaaggtgt ccagtgtgag 60

gttcagctgg tgcagtctgg gggaggcttg gtacatcctg gggggtccct gagactctcc 120

tgtgcaggct ctggattcac cttcagtaac tatgctatgc actgggttcg ccaggctcca 180

ggaaaaggtc tggagtgggt atcaactatt ggtactggtg gtggcacacc ctatgcagac 240

tccgtgaagg gccgcttcac catctccaga gacaatgcca agaactcctt gtatcttcaa 300

atgaacagcc tgagagccga ggacatggct gtgtattact gtgcattaag tgcttttgat 360

gtctggggcc aagggacaat ggtcaccgtc tcttcagcct ccaccaaggg cccatcggtc 420

ttcccccctgg cac 433

<210> 63
<211> 144
<212> PRT
<213> Homo sapiens

<400> 63
Met Glu Phe Val Leu Ser Trp Val Leu Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Thr Ile Gly Thr Gly Gly Gly Thr Pro Tyr Ala Asp
65 70 75 80

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

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

Tyr Cys Ala Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val
115 120 125

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

<210> 64
<211> 125
<212> PRT
<213> Homo sapiens

<400> 64
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Gly Thr Gly Gly Gly Thr Pro Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
100 105 110

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

<210> 65
<211> 5
<212> PRT
<213> Homo sapiens

<400> 65
Asn Tyr Ala Met His
1 5

<210> 66
<211> 16
<212> PRT
<213> Homo sapiens

<400> 66
Thr Ile Gly Thr Gly Gly Gly Thr Pro Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 67
<211> 5
<212> PRT
<213> Homo sapiens

<400> 67
Ser Ala Phe Asp Val

1 5

<210> 68
<211> 466
<212> DNA
<213> Homo sapiens

<400> 68
atggagtttg tgctgagctg ggttttcctt gttgctatat taaaaggtgt ccagtgtgag 60

gttcagctgg tgcagtctgg gggaggcttg gtacatcctg gggggtccct gagactctcc 120

tgtgcaggct ctggattcac cttcagtagc tatgctatgc actgggttcg ccaggctcca 180

ggaaaaggtc tggagtgggt atcagctatt ggtactggtg gttacacata ctatgtagac 240

tccgtgaagg gccgattcac catctccaga gacaatgcca agaagtcctt gtatcttcaa 300

atgaacagcc tgagagccga ggacatggct gtgtattact gtgcaagaga gccgttttac 360

gatattttga ctggttattc cccatacttt gactactggg gccagggaac cctggtcacc 420

gtctcctcag cctccaccaa gggcccatcg gtcttccccc tggcac 466

<210> 69
<211> 143
<212> PRT
<213> Homo sapiens

<400> 69
Met Glu Phe Val Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp
65 70 75 80

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

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

Tyr Cys Ala Arg Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro
115 120 125

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

<210> 70

<211> 124
<212> PRT
<213> Homo sapiens

<400> 70
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp Ser Val Lys
50 55 60

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

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

Arg Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 71
<211> 5
<212> PRT
<213> Homo sapiens

<400> 71
Ser Tyr Ala Met His
1 5

<210> 72
<211> 16
<212> PRT
<213> Homo sapiens

<400> 72
Ala Ile Gly Thr Gly Gly Tyr Thr Tyr Tyr Val Asp Ser Val Lys Gly
1 5 10 15

<210> 73
<211> 16
<212> PRT
<213> Homo sapiens

<400> 73
Glu Pro Phe Tyr Asp Ile Leu Thr Gly Tyr Ser Pro Tyr Phe Asp Tyr
1 5 10 15

<210> 74
<211> 454

<212> DNA
<213> Homo sapiens

<400> 74
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tataacatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgga 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agaagagctg 360

gggatcgggt ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctcagcc 420

tccaccaagg gcccatcggt cttccccctg gcac 454

<210> 75
<211> 139
<212> PRT
<213> Homo sapiens

<400> 75
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
115 120 125

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 76
<211> 120
<212> PRT
<213> Homo sapiens

<400> 76

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
    50                  55                  60

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

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

Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 77
<211> 5
<212> PRT
<213> Homo sapiens

<400> 77
```
Ser Tyr Asn Met His
1               5
```

<210> 78
<211> 17
<212> PRT
<213> Homo sapiens

<400> 78
```
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys
1               5                   10                  15

Gly
```

<210> 79
<211> 11
<212> PRT
<213> Homo sapiens

<400> 79
```
Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu
1               5                   10
```

<210> 80
<211> 475
<212> DNA

<213> Homo sapiens

<400> 80
atggacatga gggtccccgc tcagctcctg gggcttctgc tgctctggct cccaggtgcc 60

agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120

gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180

aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tcacttcggc 360

caagggacac gactggagat taaacgaact gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgca agggc 475

<210> 81
<211> 128
<212> PRT
<213> Homo sapiens

<400> 81
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65 70 75 80

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

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

Phe Asn Ser Tyr Pro His Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
115 120 125

<210> 82
<211> 106
<212> PRT
<213> Homo sapiens

<400> 82
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala

20 25 30

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro His
85 90 95

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

<210> 83
<211> 11
<212> PRT
<213> Homo sapiens

<400> 83
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 84
<211> 7
<212> PRT
<213> Homo sapiens

<400> 84
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 85
<211> 8
<212> PRT
<213> Homo sapiens

<400> 85
Gln Gln Phe Asn Ser Tyr Pro His
1 5

<210> 86
<211> 445
<212> DNA
<213> Homo sapiens

<400> 86
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtagc tatggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggccccccct 360

cggtacttcg atctctgggg ccgtggcacc ctggtcactg tctcctcagc ctccaccaag 420

ggcccatcgg tcttcccccct ggcac 445

<210> 87
<211> 136
<212> PRT
<213> Homo sapiens

<400> 87
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

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

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Pro Pro Arg Tyr Phe Asp Leu Trp Gly Arg
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 88
<211> 117
<212> PRT
<213> Homo sapiens

<400> 88
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Pro Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 89
<211> 5
<212> PRT
<213> Homo sapiens

<400> 89
Ser Tyr Gly Met His
1 5

<210> 90
<211> 17
<212> PRT
<213> Homo sapiens

<400> 90
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 91
<211> 8
<212> PRT
<213> Homo sapiens

<400> 91
Gly Pro Pro Arg Tyr Phe Asp Leu
1 5

<210> 92
<211> 95
<212> PRT
<213> Homo sapiens

<400> 92
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro
85 90 95

<210> 93
<211> 95
<212> PRT
<213> Homo sapiens

<400> 93
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro
85 90 95

<210> 94
<211> 95
<212> PRT
<213> Homo sapiens

<400> 94
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
85 90 95

<210> 95
<211> 98
<212> PRT
<213> Homo sapiens

<400> 95
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg

<210> 96
<211> 97
<212> PRT
<213> Homo sapiens

<400> 96
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg

<210> 97
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Asn" or "Thr" or "Ser"

<220>
<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Asn" or "Ala"

<220>
<221> misc_feature
<222> (3)..(3)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Tyr"

<220>
<221> misc_feature
<222> (5)..(5)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 97
Ile Tyr Gly Met His
1 5

<210> 98
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Ile" or "Phe" or "Thr" or "Ala"

<220>

<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Gly"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Gly"

<220>
<221> misc_feature
<222> (3)..(5)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Gly" or "Tyr"

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Pro"

<220>
<221> misc_feature
<222> (7)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="Ala" or "Val"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Gly" or " "

<220>
<221> misc_feature
<222> (11)..(12)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 98
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 99
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Gly" or "Tyr" or "Ser" or "Pro" or " "

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Trp" or "Ser" or "Arg"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Ala" or "His"

<220>
<221> misc_feature
<222> (1)..(3)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Leu" or "Val"

<220>
<221> misc_feature
<222> (6)..(6)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 99
Ala Pro Tyr Phe Asp Tyr
1 5

<210> 100
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Gly"

<220>
<221> VARIANT

<222> (6)..(6)
<223> /replace="Val"

<220>
<221> misc_feature
<222> (5)..(6)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Trp" or "Ala"

<220>
<221> misc_feature
<222> (9)..(9)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<400> 100
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala
1 5 10

<210> 101
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (1)..(1)
<223> /replace="Ala"

<220>
<221> misc_feature
<222> (1)..(1)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotation for said position"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Ser"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Leu"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Gln" or "Glu"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Ser"

<220>
<221> misc_feature

<222> (4)..(7)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 101
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 102
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<221> source
<223> /note="Description of artificial sequence: Synthetic
consensus sequence"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Tyr" or "Phe"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Asn"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Ser" or "Asn"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace="Trp" or " "

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace=" "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Leu" or "His" or " "

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace=" "

<220>
<221> misc_feature
<222> (3)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 102
Gln Gln Arg Arg Thr Tyr Pro Tyr Thr
1 5

<210> 103
<211> 118
<212> PRT

<213> Homo sapiens

<400> 103
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Leu Trp Gly Trp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115

<210> 104
<211> 117
<212> PRT
<213> Homo sapiens

<400> 104
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Phe Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
115

<210> 105
<211> 120
<212> PRT
<213> Homo sapiens

<400> 105
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
50 55 60

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

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

Ala Arg Glu Glu Leu Gly Ile Gly Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 106
<211> 113
<212> PRT
<213> Homo sapiens

<400> 106
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Gly Thr Gly Gly Gly Thr Pro Tyr Ala Asp Ser Val Lys
50 55 60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala

85 90 95

Leu Ser Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
100 105 110

Ser