

P108399_seqlist_ST25.txt
SEQUENCE LISTING

<110> Agency for Science, Technology and Research
 <120> PROTEASE-RESPONSIVE PEPTIDE BIOSENSORS AND METHODS FOR ANALYTE
 DETECTION
 <130> P108399
 <150> SG201304395-5
 <151> 2013-06-06
 <160> 23
 <170> PatentIn version 3.5
 <210> 1
 <211> 5
 <212> PRT
 <213> Artificial
 <220>
 <223> Enterokinase protease recognition site
 <400> 1

Asp Asp Asp Asp Arg
 1 5

<210> 2
 <211> 9
 <212> PRT
 <213> Artificial
 <220>
 <223> Influenza virus hemagglutinin epitope
 <400> 2

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 3
 <211> 12
 <212> PRT
 <213> Artificial
 <220>
 <223> p53-derived binding site for mdm2
 <400> 3

Thr Ser Phe Ala Glu Tyr Trp Asn Leu Leu Ser Pro
 1 5 10

<210> 4
 <211> 286
 <212> PRT
 <213> Salmonella typhimurium
 <400> 4

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

P108399_seqlist_ST25.txt

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 275 280 285

P108399_seqlist_ST25.txt

<210> 5
 <211> 1743
 <212> PRT
 <213> Clostridium difficile

<400> 5

Met Lys Gln Asn Lys Leu Leu Gln Arg Gly Ala Tyr Phe Asn Asp Lys
 1 5 10 15

Asn Ile Leu Ile Asp Asp Phe Asp Lys Arg Tyr Asn Asp Tyr Asp Phe
 20 25 30

Val Glu Phe Phe Thr Gly Ile Ser Asn Ser Thr Phe Gly Leu Lys Ser
 35 40 45

Asp Gly Asn Leu Tyr Ala Cys Gly Asp Asn Thr Gly Phe Gln Leu Gly
 50 55 60

Leu Gly Lys Asp Ser Ser Glu Arg Arg Met Phe Ser Lys Val Lys Ile
 65 70 75 80

Asp Asn Val Lys Tyr Val Ser Cys Gly Ser Lys His Ser Val Ala Val
 85 90 95

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

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

Ile Asp Asp Val Lys Thr Val Ala Cys Gly Tyr Asp Phe Thr Phe Val
 130 135 140

Leu Lys Asn Asp Gly Thr Leu Tyr Ser Ala Gly Leu Asn Ser Ser Gly
 145 150 155 160

Gln Leu Gly Leu Gly Asp Thr Asn Asn Arg Val Thr Phe Thr Lys Val
 165 170 175

Asn Ile Asp Ser Val Lys Asp Val Val Thr Tyr Asn Gln Ser Val Phe
 180 185 190

Ile Ile Lys Met Asp Gly Thr Ala His Ala Cys Gly Leu Asn Ser Asn
 195 200 205

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

Ile Glu Gly Met Asp Asn Val Lys Gln Ile Ala Cys Gly Ser Ser His
 225 230 235 240

P108399_seqlist_ST25.txt

Thr Ile Leu Ile Lys Asn Asp Gly Thr Met Tyr Thr Thr Gly Ser Asn
245 250 255

Gly Tyr Gly Gln Leu Gly Thr Gly Asn Asn Asn Asn Ser Ile Val Phe
260 265 270

Thr Leu Ser Ser Ile Asn Asn Val Lys Tyr Ala Ser Cys Gly Asn Asn
275 280 285

His Thr Met Ile Leu Lys Tyr Asp Asn Thr Leu Phe Ser Thr Gly Gln
290 295 300

Asn Asn Tyr Gly Gln Leu Ala Asn Ala Asn Lys Asp Val Ala Ser Arg
305 310 315 320

Asn Thr Phe Val Lys Val Asn Val Glu Asn Ile Lys Asp Ile Lys Cys
325 330 335

Gly Ser Gln Phe Asn Phe Leu Ile Asn Gly Ser Lys Glu Ile Phe Val
340 345 350

Ser Gly Cys Asn Leu Ala Gly Gln Leu Gly Ser Phe Phe His Thr Thr
355 360 365

Phe Leu Tyr Glu Phe Ser Lys Val Gln Ser Ser Asn Leu Asp Asn Tyr
370 375 380

Ser Gly Leu Leu Val Asn Asp Asp Tyr Leu Tyr Val Thr Lys Asp Asn
385 390 395 400

Ser Glu Phe Leu Asn Val Lys Leu Ser Asp Asn Phe Gln Asp Tyr Lys
405 410 415

Lys Ile Glu Leu Thr Asp Asn Asn Met Phe Ile Val Met Asn Asp Gly
420 425 430

Thr Leu Tyr Ala Cys Gly Leu Asn Asn Tyr Gly Gln Leu Gly Leu Gly
435 440 445

Asp Thr Val Asn Arg Ser Val Met Thr Lys Val Asp Ile Asp Asn Val
450 455 460

Leu Asp Ile Lys Gly Asn Gly Asn Ser Thr Phe Val Leu Lys Asn Asn
465 470 475 480

Gly Thr Leu Tyr Ser Cys Gly Tyr Asn Ser Ser Gly Ile Leu Gly Leu
485 490 495

Lys Asp Asn Thr Asn Arg Asn Ile Phe Thr Lys Ile Glu Ile Glu Asn
500 505 510

P108399_seqlist_ST25.txt

Ile Lys Glu Phe Cys Val Glu Ser Asn Tyr Ile Val Ala Leu Asn His
 515 520 525

Ser Lys Glu Leu Tyr Gly Trp Gly Asn Gln Ser Tyr Ile Val Tyr Gly
 530 535 540

Asp Asn Arg Asn Tyr Pro Tyr Lys Asp Thr Arg Val Ser Asn Val Glu
 545 550 555 560

Lys Ile Ala Thr Trp Ser Asp Thr Leu Tyr Ile Leu Asp Ser Thr Gly
 565 570 575

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

Ala Pro Ser Ser Ser Ser Thr Tyr Arg Glu Gly Gly Tyr Ile Asn Lys
 595 600 605

Asn Thr Ser Tyr Arg Thr Leu Glu Phe Tyr Asn Thr Ser Lys Thr Lys
 610 615 620

Leu Val Asn Leu Phe Ala Phe Tyr Asn Gly Cys Val Phe Val Asp Glu
 625 630 635 640

Asn Gly Leu Ala Tyr Cys Ile Gly Glu Asn Asn Ile Asn Phe Arg Gly
 645 650 655

Gly Ser Thr Thr Asn Glu Asn Asn Ser Leu Arg Phe Ile Asn Asn Ser
 660 665 670

Gly Val Tyr Tyr Thr Asn Thr Asp Gly Thr Asp Tyr Thr Cys Tyr Gln
 675 680 685

Trp Thr Tyr Lys Leu Ile Arg Cys Ser Ile Phe Asp Ser Pro Gln Asn
 690 695 700

Ile Ile Gly Asn Ser Lys Asn Ile Leu Tyr Leu Ser Lys Asn Asn Ser
 705 710 715 720

Thr Phe Lys Cys Thr Gly Asn Cys Ile Thr Tyr Gly Ile Asn Ser Gln
 725 730 735

Asn Trp Tyr Ser Tyr Phe Ser Asp Ser Ser Asn Gly Ala Ile Ala Leu
 740 745 750

Gly Asn Glu Phe Ile Leu Lys Asn Tyr Ser Gly Glu Cys Leu Leu Lys
 755 760 765

Gly Tyr Gly Lys Ala Thr Asn Gly Glu Phe Gly Asn Ser Thr Asn Ile
 770 775 780

P108399_seqlist_ST25.txt

Ser Ser Ile Ser Asn Tyr Asp Thr Gly Leu Lys Asp Ile Lys Asp Ile
785 790 795 800

Ile Val Lys Asn Asn Thr Val Val Val Val Asp Lys Asn Asn Asn Ile
805 810 815

Tyr Val Thr Gly Ala Asn Gln Phe Asn Lys Leu Gly Ile Gly Glu Tyr
820 825 830

Asn Asn Gln Pro Ile Arg Lys Phe Thr Asn Ile Thr Glu Gln Ser Asn
835 840 845

Ser Phe Ile Phe Met Asp Asp Ile Lys Glu Ile Thr Thr Ser Arg Asn
850 855 860

Thr Met Phe Ile Val Lys Asn Asp Gly Thr Ala Tyr Ala Thr Gly Asn
865 870 875 880

Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Ile Asn Arg Asn Lys
885 890 895

Phe Thr Gln Ile Asn Leu Asp Asn Ile Lys Lys Ile Ser Thr Ser Ile
900 905 910

Asp Gly Asn Thr Thr Phe Ala Ile Arg Asn Asp Gly Thr Leu Tyr Ser
915 920 925

Thr Gly Leu Asn Thr Lys Gly Gln Leu Gly Leu Gly Asp Ile Val Asn
930 935 940

Arg Asn Thr Phe Thr Lys Val Asn Ile Gln Asn Val Arg Asp Val Val
945 950 955 960

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

Ser Cys Gly Glu Asn Thr His Gly Gln Leu Gly Leu Gly Ser Glu Ser
980 985 990

Asn His Pro Asp Val Leu Thr Phe Thr Val Asn Asn Ile Thr Asn Val
995 1000 1005

Arg Asp Val Tyr Cys Ser Asp Thr Thr Thr Phe Ile Val Lys Asp
1010 1015 1020

Thr Asn Ile Ala Tyr Cys Cys Gly Tyr Asn Asn Asn Ser Gln Leu
1025 1030 1035

Gly Met Gly Asn Thr Thr Asp Gln Tyr Ser Phe Ile Lys Cys Met
1040 1045 1050

P108399_seqlist_ST25.txt

Glu Asn Val Lys Glu Val Ile Pro Asn Glu Ile Asn Thr Tyr Ile
 1055 1060 1065
 Ile Thr Ile Tyr Asn Thr Ala Tyr Ser Thr Gly Leu Asn Thr Asp
 1070 1075 1080
 Tyr Cys Leu Gly Leu Asn Ser Asn Ser Asn Gln Ser Ser Phe Ser
 1085 1090 1095
 Glu Ile Pro Ile Ser Asn Val Val Lys Val Ala Pro Asn Arg Asn
 1100 1105 1110
 Asn Ala Val Leu Leu Leu Thr Ser Glu Gly Asp Val Tyr Thr Ala
 1115 1120 1125
 Gly Lys Cys Ser Asn Gly Ser Gly Thr Gly Ser Glu Thr Pro Glu
 1130 1135 1140
 Lys Ile Lys Lys Ile Ala Ser Lys Ala Lys Asp Ile Gly Met Asn
 1145 1150 1155
 Tyr Arg Cys Gly His Tyr Val Ser Asp Asn Gly Asp Leu Tyr Gly
 1160 1165 1170
 Thr Gly Phe Asn Asp Cys Gly Gln Leu Gly Val Gly Asn Val Thr
 1175 1180 1185
 Lys Arg Asp Thr Phe Ile Lys Thr Asn Thr Arg Val Lys Lys Ile
 1190 1195 1200
 Leu Pro Leu Glu Tyr Ala Asn Ile Ala Ile Lys Asp Thr Asn Asp
 1205 1210 1215
 Ile Tyr Ile Cys Gly Leu Asn Asn Tyr Gly Gln Leu Gly Val Gly
 1220 1225 1230
 Asn Arg Tyr Asp Ser Arg Asn Asn Asp Asn Arg Ile Phe Asn Tyr
 1235 1240 1245
 Lys His Met Asn Phe Val Met Gly Asp Leu Thr Ser Ile Lys Asn
 1250 1255 1260
 Arg His Asn Phe Ile Leu Leu Asn Asn Lys Ile Val Ile Pro Thr
 1265 1270 1275
 Thr Lys Asp Ile Asp Tyr Gly Leu Val Leu Gly Asn Leu Tyr Lys
 1280 1285 1290
 Gly Asp Leu Tyr Thr Glu Leu Pro Tyr Glu Asp Ile Lys Glu Val
 1295 1300 1305

P108399_seqlist_ST25.txt

Ser Ile Ser Lys Thr His Ile Ile Ile Leu Leu Asn Asp Gly Thr
 1310 1315 1320
 Met Tyr Gly Cys Gly Thr Asn Tyr His Gly Glu Leu Leu Gln Asp
 1325 1330 1335
 Leu Ser Ile Asn Gln Val Asp Glu Phe Val Gln Ile Asn Val Ser
 1340 1345 1350
 Asp Val Lys His Val Ser Cys Gly Asp Asn Phe Thr Tyr Phe Ile
 1355 1360 1365
 Lys Ser Asp Asp Ser Leu Trp Ser Ile Gly Lys Asn Ser Glu Tyr
 1370 1375 1380
 Gln Leu Gly Ile Gly His Asn Asn Pro Val Thr Glu Leu Gln Arg
 1385 1390 1395
 Ile Thr Thr Ile Ser Ser Cys Lys Glu Val His Cys Gly Lys Asn
 1400 1405 1410
 Tyr Thr Leu Val Val Thr Thr Ser Asn Glu Leu Phe Val Gln Gly
 1415 1420 1425
 Tyr Asn Asp Lys Gly Ala Leu Gly Leu Gly Ser Asp Ser Glu Asn
 1430 1435 1440
 Thr Ile Ile Lys Phe Phe Thr Lys Ala Leu Thr Asp Ile Arg Glu
 1445 1450 1455
 Ile Lys Ser Tyr Gly Ser Asp His Ile Leu Val Leu Lys Asn Asp
 1460 1465 1470
 Asn Ser Val Trp Val Thr Gly Lys Asn Arg Asp Val Tyr Lys Ile
 1475 1480 1485
 Glu Gln Pro Val Glu Phe Leu Lys Glu Phe Thr Ile Val Pro Ile
 1490 1495 1500
 Ser Glu Asp Val Asn Thr Val Lys Asp Val Leu Ala Thr Asp Asn
 1505 1510 1515
 Thr Leu Tyr Ile Ile Ser Glu Val Gly Thr Thr Asn Ala Ala Ile
 1520 1525 1530
 Glu Ile Thr Glu Lys Ser Ile Ser Ser Ile Lys Ile Lys Ile Gln
 1535 1540 1545
 Asp Pro Asn Lys Asp Ile Ser Arg Ile Glu Met Leu Ile Asn Gly
 1550 1555 1560

P108399_seqlist_ST25.txt

Glu Ser Val Lys Ser Val Ser Asp Leu Ile Thr Glu Lys Ile Ser
1565 1570 1575

Phe Glu Val Pro Pro Asp Lys Ile Lys Ile Gly Glu Asn Lys Ile
1580 1585 1590

Leu Phe Arg Ala Tyr Cys Lys Gly Asp Asp Leu Tyr Ala Ser Leu
1595 1600 1605

Phe Ile Phe Lys Glu Ser Thr Gly Asn Ser Ile Ile Lys Asp Ser
1610 1615 1620

Tyr Val Met Ile Gly Asn Arg Met Tyr Lys Val Val Asn Thr Thr
1625 1630 1635

Ser Asn Glu Gln Asp Ile Thr Ile Thr Leu Asp Arg Gly Leu Glu
1640 1645 1650

Glu Asp Leu Asn Leu Gly Asp Pro Ile Tyr Gln Leu Ile Asn Lys
1655 1660 1665

Thr Lys Val Gln Val Lys Ile Asn Lys Ser Asp Leu Phe Lys Asp
1670 1675 1680

Met Lys Leu Val Glu Ile Lys Lys Ser Asp Ser Ser Tyr Gln Glu
1685 1690 1695

Ile Tyr Glu Leu Glu Glu Ala Asn Ile Lys Ser Ala Gln Pro Lys
1700 1705 1710

Ile Ile Val Glu Lys Gly Asp Lys Trp Thr Ala Ile Lys Arg Pro
1715 1720 1725

Ser Met Ile Phe Arg Tyr Asp Ala Glu Asn Asn Glu Pro Gln Ala
1730 1735 1740

<210> 6
<211> 24
<212> PRT
<213> Artificial

<220>
<223> Artificial peptide, E at position 1 side chain modified with
EDANS, K at position 10 side chain modified with Dabcyl

<400> 6

Glu Ser Gly Asp Asp Asp Asp Arg Gly Lys Thr Ser Phe Ala Glu Tyr
1 5 10 15

Trp Asn Leu Leu Ser Pro Gly Ser
20

<210> 7

P108399_seqlist_ST25.txt

<211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> p53 wt peptide

<400> 7

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Ser
 1 5 10

<210> 8
 <211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> mutated p53 peptide

<400> 8

Glu Thr Ala Ser Asp Leu Ala Lys Leu Ala Pro
 1 5 10

<210> 9
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide primer

<400> 9
 aacatcgtagc ggatagccac ggtagatcgtagc atcgtagtagc cccca

45

<210> 10
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide primer

<400> 10
 tatccgtacg atgttccgga ctacgccgga ggtgtt

36

<210> 11
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide primer

<400> 11
 ctgaaaatac aggtttttcgc taccgccccca atgttt

36

<210> 12
 <211> 33
 <212> DNA
 <213> Artificial

P108399_seqlist_ST25.txt

<220>
 <223> oligonucleotide primer
 <400> 12
 aacctgtatt ttcagtctgg ctatccgtac gat 33
 <210> 13
 <211> 33
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide primer
 <400> 13
 acgatcgta tcgtcaccac taccgcccc atg 33
 <210> 14
 <211> 42
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide primer
 <400> 14
 gacgatgacg atcgtggtgg tactagcttt gcagaatatt gg 42
 <210> 15
 <211> 42
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide primer
 <400> 15
 gcagaatatt ggaacctgtt gtctccggga tccgaagaga tt 42
 <210> 16
 <211> 42
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide primer
 <400> 16
 gacgatgacg atcgtggtgg taaaaagcgt tatagccgtg at 42
 <210> 17
 <211> 42
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide primer
 <400> 17
 tatagccgtg atcaactgtt agcgctggga tccgaagaga tt 42
 <210> 18

P108399_seqlist_ST25.txt

<211> 2057

<212> PRT

<213> Artificial

<220>

<223> Peptide biosensor HA-enterokinase

<400> 18

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

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

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

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

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

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

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

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

P108399_seqlist_ST25.txt

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Lys His
 275 280 285
 Trp Gly Gly Ser Asp Asp Asp Arg Gly Tyr Pro Tyr Asp Val Pro
 290 295 300
 Asp Tyr Ala Gly Gly Val Met Thr Met Lys Gln Asn Lys Leu Leu Gln
 305 310 315 320
 Arg Gly Ala Tyr Phe Asn Asp Lys Asn Ile Leu Ile Asp Asp Phe Asp
 325 330 335
 Lys Arg Tyr Asn Asp Tyr Asp Phe Val Glu Phe Phe Thr Gly Ile Ser
 340 345 350
 Asn Ser Thr Phe Gly Leu Lys Ser Asp Gly Asn Leu Tyr Ala Cys Gly
 355 360 365
 Asp Asn Thr Gly Phe Gln Leu Gly Leu Gly Lys Asp Ser Ser Glu Arg
 370 375 380
 Arg Met Phe Ser Lys Val Lys Ile Asp Asn Val Lys Tyr Val Ser Cys
 385 390 395 400
 Gly Ser Lys His Ser Val Ala Val Thr Lys Asp Gly Phe Ala Tyr Gly
 405 410 415
 Ala Gly Thr Ser Asn Val Gly Gln Leu Gly Val Ile Glu Ser Thr Val
 420 425 430
 Tyr Tyr Glu Phe Thr Lys Leu Pro Ile Asp Asp Val Lys Thr Val Ala
 435 440 445
 Cys Gly Tyr Asp Phe Thr Phe Val Leu Lys Asn Asp Gly Thr Leu Tyr
 450 455 460
 Ser Ala Gly Leu Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Asn
 465 470 475 480
 Asn Arg Val Thr Phe Thr Lys Val Asn Ile Asp Ser Val Lys Asp Val
 485 490 495
 Val Thr Tyr Asn Gln Ser Val Phe Ile Ile Lys Met Asp Gly Thr Ala
 500 505 510

P108399_seqlist_ST25.txt

His Ala Cys Gly Leu Asn Ser Asn Gly Gln Leu Gly Ile Asn Ser Thr
 515 520 525
 Leu Asn Lys Ser Val Phe Asn Lys Ile Glu Gly Met Asp Asn Val Lys
 530 535 540
 Gln Ile Ala Cys Gly Ser Ser His Thr Ile Leu Ile Lys Asn Asp Gly
 545 550 555 560
 Thr Met Tyr Thr Thr Gly Ser Asn Gly Tyr Gly Gln Leu Gly Thr Gly
 565 570 575
 Asn Asn Asn Asn Ser Ile Val Phe Thr Leu Ser Ser Ile Asn Asn Val
 580 585 590
 Lys Tyr Ala Ser Cys Gly Asn Asn His Thr Met Ile Leu Lys Tyr Asp
 595 600 605
 Asn Thr Leu Phe Ser Thr Gly Gln Asn Asn Tyr Gly Gln Leu Ala Asn
 610 615 620
 Ala Asn Lys Asp Val Ala Ser Arg Asn Thr Phe Val Lys Val Asn Val
 625 630 635 640
 Glu Asn Ile Lys Asp Ile Lys Cys Gly Ser Gln Phe Asn Phe Leu Ile
 645 650 655
 Asn Gly Ser Lys Glu Ile Phe Val Ser Gly Cys Asn Leu Ala Gly Gln
 660 665 670
 Leu Gly Ser Phe Phe His Thr Thr Phe Leu Tyr Glu Phe Ser Lys Val
 675 680 685
 Gln Ser Ser Asn Leu Asp Asn Tyr Ser Gly Leu Leu Val Asn Asp Asp
 690 695 700
 Tyr Leu Tyr Val Thr Lys Asp Asn Ser Glu Phe Leu Asn Val Lys Leu
 705 710 715 720
 Ser Asp Asn Phe Gln Asp Tyr Lys Lys Ile Glu Leu Thr Asp Asn Asn
 725 730 735
 Met Phe Ile Val Met Asn Asp Gly Thr Leu Tyr Ala Cys Gly Leu Asn
 740 745 750
 Asn Tyr Gly Gln Leu Gly Leu Gly Asp Thr Val Asn Arg Ser Val Met
 755 760 765
 Thr Lys Val Asp Ile Asp Asn Val Leu Asp Ile Lys Gly Asn Gly Asn
 770 775 780

P108399_seqlist_ST25.txt

Ser Thr Phe Val Leu Lys Asn Asn Gly Thr Leu Tyr Ser Cys Gly Tyr
785 790 795 800

Asn Ser Ser Gly Ile Leu Gly Leu Lys Asp Asn Thr Asn Arg Asn Ile
805 810 815

Phe Thr Lys Ile Glu Ile Glu Asn Ile Lys Glu Phe Cys Val Glu Ser
820 825 830

Asn Tyr Ile Val Ala Leu Asn His Ser Lys Glu Leu Tyr Gly Trp Gly
835 840 845

Asn Gln Ser Tyr Ile Val Tyr Gly Asp Asn Arg Asn Tyr Pro Tyr Lys
850 855 860

Asp Thr Arg Val Ser Asn Val Glu Lys Ile Ala Thr Trp Ser Asp Thr
865 870 875 880

Leu Tyr Ile Leu Asp Ser Thr Gly Ala Thr Lys Thr Ile Gly Tyr Ser
885 890 895

Tyr Asn Gly Ser Gly Gly Tyr Pro Ala Pro Ser Ser Ser Ser Thr Tyr
900 905 910

Arg Glu Gly Gly Tyr Ile Asn Lys Asn Thr Ser Tyr Arg Thr Leu Glu
915 920 925

Phe Tyr Asn Thr Ser Lys Thr Lys Leu Val Asn Leu Phe Ala Phe Tyr
930 935 940

Asn Gly Cys Val Phe Val Asp Glu Asn Gly Leu Ala Tyr Cys Ile Gly
945 950 955 960

Glu Asn Asn Ile Asn Phe Arg Gly Gly Ser Thr Thr Asn Glu Asn Asn
965 970 975

Ser Leu Arg Phe Ile Asn Asn Ser Gly Val Tyr Tyr Thr Asn Thr Asp
980 985 990

Gly Thr Asp Tyr Thr Cys Tyr Gln Trp Thr Tyr Lys Leu Ile Arg Cys
995 1000 1005

Ser Ile Phe Asp Ser Pro Gln Asn Ile Ile Gly Asn Ser Lys Asn
1010 1015 1020

Ile Leu Tyr Leu Ser Lys Asn Asn Ser Thr Phe Lys Cys Thr Gly
1025 1030 1035

Asn Cys Ile Thr Tyr Gly Ile Asn Ser Gln Asn Trp Tyr Ser Tyr
1040 1045 1050

P108399_seqlist_ST25.txt

Phe Ser Asp Ser Ser Asn Gly Ala Ile Ala Leu Gly Asn Glu Phe
 1055 1060 1065
 Ile Leu Lys Asn Tyr Ser Gly Glu Cys Leu Leu Lys Gly Tyr Gly
 1070 1075 1080
 Lys Ala Thr Asn Gly Glu Phe Gly Asn Ser Thr Asn Ile Ser Ser
 1085 1090 1095
 Ile Ser Asn Tyr Asp Thr Gly Leu Lys Asp Ile Lys Asp Ile Ile
 1100 1105 1110
 Val Lys Asn Asn Thr Val Val Val Val Asp Lys Asn Asn Asn Ile
 1115 1120 1125
 Tyr Val Thr Gly Ala Asn Gln Phe Asn Lys Leu Gly Ile Gly Glu
 1130 1135 1140
 Tyr Asn Asn Gln Pro Ile Arg Lys Phe Thr Asn Ile Thr Glu Gln
 1145 1150 1155
 Ser Asn Ser Phe Ile Phe Met Asp Asp Ile Lys Glu Ile Thr Thr
 1160 1165 1170
 Ser Arg Asn Thr Met Phe Ile Val Lys Asn Asp Gly Thr Ala Tyr
 1175 1180 1185
 Ala Thr Gly Asn Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr
 1190 1195 1200
 Ile Asn Arg Asn Lys Phe Thr Gln Ile Asn Leu Asp Asn Ile Lys
 1205 1210 1215
 Lys Ile Ser Thr Ser Ile Asp Gly Asn Thr Thr Phe Ala Ile Arg
 1220 1225 1230
 Asn Asp Gly Thr Leu Tyr Ser Thr Gly Leu Asn Thr Lys Gly Gln
 1235 1240 1245
 Leu Gly Leu Gly Asp Ile Val Asn Arg Asn Thr Phe Thr Lys Val
 1250 1255 1260
 Asn Ile Gln Asn Val Arg Asp Val Val Leu Gly Thr Thr His Ser
 1265 1270 1275
 His Ala Ile Lys Asp Asp Asn Thr Leu Tyr Ser Cys Gly Glu Asn
 1280 1285 1290
 Thr His Gly Gln Leu Gly Leu Gly Ser Glu Ser Asn His Pro Asp
 1295 1300 1305

P108399_seqlist_ST25.txt

Val Leu Thr Phe Thr Val Asn Asn Ile Thr Asn Val Arg Asp Val
 1310 1315 1320
 Tyr Cys Ser Asp Thr Thr Thr Phe Ile Val Lys Asp Thr Asn Ile
 1325 1330 1335
 Ala Tyr Cys Cys Gly Tyr Asn Asn Asn Ser Gln Leu Gly Met Gly
 1340 1345 1350
 Asn Thr Thr Asp Gln Tyr Ser Phe Ile Lys Cys Met Glu Asn Val
 1355 1360 1365
 Lys Glu Val Ile Pro Asn Glu Ile Asn Thr Tyr Ile Ile Thr Ile
 1370 1375 1380
 Tyr Asn Thr Ala Tyr Ser Thr Gly Leu Asn Thr Asp Tyr Cys Leu
 1385 1390 1395
 Gly Leu Asn Ser Asn Ser Asn Gln Ser Ser Phe Ser Glu Ile Pro
 1400 1405 1410
 Ile Ser Asn Val Val Lys Val Ala Pro Asn Arg Asn Asn Ala Val
 1415 1420 1425
 Leu Leu Leu Thr Ser Glu Gly Asp Val Tyr Thr Ala Gly Lys Cys
 1430 1435 1440
 Ser Asn Gly Ser Gly Thr Gly Ser Glu Thr Pro Glu Lys Ile Lys
 1445 1450 1455
 Lys Ile Ala Ser Lys Ala Lys Asp Ile Gly Met Asn Tyr Arg Cys
 1460 1465 1470
 Gly His Tyr Val Ser Asp Asn Gly Asp Leu Tyr Gly Thr Gly Phe
 1475 1480 1485
 Asn Asp Cys Gly Gln Leu Gly Val Gly Asn Val Thr Lys Arg Asp
 1490 1495 1500
 Thr Phe Ile Lys Thr Asn Thr Arg Val Lys Lys Ile Leu Pro Leu
 1505 1510 1515
 Glu Tyr Ala Asn Ile Ala Ile Lys Asp Thr Asn Asp Ile Tyr Ile
 1520 1525 1530
 Cys Gly Leu Asn Asn Tyr Gly Gln Leu Gly Val Gly Asn Arg Tyr
 1535 1540 1545
 Asp Ser Arg Asn Asn Asp Asn Arg Ile Phe Asn Tyr Lys His Met
 1550 1555 1560

P108399_seqlist_ST25.txt

Asn Phe Val Met Gly Asp Leu Thr Ser Ile Lys Asn Arg His Asn
 1565 1570 1575
 Phe Ile Leu Leu Asn Asn Lys Ile Val Ile Pro Thr Thr Lys Asp
 1580 1585 1590
 Ile Asp Tyr Gly Leu Val Leu Gly Asn Leu Tyr Lys Gly Asp Leu
 1595 1600 1605
 Tyr Thr Glu Leu Pro Tyr Glu Asp Ile Lys Glu Val Ser Ile Ser
 1610 1615 1620
 Lys Thr His Ile Ile Ile Leu Leu Asn Asp Gly Thr Met Tyr Gly
 1625 1630 1635
 Cys Gly Thr Asn Tyr His Gly Glu Leu Leu Gln Asp Leu Ser Ile
 1640 1645 1650
 Asn Gln Val Asp Glu Phe Val Gln Ile Asn Val Ser Asp Val Lys
 1655 1660 1665
 His Val Ser Cys Gly Asp Asn Phe Thr Tyr Phe Ile Lys Ser Asp
 1670 1675 1680
 Asp Ser Leu Trp Ser Ile Gly Lys Asn Ser Glu Tyr Gln Leu Gly
 1685 1690 1695
 Ile Gly His Asn Asn Pro Val Thr Glu Leu Gln Arg Ile Thr Thr
 1700 1705 1710
 Ile Ser Ser Cys Lys Glu Val His Cys Gly Lys Asn Tyr Thr Leu
 1715 1720 1725
 Val Val Thr Thr Ser Asn Glu Leu Phe Val Gln Gly Tyr Asn Asp
 1730 1735 1740
 Lys Gly Ala Leu Gly Leu Gly Ser Asp Ser Glu Asn Thr Ile Ile
 1745 1750 1755
 Lys Phe Phe Thr Lys Ala Leu Thr Asp Ile Arg Glu Ile Lys Ser
 1760 1765 1770
 Tyr Gly Ser Asp His Ile Leu Val Leu Lys Asn Asp Asn Ser Val
 1775 1780 1785
 Trp Val Thr Gly Lys Asn Arg Asp Val Tyr Lys Ile Glu Gln Pro
 1790 1795 1800
 Val Glu Phe Leu Lys Glu Phe Thr Ile Val Pro Ile Ser Glu Asp
 1805 1810 1815

P108399_seqlist_ST25.txt

Val Asn Thr Val Lys Asp Val Leu Ala Thr Asp Asn Thr Leu Tyr
 1820 1825 1830
 Ile Ile Ser Glu Val Gly Thr Thr Asn Ala Ala Ile Glu Ile Thr
 1835 1840 1845
 Glu Lys Ser Ile Ser Ser Ile Lys Ile Lys Ile Gln Asp Pro Asn
 1850 1855 1860
 Lys Asp Ile Ser Arg Ile Glu Met Leu Ile Asn Gly Glu Ser Val
 1865 1870 1875
 Lys Ser Val Ser Asp Leu Ile Thr Glu Lys Ile Ser Phe Glu Val
 1880 1885 1890
 Pro Pro Asp Lys Ile Lys Ile Gly Glu Asn Lys Ile Leu Phe Arg
 1895 1900 1905
 Ala Tyr Cys Lys Gly Asp Asp Leu Tyr Ala Ser Leu Phe Ile Phe
 1910 1915 1920
 Lys Glu Ser Thr Gly Asn Ser Ile Ile Lys Asp Ser Tyr Val Met
 1925 1930 1935
 Ile Gly Asn Arg Met Tyr Lys Val Val Asn Thr Thr Ser Asn Glu
 1940 1945 1950
 Gln Asp Ile Thr Ile Thr Leu Asp Arg Gly Leu Glu Glu Asp Leu
 1955 1960 1965
 Asn Leu Gly Asp Pro Ile Tyr Gln Leu Ile Asn Lys Thr Lys Val
 1970 1975 1980
 Gln Val Lys Ile Asn Lys Ser Asp Leu Phe Lys Asp Met Lys Leu
 1985 1990 1995
 Val Glu Ile Lys Lys Ser Asp Ser Ser Tyr Gln Glu Ile Tyr Glu
 2000 2005 2010
 Leu Glu Glu Ala Asn Ile Lys Ser Ala Gln Pro Lys Ile Ile Val
 2015 2020 2025
 Glu Lys Gly Asp Lys Trp Thr Ala Ile Lys Arg Pro Ser Met Ile
 2030 2035 2040
 Phe Arg Tyr Asp Ala Glu Asn Asn Glu Pro Gln Ala His Ala
 2045 2050 2055

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 <211> 2070
 <212> PRT

P108399_seqlist_ST25.txt

<213> Artificial

<220>

<223> Peptide biosensor mdm2-enterokinase

<400> 19

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 1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

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

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

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

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

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

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 Page 20

P108399_seqlist_ST25.txt

245

250

255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Lys His
 275 280 285

Trp Gly Gly Ser Gly Asp Asp Asp Asp Arg Gly Gly Thr Ser Phe Ala
 290 295 300

Glu Tyr Trp Asn Leu Leu Ser Pro Gly Ser Glu Glu Ile Gly Leu Gly
 305 310 315 320

Ala Gly Val Met Thr Met Lys Gln Asn Lys Leu Leu Gln Arg Gly Ala
 325 330 335

Tyr Phe Asn Asp Lys Asn Ile Leu Ile Asp Asp Phe Asp Lys Arg Tyr
 340 345 350

Asn Asp Tyr Asp Phe Val Glu Phe Phe Thr Gly Ile Ser Asn Ser Thr
 355 360 365

Phe Gly Leu Lys Ser Asp Gly Asn Leu Tyr Ala Cys Gly Asp Asn Thr
 370 375 380

Gly Phe Gln Leu Gly Leu Gly Lys Asp Ser Ser Glu Arg Arg Met Phe
 385 390 395 400

Ser Lys Val Lys Ile Asp Asn Val Lys Tyr Val Ser Cys Gly Ser Lys
 405 410 415

His Ser Val Ala Val Thr Lys Asp Gly Phe Ala Tyr Gly Ala Gly Thr
 420 425 430

Ser Asn Val Gly Gln Leu Gly Val Ile Glu Ser Thr Val Tyr Tyr Glu
 435 440 445

Phe Thr Lys Leu Pro Ile Asp Asp Val Lys Thr Val Ala Cys Gly Tyr
 450 455 460

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

Leu Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Asn Asn Arg Val
 485 490 495

Thr Phe Thr Lys Val Asn Ile Asp Ser Val Lys Asp Val Val Thr Tyr
 500 505 510

Asn Gln Ser Val Phe Ile Ile Lys Met Asp Gly Thr Ala His Ala Cys

P108399_seqlist_ST25.txt
520 525

515

Gly Leu Asn Ser Asn Gly Gln Leu Gly Ile Asn Ser Thr Leu Asn Lys
530 535 540

Ser Val Phe Asn Lys Ile Glu Gly Met Asp Asn Val Lys Gln Ile Ala
545 550 555 560

Cys Gly Ser Ser His Thr Ile Leu Ile Lys Asn Asp Gly Thr Met Tyr
565 570 575

Thr Thr Gly Ser Asn Gly Tyr Gly Gln Leu Gly Thr Gly Asn Asn Asn
580 585 590

Asn Ser Ile Val Phe Thr Leu Ser Ser Ile Asn Asn Val Lys Tyr Ala
595 600 605

Ser Cys Gly Asn Asn His Thr Met Ile Leu Lys Tyr Asp Asn Thr Leu
610 615 620

Phe Ser Thr Gly Gln Asn Asn Tyr Gly Gln Leu Ala Asn Ala Asn Lys
625 630 635 640

Asp Val Ala Ser Arg Asn Thr Phe Val Lys Val Asn Val Glu Asn Ile
645 650 655

Lys Asp Ile Lys Cys Gly Ser Gln Phe Asn Phe Leu Ile Asn Gly Ser
660 665 670

Lys Glu Ile Phe Val Ser Gly Cys Asn Leu Ala Gly Gln Leu Gly Ser
675 680 685

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

Asn Leu Asp Asn Tyr Ser Gly Leu Leu Val Asn Asp Asp Tyr Leu Tyr
705 710 715 720

Val Thr Lys Asp Asn Ser Glu Phe Leu Asn Val Lys Leu Ser Asp Asn
725 730 735

Phe Gln Asp Tyr Lys Lys Ile Glu Leu Thr Asp Asn Asn Met Phe Ile
740 745 750

Val Met Asn Asp Gly Thr Leu Tyr Ala Cys Gly Leu Asn Asn Tyr Gly
755 760 765

Gln Leu Gly Leu Gly Asp Thr Val Asn Arg Ser Val Met Thr Lys Val
770 775 780

Asp Ile Asp Asn Val Leu Asp Ile Lys Gly Asn Gly Asn Ser Thr Phe
Page 22

P108399_seqlist_ST25.txt

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785                               790          795          800
Val Leu Lys Asn Asn Gly Thr Leu Tyr Ser Cys Gly Tyr Asn Ser Ser
      805                      810
Gly Ile Leu Gly Leu Lys Asp Asn Thr Asn Arg Asn Ile Phe Thr Lys
      820                      825                      830
Ile Glu Ile Glu Asn Ile Lys Glu Phe Cys Val Glu Ser Asn Tyr Ile
      835                      840                      845
Val Ala Leu Asn His Ser Lys Glu Leu Tyr Gly Trp Gly Asn Gln Ser
      850                      855                      860
Tyr Ile Val Tyr Gly Asp Asn Arg Asn Tyr Pro Tyr Lys Asp Thr Arg
      865                      870                      875                      880
Val Ser Asn Val Glu Lys Ile Ala Thr Trp Ser Asp Thr Leu Tyr Ile
      885                      890                      895
Leu Asp Ser Thr Gly Ala Thr Lys Thr Ile Gly Tyr Ser Tyr Asn Gly
      900                      905                      910
Ser Gly Gly Tyr Pro Ala Pro Ser Ser Ser Ser Thr Tyr Arg Glu Gly
      915                      920                      925
Gly Tyr Ile Asn Lys Asn Thr Ser Tyr Arg Thr Leu Glu Phe Tyr Asn
      930                      935                      940
Thr Ser Lys Thr Lys Leu Val Asn Leu Phe Ala Phe Tyr Asn Gly Cys
      945                      950                      955                      960
Val Phe Val Asp Glu Asn Gly Leu Ala Tyr Cys Ile Gly Glu Asn Asn
      965                      970                      975
Ile Asn Phe Arg Gly Gly Ser Thr Thr Asn Glu Asn Asn Ser Leu Arg
      980                      985                      990
Phe Ile Asn Asn Ser Gly Val Tyr Tyr Thr Asn Thr Asp Gly Thr Asp
      995                      1000                      1005
Tyr Thr Cys Tyr Gln Trp Thr Tyr Lys Leu Ile Arg Cys Ser Ile
      1010                      1015                      1020
Phe Asp Ser Pro Gln Asn Ile Ile Gly Asn Ser Lys Asn Ile Leu
      1025                      1030                      1035
Tyr Leu Ser Lys Asn Asn Ser Thr Phe Lys Cys Thr Gly Asn Cys
      1040                      1045                      1050
Ile Thr Tyr Gly Ile Asn Ser Gln Asn Trp Tyr Ser Tyr Phe Ser

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P108399_seq1list_ST25.txt

1055

1060

1065

Asp Ser Ser Asn Gly Ala Ile Ala Leu Gly Asn Glu Phe Ile Leu
1070 1075 1080

Lys Asn Tyr Ser Gly Glu Cys Leu Leu Lys Gly Tyr Gly Lys Ala
1085 1090 1095

Thr Asn Gly Glu Phe Gly Asn Ser Thr Asn Ile Ser Ser Ile Ser
1100 1105 1110

Asn Tyr Asp Thr Gly Leu Lys Asp Ile Lys Asp Ile Ile Val Lys
1115 1120 1125

Asn Asn Thr Val Val Val Val Asp Lys Asn Asn Asn Ile Tyr Val
1130 1135 1140

Thr Gly Ala Asn Gln Phe Asn Lys Leu Gly Ile Gly Glu Tyr Asn
1145 1150 1155

Asn Gln Pro Ile Arg Lys Phe Thr Asn Ile Thr Glu Gln Ser Asn
1160 1165 1170

Ser Phe Ile Phe Met Asp Asp Ile Lys Glu Ile Thr Thr Ser Arg
1175 1180 1185

Asn Thr Met Phe Ile Val Lys Asn Asp Gly Thr Ala Tyr Ala Thr
1190 1195 1200

Gly Asn Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Ile Asn
1205 1210 1215

Arg Asn Lys Phe Thr Gln Ile Asn Leu Asp Asn Ile Lys Lys Ile
1220 1225 1230

Ser Thr Ser Ile Asp Gly Asn Thr Thr Phe Ala Ile Arg Asn Asp
1235 1240 1245

Gly Thr Leu Tyr Ser Thr Gly Leu Asn Thr Lys Gly Gln Leu Gly
1250 1255 1260

Leu Gly Asp Ile Val Asn Arg Asn Thr Phe Thr Lys Val Asn Ile
1265 1270 1275

Gln Asn Val Arg Asp Val Val Leu Gly Thr Thr His Ser His Ala
1280 1285 1290

Ile Lys Asp Asp Asn Thr Leu Tyr Ser Cys Gly Glu Asn Thr His
1295 1300 1305

Gly Gln Leu Gly Leu Gly Ser Glu Ser Asn His Pro Asp Val Leu

Page 25

P108399_seq1list_ST25.txt

	1565						1570						1575					
Val	Met 1580	Gly	Asp	Leu	Thr	Ser 1585	Ile	Lys	Asn	Arg	His 1590	Asn	Phe	Ile				
Leu	Leu 1595	Asn	Asn	Lys	Ile	Val 1600	Ile	Pro	Thr	Thr	Lys 1605	Asp	Ile	Asp				
Tyr	Gly 1610	Leu	Val	Leu	Gly	Asn 1615	Leu	Tyr	Lys	Gly	Asp 1620	Leu	Tyr	Thr				
Glu	Leu 1625	Pro	Tyr	Glu	Asp	Ile 1630	Lys	Glu	Val	Ser	Ile 1635	Ser	Lys	Thr				
His	Ile 1640	Ile	Ile	Leu	Leu	Asn 1645	Asp	Gly	Thr	Met	Tyr 1650	Gly	Cys	Gly				
Thr	Asn 1655	Tyr	His	Gly	Glu	Leu 1660	Leu	Gln	Asp	Leu	Ser 1665	Ile	Asn	Gln				
Val	Asp 1670	Glu	Phe	Val	Gln	Ile 1675	Asn	Val	Ser	Asp	Val 1680	Lys	His	Val				
Ser	Cys 1685	Gly	Asp	Asn	Phe	Thr 1690	Tyr	Phe	Ile	Lys	Ser 1695	Asp	Asp	Ser				
Leu	Trp 1700	Ser	Ile	Gly	Lys	Asn 1705	Ser	Glu	Tyr	Gln	Leu 1710	Gly	Ile	Gly				
His	Asn 1715	Asn	Pro	Val	Thr	Glu 1720	Leu	Gln	Arg	Ile	Thr 1725	Thr	Ile	Ser				
Ser	Cys 1730	Lys	Glu	Val	His	Cys 1735	Gly	Lys	Asn	Tyr	Thr 1740	Leu	Val	Val				
Thr	Thr 1745	Ser	Asn	Glu	Leu	Phe 1750	Val	Gln	Gly	Tyr	Asn 1755	Asp	Lys	Gly				
Ala	Leu 1760	Gly	Leu	Gly	Ser	Asp 1765	Ser	Glu	Asn	Thr	Ile 1770	Ile	Lys	Phe				
Phe	Thr 1775	Lys	Ala	Leu	Thr	Asp 1780	Ile	Arg	Glu	Ile	Lys 1785	Ser	Tyr	Gly				
Ser	Asp 1790	His	Ile	Leu	Val	Leu 1795	Lys	Asn	Asp	Asn	Ser 1800	Val	Trp	Val				
Thr	Gly 1805	Lys	Asn	Arg	Asp	Val 1810	Tyr	Lys	Ile	Glu	Gln 1815	Pro	Val	Glu				
Phe	Leu	Lys	Glu	Phe	Thr	Ile	Val	Pro	Ile	Ser	Glu	Asp	Val	Asn				

P108399_seqlist_ST25.txt

1820 1825 1830
 Thr Val Lys Asp Val Leu Ala Thr Asp Asn Thr Leu Tyr Ile Ile
 1835 1840 1845
 Ser Glu Val Gly Thr Thr Asn Ala Ala Ile Glu Ile Thr Glu Lys
 1850 1855 1860
 Ser Ile Ser Ser Ile Lys Ile Lys Ile Gln Asp Pro Asn Lys Asp
 1865 1870 1875
 Ile Ser Arg Ile Glu Met Leu Ile Asn Gly Glu Ser Val Lys Ser
 1880 1885 1890
 Val Ser Asp Leu Ile Thr Glu Lys Ile Ser Phe Glu Val Pro Pro
 1895 1900 1905
 Asp Lys Ile Lys Ile Gly Glu Asn Lys Ile Leu Phe Arg Ala Tyr
 1910 1915 1920
 Cys Lys Gly Asp Asp Leu Tyr Ala Ser Leu Phe Ile Phe Lys Glu
 1925 1930 1935
 Ser Thr Gly Asn Ser Ile Ile Lys Asp Ser Tyr Val Met Ile Gly
 1940 1945 1950
 Asn Arg Met Tyr Lys Val Val Asn Thr Thr Ser Asn Glu Gln Asp
 1955 1960 1965
 Ile Thr Ile Thr Leu Asp Arg Gly Leu Glu Glu Asp Leu Asn Leu
 1970 1975 1980
 Gly Asp Pro Ile Tyr Gln Leu Ile Asn Lys Thr Lys Val Gln Val
 1985 1990 1995
 Lys Ile Asn Lys Ser Asp Leu Phe Lys Asp Met Lys Leu Val Glu
 2000 2005 2010
 Ile Lys Lys Ser Asp Ser Ser Tyr Gln Glu Ile Tyr Glu Leu Glu
 2015 2020 2025
 Glu Ala Asn Ile Lys Ser Ala Gln Pro Lys Ile Ile Val Glu Lys
 2030 2035 2040
 Gly Asp Lys Trp Thr Ala Ile Lys Arg Pro Ser Met Ile Phe Arg
 2045 2050 2055
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 2060 2065 2070

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P108399_seqlist_ST25.txt

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 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

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

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

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

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
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Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

P108399_seqlist_ST25.txt

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Lys His
275 280 285

Trp Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Gly Tyr Pro Tyr Asp
290 295 300

Val Pro Asp Tyr Ala Ala Gly Val Met Thr Met Lys Gln Asn Lys Leu
305 310 315 320

Leu Gln Arg Gly Ala Tyr Phe Asn Asp Lys Asn Ile Leu Ile Asp Asp
325 330 335

Phe Asp Lys Arg Tyr Asn Asp Tyr Asp Phe Val Glu Phe Phe Thr Gly
340 345 350

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

Cys Gly Asp Asn Thr Gly Phe Gln Leu Gly Leu Gly Lys Asp Ser Ser
370 375 380

Glu Arg Arg Met Phe Ser Lys Val Lys Ile Asp Asn Val Lys Tyr Val
385 390 395 400

Ser Cys Gly Ser Lys His Ser Val Ala Val Thr Lys Asp Gly Phe Ala
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Tyr Gly Ala Gly Thr Ser Asn Val Gly Gln Leu Gly Val Ile Glu Ser
420 425 430

Thr Val Tyr Tyr Glu Phe Thr Lys Leu Pro Ile Asp Asp Val Lys Thr
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Val Ala Cys Gly Tyr Asp Phe Thr Phe Val Leu Lys Asn Asp Gly Thr
450 455 460

Leu Tyr Ser Ala Gly Leu Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp
465 470 475 480

Thr Asn Asn Arg Val Thr Phe Thr Lys Val Asn Ile Asp Ser Val Lys
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Asp Val Val Thr Tyr Asn Gln Ser Val Phe Ile Ile Lys Met Asp Gly
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P108399_seqlist_ST25.txt

Thr Ala His Ala Cys Gly Leu Asn Ser Asn Gly Gln Leu Gly Ile Asn
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 Ser Thr Leu Asn Lys Ser Val Phe Asn Lys Ile Glu Gly Met Asp Asn
 530 535 540
 Val Lys Gln Ile Ala Cys Gly Ser Ser His Thr Ile Leu Ile Lys Asn
 545 550 555 560
 Asp Gly Thr Met Tyr Thr Thr Gly Ser Asn Gly Tyr Gly Gln Leu Gly
 565 570 575
 Thr Gly Asn Asn Asn Asn Ser Ile Val Phe Thr Leu Ser Ser Ile Asn
 580 585 590
 Asn Val Lys Tyr Ala Ser Cys Gly Asn Asn His Thr Met Ile Leu Lys
 595 600 605
 Tyr Asp Asn Thr Leu Phe Ser Thr Gly Gln Asn Asn Tyr Gly Gln Leu
 610 615 620
 Ala Asn Ala Asn Lys Asp Val Ala Ser Arg Asn Thr Phe Val Lys Val
 625 630 635 640
 Asn Val Glu Asn Ile Lys Asp Ile Lys Cys Gly Ser Gln Phe Asn Phe
 645 650 655
 Leu Ile Asn Gly Ser Lys Glu Ile Phe Val Ser Gly Cys Asn Leu Ala
 660 665 670
 Gly Gln Leu Gly Ser Phe Phe His Thr Thr Phe Leu Tyr Glu Phe Ser
 675 680 685
 Lys Val Gln Ser Ser Asn Leu Asp Asn Tyr Ser Gly Leu Leu Val Asn
 690 695 700
 Asp Asp Tyr Leu Tyr Val Thr Lys Asp Asn Ser Glu Phe Leu Asn Val
 705 710 715 720
 Lys Leu Ser Asp Asn Phe Gln Asp Tyr Lys Lys Ile Glu Leu Thr Asp
 725 730 735
 Asn Asn Met Phe Ile Val Met Asn Asp Gly Thr Leu Tyr Ala Cys Gly
 740 745 750
 Leu Asn Asn Tyr Gly Gln Leu Gly Leu Gly Asp Thr Val Asn Arg Ser
 755 760 765
 Val Met Thr Lys Val Asp Ile Asp Asn Val Leu Asp Ile Lys Gly Asn
 770 775 780

P108399_seqlist_ST25.txt

Gly Asn Ser Thr Phe Val Leu Lys Asn Asn Gly Thr Leu Tyr Ser Cys
785 790 795 800

Gly Tyr Asn Ser Ser Gly Ile Leu Gly Leu Lys Asp Asn Thr Asn Arg
805 810 815

Asn Ile Phe Thr Lys Ile Glu Ile Glu Asn Ile Lys Glu Phe Cys Val
820 825 830

Glu Ser Asn Tyr Ile Val Ala Leu Asn His Ser Lys Glu Leu Tyr Gly
835 840 845

Trp Gly Asn Gln Ser Tyr Ile Val Tyr Gly Asp Asn Arg Asn Tyr Pro
850 855 860

Tyr Lys Asp Thr Arg Val Ser Asn Val Glu Lys Ile Ala Thr Trp Ser
865 870 875 880

Asp Thr Leu Tyr Ile Leu Asp Ser Thr Gly Ala Thr Lys Thr Ile Gly
885 890 895

Tyr Ser Tyr Asn Gly Ser Gly Gly Tyr Pro Ala Pro Ser Ser Ser Ser
900 905 910

Thr Tyr Arg Glu Gly Gly Tyr Ile Asn Lys Asn Thr Ser Tyr Arg Thr
915 920 925

Leu Glu Phe Tyr Asn Thr Ser Lys Thr Lys Leu Val Asn Leu Phe Ala
930 935 940

Phe Tyr Asn Gly Cys Val Phe Val Asp Glu Asn Gly Leu Ala Tyr Cys
945 950 955 960

Ile Gly Glu Asn Asn Ile Asn Phe Arg Gly Gly Ser Thr Thr Asn Glu
965 970 975

Asn Asn Ser Leu Arg Phe Ile Asn Asn Ser Gly Val Tyr Tyr Thr Asn
980 985 990

Thr Asp Gly Thr Asp Tyr Thr Cys Tyr Gln Trp Thr Tyr Lys Leu Ile
995 1000 1005

Arg Cys Ser Ile Phe Asp Ser Pro Gln Asn Ile Ile Gly Asn Ser
1010 1015 1020

Lys Asn Ile Leu Tyr Leu Ser Lys Asn Asn Ser Thr Phe Lys Cys
1025 1030 1035

Thr Gly Asn Cys Ile Thr Tyr Gly Ile Asn Ser Gln Asn Trp Tyr
1040 1045 1050

P108399_seqlist_ST25.txt

Ser Tyr Phe Ser Asp Ser Ser Asn Gly Ala Ile Ala Leu Gly Asn
 1055 1060 1065
 Glu Phe Ile Leu Lys Asn Tyr Ser Gly Glu Cys Leu Leu Lys Gly
 1070 1075 1080
 Tyr Gly Lys Ala Thr Asn Gly Glu Phe Gly Asn Ser Thr Asn Ile
 1085 1090 1095
 Ser Ser Ile Ser Asn Tyr Asp Thr Gly Leu Lys Asp Ile Lys Asp
 1100 1105 1110
 Ile Ile Val Lys Asn Asn Thr Val Val Val Val Asp Lys Asn Asn
 1115 1120 1125
 Asn Ile Tyr Val Thr Gly Ala Asn Gln Phe Asn Lys Leu Gly Ile
 1130 1135 1140
 Gly Glu Tyr Asn Asn Gln Pro Ile Arg Lys Phe Thr Asn Ile Thr
 1145 1150 1155
 Glu Gln Ser Asn Ser Phe Ile Phe Met Asp Asp Ile Lys Glu Ile
 1160 1165 1170
 Thr Thr Ser Arg Asn Thr Met Phe Ile Val Lys Asn Asp Gly Thr
 1175 1180 1185
 Ala Tyr Ala Thr Gly Asn Asn Ser Ser Gly Gln Leu Gly Leu Gly
 1190 1195 1200
 Asp Thr Ile Asn Arg Asn Lys Phe Thr Gln Ile Asn Leu Asp Asn
 1205 1210 1215
 Ile Lys Lys Ile Ser Thr Ser Ile Asp Gly Asn Thr Thr Phe Ala
 1220 1225 1230
 Ile Arg Asn Asp Gly Thr Leu Tyr Ser Thr Gly Leu Asn Thr Lys
 1235 1240 1245
 Gly Gln Leu Gly Leu Gly Asp Ile Val Asn Arg Asn Thr Phe Thr
 1250 1255 1260
 Lys Val Asn Ile Gln Asn Val Arg Asp Val Val Leu Gly Thr Thr
 1265 1270 1275
 His Ser His Ala Ile Lys Asp Asp Asn Thr Leu Tyr Ser Cys Gly
 1280 1285 1290
 Glu Asn Thr His Gly Gln Leu Gly Leu Gly Ser Glu Ser Asn His
 1295 1300 1305

P108399_seqlist_ST25.txt

Pro Asp Val Leu Thr Phe Thr Val Asn Asn Ile Thr Asn Val Arg
 1310 1315 1320
 Asp Val Tyr Cys Ser Asp Thr Thr Thr Phe Ile Val Lys Asp Thr
 1325 1330 1335
 Asn Ile Ala Tyr Cys Cys Gly Tyr Asn Asn Asn Ser Gln Leu Gly
 1340 1345 1350
 Met Gly Asn Thr Thr Asp Gln Tyr Ser Phe Ile Lys Cys Met Glu
 1355 1360 1365
 Asn Val Lys Glu Val Ile Pro Asn Glu Ile Asn Thr Tyr Ile Ile
 1370 1375 1380
 Thr Ile Tyr Asn Thr Ala Tyr Ser Thr Gly Leu Asn Thr Asp Tyr
 1385 1390 1395
 Cys Leu Gly Leu Asn Ser Asn Ser Asn Gln Ser Ser Phe Ser Glu
 1400 1405 1410
 Ile Pro Ile Ser Asn Val Val Lys Val Ala Pro Asn Arg Asn Asn
 1415 1420 1425
 Ala Val Leu Leu Leu Thr Ser Glu Gly Asp Val Tyr Thr Ala Gly
 1430 1435 1440
 Lys Cys Ser Asn Gly Ser Gly Thr Gly Ser Glu Thr Pro Glu Lys
 1445 1450 1455
 Ile Lys Lys Ile Ala Ser Lys Ala Lys Asp Ile Gly Met Asn Tyr
 1460 1465 1470
 Arg Cys Gly His Tyr Val Ser Asp Asn Gly Asp Leu Tyr Gly Thr
 1475 1480 1485
 Gly Phe Asn Asp Cys Gly Gln Leu Gly Val Gly Asn Val Thr Lys
 1490 1495 1500
 Arg Asp Thr Phe Ile Lys Thr Asn Thr Arg Val Lys Lys Ile Leu
 1505 1510 1515
 Pro Leu Glu Tyr Ala Asn Ile Ala Ile Lys Asp Thr Asn Asp Ile
 1520 1525 1530
 Tyr Ile Cys Gly Leu Asn Asn Tyr Gly Gln Leu Gly Val Gly Asn
 1535 1540 1545
 Arg Tyr Asp Ser Arg Asn Asn Asp Asn Arg Ile Phe Asn Tyr Lys
 1550 1555 1560

P108399_seqlist_ST25.txt

His Met Asn Phe Val Met Gly Asp Leu Thr Ser Ile Lys Asn Arg
 1565 1570 1575
 His Asn Phe Ile Leu Leu Asn Asn Lys Ile Val Ile Pro Thr Thr
 1580 1585 1590
 Lys Asp Ile Asp Tyr Gly Leu Val Leu Gly Asn Leu Tyr Lys Gly
 1595 1600 1605
 Asp Leu Tyr Thr Glu Leu Pro Tyr Glu Asp Ile Lys Glu Val Ser
 1610 1615 1620
 Ile Ser Lys Thr His Ile Ile Ile Leu Leu Asn Asp Gly Thr Met
 1625 1630 1635
 Tyr Gly Cys Gly Thr Asn Tyr His Gly Glu Leu Leu Gln Asp Leu
 1640 1645 1650
 Ser Ile Asn Gln Val Asp Glu Phe Val Gln Ile Asn Val Ser Asp
 1655 1660 1665
 Val Lys His Val Ser Cys Gly Asp Asn Phe Thr Tyr Phe Ile Lys
 1670 1675 1680
 Ser Asp Asp Ser Leu Trp Ser Ile Gly Lys Asn Ser Glu Tyr Gln
 1685 1690 1695
 Leu Gly Ile Gly His Asn Asn Pro Val Thr Glu Leu Gln Arg Ile
 1700 1705 1710
 Thr Thr Ile Ser Ser Cys Lys Glu Val His Cys Gly Lys Asn Tyr
 1715 1720 1725
 Thr Leu Val Val Thr Thr Ser Asn Glu Leu Phe Val Gln Gly Tyr
 1730 1735 1740
 Asn Asp Lys Gly Ala Leu Gly Leu Gly Ser Asp Ser Glu Asn Thr
 1745 1750 1755
 Ile Ile Lys Phe Phe Thr Lys Ala Leu Thr Asp Ile Arg Glu Ile
 1760 1765 1770
 Lys Ser Tyr Gly Ser Asp His Ile Leu Val Leu Lys Asn Asp Asn
 1775 1780 1785
 Ser Val Trp Val Thr Gly Lys Asn Arg Asp Val Tyr Lys Ile Glu
 1790 1795 1800
 Gln Pro Val Glu Phe Leu Lys Glu Phe Thr Ile Val Pro Ile Ser
 1805 1810 1815

P108399_seqlist_ST25.txt

Glu Asp Val Asn Thr Val Lys Asp Val Leu Ala Thr Asp Asn Thr
 1820 1825 1830
 Leu Tyr Ile Ile Ser Glu Val Gly Thr Thr Asn Ala Ala Ile Glu
 1835 1840 1845
 Ile Thr Glu Lys Ser Ile Ser Ser Ile Lys Ile Lys Ile Gln Asp
 1850 1855 1860
 Pro Asn Lys Asp Ile Ser Arg Ile Glu Met Leu Ile Asn Gly Glu
 1865 1870 1875
 Ser Val Lys Ser Val Ser Asp Leu Ile Thr Glu Lys Ile Ser Phe
 1880 1885 1890
 Glu Val Pro Pro Asp Lys Ile Lys Ile Gly Glu Asn Lys Ile Leu
 1895 1900 1905
 Phe Arg Ala Tyr Cys Lys Gly Asp Asp Leu Tyr Ala Ser Leu Phe
 1910 1915 1920
 Ile Phe Lys Glu Ser Thr Gly Asn Ser Ile Ile Lys Asp Ser Tyr
 1925 1930 1935
 Val Met Ile Gly Asn Arg Met Tyr Lys Val Val Asn Thr Thr Ser
 1940 1945 1950
 Asn Glu Gln Asp Ile Thr Ile Thr Leu Asp Arg Gly Leu Glu Glu
 1955 1960 1965
 Asp Leu Asn Leu Gly Asp Pro Ile Tyr Gln Leu Ile Asn Lys Thr
 1970 1975 1980
 Lys Val Gln Val Lys Ile Asn Lys Ser Asp Leu Phe Lys Asp Met
 1985 1990 1995
 Lys Leu Val Glu Ile Lys Lys Ser Asp Ser Ser Tyr Gln Glu Ile
 2000 2005 2010
 Tyr Glu Leu Glu Glu Ala Asn Ile Lys Ser Ala Gln Pro Lys Ile
 2015 2020 2025
 Ile Val Glu Lys Gly Asp Lys Trp Thr Ala Ile Lys Arg Pro Ser
 2030 2035 2040
 Met Ile Phe Arg Tyr Asp Ala Glu Asn Asn Glu Pro Gln Ala His
 2045 2050 2055
 Ala

P108399_seqlist_ST25.txt

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 <211> 2069
 <212> PRT
 <213> Artificial

<220>
 <223> Peptide biosensor eiF4E-enterokinase

<400> 21

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 1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

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

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

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

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

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

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 Page 36

P108399_seq1ist_ST25.txt

225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Lys His
 275 280 285
 Trp Gly Gly Ser Gly Asp Asp Asp Asp Arg Gly Lys Lys Arg Tyr Ser
 290 295 300
 Arg Asp Gln Leu Leu Ala Leu Gly Ser Glu Glu Ile Gly Leu Gly Ala
 305 310 315 320
 Gly Val Met Thr Met Lys Gln Asn Lys Leu Leu Gln Arg Gly Ala Tyr
 325 330 335
 Phe Asn Asp Lys Asn Ile Leu Ile Asp Asp Phe Asp Lys Arg Tyr Asn
 340 345 350
 Asp Tyr Asp Phe Val Glu Phe Phe Thr Gly Ile Ser Asn Ser Thr Phe
 355 360 365
 Gly Leu Lys Ser Asp Gly Asn Leu Tyr Ala Cys Gly Asp Asn Thr Gly
 370 375 380
 Phe Gln Leu Gly Leu Gly Lys Asp Ser Ser Glu Arg Arg Met Phe Ser
 385 390 395 400
 Lys Val Lys Ile Asp Asn Val Lys Tyr Val Ser Cys Gly Ser Lys His
 405 410 415
 Ser Val Ala Val Thr Lys Asp Gly Phe Ala Tyr Gly Ala Gly Thr Ser
 420 425 430
 Asn Val Gly Gln Leu Gly Val Ile Glu Ser Thr Val Tyr Tyr Glu Phe
 435 440 445
 Thr Lys Leu Pro Ile Asp Asp Val Lys Thr Val Ala Cys Gly Tyr Asp
 450 455 460
 Phe Thr Phe Val Leu Lys Asn Asp Gly Thr Leu Tyr Ser Ala Gly Leu
 465 470 475 480
 Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Asn Asn Arg Val Thr
 485 490 495
 Phe Thr Lys Val Asn Ile Asp Ser Val Lys Asp Val Val Thr Tyr Asn

P108399_seqlist_ST25.txt

500

505

510

Gln Ser Val Phe Ile Ile Lys Met Asp Gly Thr Ala His Ala Cys Gly
 515 520 525
 Leu Asn Ser Asn Gly Gln Leu Gly Ile Asn Ser Thr Leu Asn Lys Ser
 530 535 540
 Val Phe Asn Lys Ile Glu Gly Met Asp Asn Val Lys Gln Ile Ala Cys
 545 550 555 560
 Gly Ser Ser His Thr Ile Leu Ile Lys Asn Asp Gly Thr Met Tyr Thr
 565 570 575
 Thr Gly Ser Asn Gly Tyr Gly Gln Leu Gly Thr Gly Asn Asn Asn Asn
 580 585 590
 Ser Ile Val Phe Thr Leu Ser Ser Ile Asn Asn Val Lys Tyr Ala Ser
 595 600 605
 Cys Gly Asn Asn His Thr Met Ile Leu Lys Tyr Asp Asn Thr Leu Phe
 610 615 620
 Ser Thr Gly Gln Asn Asn Tyr Gly Gln Leu Ala Asn Ala Asn Lys Asp
 625 630 635 640
 Val Ala Ser Arg Asn Thr Phe Val Lys Val Asn Val Glu Asn Ile Lys
 645 650 655
 Asp Ile Lys Cys Gly Ser Gln Phe Asn Phe Leu Ile Asn Gly Ser Lys
 660 665 670
 Glu Ile Phe Val Ser Gly Cys Asn Leu Ala Gly Gln Leu Gly Ser Phe
 675 680 685
 Phe His Thr Thr Phe Leu Tyr Glu Phe Ser Lys Val Gln Ser Ser Asn
 690 695 700
 Leu Asp Asn Tyr Ser Gly Leu Leu Val Asn Asp Asp Tyr Leu Tyr Val
 705 710 715 720
 Thr Lys Asp Asn Ser Glu Phe Leu Asn Val Lys Leu Ser Asp Asn Phe
 725 730 735
 Gln Asp Tyr Lys Lys Ile Glu Leu Thr Asp Asn Asn Met Phe Ile Val
 740 745 750
 Met Asn Asp Gly Thr Leu Tyr Ala Cys Gly Leu Asn Asn Tyr Gly Gln
 755 760 765
 Leu Gly Leu Gly Asp Thr Val Asn Arg Ser Val Met Thr Lys Val Asp

P108399_seqlist_ST25.txt

770

775

780

Ile Asp Asn Val Leu Asp Ile Lys Gly Asn Gly Asn Ser Thr Phe Val
 785 790 795 800

Leu Lys Asn Asn Gly Thr Leu Tyr Ser Cys Gly Tyr Asn Ser Ser Gly
 805 810 815

Ile Leu Gly Leu Lys Asp Asn Thr Asn Arg Asn Ile Phe Thr Lys Ile
 820 825 830

Glu Ile Glu Asn Ile Lys Glu Phe Cys Val Glu Ser Asn Tyr Ile Val
 835 840 845

Ala Leu Asn His Ser Lys Glu Leu Tyr Gly Trp Gly Asn Gln Ser Tyr
 850 855 860

Ile Val Tyr Gly Asp Asn Arg Asn Tyr Pro Tyr Lys Asp Thr Arg Val
 865 870 875 880

Ser Asn Val Glu Lys Ile Ala Thr Trp Ser Asp Thr Leu Tyr Ile Leu
 885 890 895

Asp Ser Thr Gly Ala Thr Lys Thr Ile Gly Tyr Ser Tyr Asn Gly Ser
 900 905 910

Gly Gly Tyr Pro Ala Pro Ser Ser Ser Thr Tyr Arg Glu Gly Gly
 915 920 925

Tyr Ile Asn Lys Asn Thr Ser Tyr Arg Thr Leu Glu Phe Tyr Asn Thr
 930 935 940

Ser Lys Thr Lys Leu Val Asn Leu Phe Ala Phe Tyr Asn Gly Cys Val
 945 950 955 960

Phe Val Asp Glu Asn Gly Leu Ala Tyr Cys Ile Gly Glu Asn Asn Ile
 965 970 975

Asn Phe Arg Gly Gly Ser Thr Thr Asn Glu Asn Asn Ser Leu Arg Phe
 980 985 990

Ile Asn Asn Ser Gly Val Tyr Tyr Thr Asn Thr Asp Gly Thr Asp Tyr
 995 1000 1005

Thr Cys Tyr Gln Trp Thr Tyr Lys Leu Ile Arg Cys Ser Ile Phe
 1010 1015 1020

Asp Ser Pro Gln Asn Ile Ile Gly Asn Ser Lys Asn Ile Leu Tyr
 1025 1030 1035

Leu Ser Lys Asn Asn Ser Thr Phe Lys Cys Thr Gly Asn Cys Ile

P108399_seqlist_ST25.txt

1040 1045 1050
 Thr Tyr Gly Ile Asn Ser Gln Asn Trp Tyr Ser Tyr Phe Ser Asp
 1055 1060 1065
 Ser Ser Asn Gly Ala Ile Ala Leu Gly Asn Glu Phe Ile Leu Lys
 1070 1075 1080
 Asn Tyr Ser Gly Glu Cys Leu Leu Lys Gly Tyr Gly Lys Ala Thr
 1085 1090 1095
 Asn Gly Glu Phe Gly Asn Ser Thr Asn Ile Ser Ser Ile Ser Asn
 1100 1105 1110
 Tyr Asp Thr Gly Leu Lys Asp Ile Lys Asp Ile Ile Val Lys Asn
 1115 1120 1125
 Asn Thr Val Val Val Val Asp Lys Asn Asn Asn Ile Tyr Val Thr
 1130 1135 1140
 Gly Ala Asn Gln Phe Asn Lys Leu Gly Ile Gly Glu Tyr Asn Asn
 1145 1150 1155
 Gln Pro Ile Arg Lys Phe Thr Asn Ile Thr Glu Gln Ser Asn Ser
 1160 1165 1170
 Phe Ile Phe Met Asp Asp Ile Lys Glu Ile Thr Thr Ser Arg Asn
 1175 1180 1185
 Thr Met Phe Ile Val Lys Asn Asp Gly Thr Ala Tyr Ala Thr Gly
 1190 1195 1200
 Asn Asn Ser Ser Gly Gln Leu Gly Leu Gly Asp Thr Ile Asn Arg
 1205 1210 1215
 Asn Lys Phe Thr Gln Ile Asn Leu Asp Asn Ile Lys Lys Ile Ser
 1220 1225 1230
 Thr Ser Ile Asp Gly Asn Thr Thr Phe Ala Ile Arg Asn Asp Gly
 1235 1240 1245
 Thr Leu Tyr Ser Thr Gly Leu Asn Thr Lys Gly Gln Leu Gly Leu
 1250 1255 1260
 Gly Asp Ile Val Asn Arg Asn Thr Phe Thr Lys Val Asn Ile Gln
 1265 1270 1275
 Asn Val Arg Asp Val Val Leu Gly Thr Thr His Ser His Ala Ile
 1280 1285 1290
 Lys Asp Asp Asn Thr Leu Tyr Ser Cys Gly Glu Asn Thr His Gly

P108399_seqlist_ST25.txt

1295						1300						1305
Gln	Leu	Gly	Leu	Gly	Ser	Glu	Ser	Asn	His	Pro	Asp	Val
1310						1315					1320	Leu
												Thr
Phe	Thr	Val	Asn	Asn	Ile	Thr	Asn	Val	Arg	Asp	Val	Tyr
1325						1330					1335	Cys
												Ser
Asp	Thr	Thr	Thr	Phe	Ile	Val	Lys	Asp	Thr	Asn	Ile	Ala
1340						1345					1350	Tyr
												Cys
Cys	Gly	Tyr	Asn	Asn	Asn	Ser	Gln	Leu	Gly	Met	Gly	Asn
1355						1360					1365	Thr
												Thr
Asp	Gln	Tyr	Ser	Phe	Ile	Lys	Cys	Met	Glu	Asn	Val	Lys
1370						1375					1380	Glu
												Val
Ile	Pro	Asn	Glu	Ile	Asn	Thr	Tyr	Ile	Ile	Thr	Ile	Tyr
1385						1390					1395	Asn
												Thr
Ala	Tyr	Ser	Thr	Gly	Leu	Asn	Thr	Asp	Tyr	Cys	Leu	Gly
1400						1405					1410	Leu
												Asn
Ser	Asn	Ser	Asn	Gln	Ser	Ser	Phe	Ser	Glu	Ile	Pro	Ile
1415						1420					1425	Ser
												Asn
Val	Val	Lys	Val	Ala	Pro	Asn	Arg	Asn	Asn	Ala	Val	Leu
1430						1435					1440	Leu
												Leu
Thr	Ser	Glu	Gly	Asp	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Ser
1445						1450					1455	Asn
												Gly
Ser	Gly	Thr	Gly	Ser	Glu	Thr	Pro	Glu	Lys	Ile	Lys	Lys
1460						1465					1470	Ile
												Ala
Ser	Lys	Ala	Lys	Asp	Ile	Gly	Met	Asn	Tyr	Arg	Cys	Gly
1475						1480					1485	His
												Tyr
Val	Ser	Asp	Asn	Gly	Asp	Leu	Tyr	Gly	Thr	Gly	Phe	Asn
1490						1495					1500	Asp
												Cys
Gly	Gln	Leu	Gly	Val	Gly	Asn	Val	Thr	Lys	Arg	Asp	Thr
1505						1510					1515	Phe
												Ile
Lys	Thr	Asn	Thr	Arg	Val	Lys	Lys	Ile	Leu	Pro	Leu	Glu
1520						1525					1530	Tyr
												Ala
Asn	Ile	Ala	Ile	Lys	Asp	Thr	Asn	Asp	Ile	Tyr	Ile	Cys
1535						1540					1545	Gly
												Leu
Asn	Asn	Tyr	Gly	Gln	Leu	Gly	Val	Gly	Asn	Arg	Tyr	Asp
												Ser
												Arg

p108399_seqlist_ST25.txt

1550													
Asn	Asn	Asp	Asn	Arg	Ile	Phe	Asn	Tyr	Lys	His	Met	Asn	Phe Val
1565						1570					1575		
Met	Gly	Asp	Leu	Thr	Ser	Ile	Lys	Asn	Arg	His	Asn	Phe	Ile Leu
1580						1585					1590		
Leu	Asn	Asn	Lys	Ile	Val	Ile	Pro	Thr	Thr	Lys	Asp	Ile	Asp Tyr
1595						1600					1605		
Gly	Leu	Val	Leu	Gly	Asn	Leu	Tyr	Lys	Gly	Asp	Leu	Tyr	Thr Glu
1610						1615					1620		
Leu	Pro	Tyr	Glu	Asp	Ile	Lys	Glu	Val	Ser	Ile	Ser	Lys	Thr His
1625						1630					1635		
Ile	Ile	Ile	Leu	Leu	Asn	Asp	Gly	Thr	Met	Tyr	Gly	Cys	Gly Thr
1640						1645					1650		
Asn	Tyr	His	Gly	Glu	Leu	Leu	Gln	Asp	Leu	Ser	Ile	Asn	Gln Val
1655						1660					1665		
Asp	Glu	Phe	Val	Gln	Ile	Asn	Val	Ser	Asp	Val	Lys	His	Val Ser
1670						1675					1680		
Cys	Gly	Asp	Asn	Phe	Thr	Tyr	Phe	Ile	Lys	Ser	Asp	Asp	Ser Leu
1685						1690					1695		
Trp	Ser	Ile	Gly	Lys	Asn	Ser	Glu	Tyr	Gln	Leu	Gly	Ile	Gly His
1700						1705					1710		
Asn	Asn	Pro	Val	Thr	Glu	Leu	Gln	Arg	Ile	Thr	Thr	Ile	Ser Ser
1715						1720					1725		
Cys	Lys	Glu	Val	His	Cys	Gly	Lys	Asn	Tyr	Thr	Leu	val	val Thr
1730						1735					1740		
Thr	Ser	Asn	Glu	Leu	Phe	Val	Gln	Gly	Tyr	Asn	Asp	Lys	Gly Ala
1745						1750					1755		
Leu	Gly	Leu	Gly	Ser	Asp	Ser	Glu	Asn	Thr	Ile	Ile	Lys	Phe Phe
1760						1765					1770		
Thr	Lys	Ala	Leu	Thr	Asp	Ile	Arg	Glu	Ile	Lys	Ser	Tyr	Gly Ser
1775						1780					1785		
Asp	His	Ile	Leu	Val	Leu	Lys	Asn	Asp	Asn	Ser	Val	Trp	Val Thr
1790						1795					1800		
Gly	Lys	Asn	Arg	Asp	Val	Tyr	Lys	Ile	Glu	Gln	Pro	val	Glu Phe

P108399_seqlist_ST25.txt

1805 1810 1815
 Leu Lys Glu Phe Thr Ile Val Pro Ile Ser Glu Asp Val Asn Thr
 1820 1825 1830
 Val Lys Asp Val Leu Ala Thr Asp Asn Thr Leu Tyr Ile Ile Ser
 1835 1840 1845
 Glu Val Gly Thr Thr Asn Ala Ala Ile Glu Ile Thr Glu Lys Ser
 1850 1855 1860
 Ile Ser Ser Ile Lys Ile Lys Ile Gln Asp Pro Asn Lys Asp Ile
 1865 1870 1875
 Ser Arg Ile Glu Met Leu Ile Asn Gly Glu Ser Val Lys Ser Val
 1880 1885 1890
 Ser Asp Leu Ile Thr Glu Lys Ile Ser Phe Glu Val Pro Pro Asp
 1895 1900 1905
 Lys Ile Lys Ile Gly Glu Asn Lys Ile Leu Phe Arg Ala Tyr Cys
 1910 1915 1920
 Lys Gly Asp Asp Leu Tyr Ala Ser Leu Phe Ile Phe Lys Glu Ser
 1925 1930 1935
 Thr Gly Asn Ser Ile Ile Lys Asp Ser Tyr Val Met Ile Gly Asn
 1940 1945 1950
 Arg Met Tyr Lys Val Val Asn Thr Thr Ser Asn Glu Gln Asp Ile
 1955 1960 1965
 Thr Ile Thr Leu Asp Arg Gly Leu Glu Glu Asp Leu Asn Leu Gly
 1970 1975 1980
 Asp Pro Ile Tyr Gln Leu Ile Asn Lys Thr Lys Val Gln Val Lys
 1985 1990 1995
 Ile Asn Lys Ser Asp Leu Phe Lys Asp Met Lys Leu Val Glu Ile
 2000 2005 2010
 Lys Lys Ser Asp Ser Ser Tyr Gln Glu Ile Tyr Glu Leu Glu Glu
 2015 2020 2025
 Ala Asn Ile Lys Ser Ala Gln Pro Lys Ile Ile Val Glu Lys Gly
 2030 2035 2040
 Asp Lys Trp Thr Ala Ile Lys Arg Pro Ser Met Ile Phe Arg Tyr
 2045 2050 2055
 Asp Ala Glu Asn Asn Glu Pro Gln Ala His Ala

2060

P108399_seqlist_ST25.txt
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36

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<212> DNA
<213> Artificial

<220>
<223> oligonucleotide primer

<400> 23
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45