SEQUENCE LISTING

<110> Steward, Lance E.
Ghanshani, Sanjiv
Fernandez-Salas, Ester
Gilmore, Marcella A.
Francis, Joseph
Aoki, Kei Roger

<120> Degradable Clostridial Toxins

<130> 17994-PCT (BOT)

<150> US 61/346,578
<151> 2010-05-20

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<170> FastSEQ for Windows Version 4.0

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Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
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Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
435 440 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
580 585 590
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860

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Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865                 870                 875                 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
                885                 890                 895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
            900                 905                 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
        915                 920                 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
            980                 985                 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
    1010                1015                1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
            1060                1065                1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
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Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
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Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Val Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Ile
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Asn Phe Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr
    370                 375                 380
Thr Ile Lys Asp Gly Phe Asn Leu Lys Gly Ala Asn Leu Ser Thr Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Pro Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ala Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545                 550                 555                 560
His Gly Asp Ser Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys
            580                 585                 590
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Lys Ile Asn Lys Ala Val Glu Ala Phe Met Phe Leu Asn Trp Ala Glu
595 600 605
Glu Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Ser Lys Gly Glu Phe Val Glu Ala Ile
645 650 655
Ile Phe Thr Gly Val Val Ala Met Leu Glu Phe Ile Pro Glu Tyr Ala
660 665 670
Leu Pro Val Phe Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
805 810 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Val Leu
820 825 830
Gln Val Asp Arg Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
850 855 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser
865 870 875 880
Ile Val Tyr Lys Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
885 890 895
Lys Ile Asn Ile Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn
900 905 910
Gln Ile Lys Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
915 920 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Lys Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val
965 970 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln
980 985 990
Asn Ile Gln Arg Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser
995 1000 1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
1010 1015 1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025 1030 1035 1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
1045 1050 1055
Leu Asp Gly Cys Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe
1060 1065 1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
1075 1080 1085
Asp Ser Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr
1090 1095 1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn
1105 1110 1115 1120
Lys Tyr Val Asp Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu
1125 1130 1135

Lys Gly Pro Arg Gly Ser Val Val Thr Thr Asn Ile Tyr Leu Asn Ser
1140 1145 1150
Thr Leu Tyr Glu Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
1155 1160 1165
Asn Glu Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
1170 1175 1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185 1190 1195 1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
1205 1210 1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg
1220 1225 1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245
Phe Ile Gly Phe His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser
1250 1255 1260
Asn Trp Tyr Asn Arg Gln Val Gly Lys Ala Ser Arg Thr Phe Gly Cys
1265 1270 1275 1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
1285 1290 1295

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Val Lys Ala Phe Lys Ile His Glu Gly Val Trp Val Ile Pro Glu Arg
35 40 45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Asp
85 90 95
Arg Ile Tyr Ser Thr Gly Leu Gly Arg Met Leu Leu Ser Phe Ile Val
100 105 110
Lys Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Glu Pro Gly Gly Ser Tyr
130 135 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Thr Gly Pro Ser Ala Asp Ile
145 150 155 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Phe Asn Leu Thr
165 170 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205
Gly Ala Gly Thr Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220
Leu Ile His Ala Ala His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240
Arg Val Leu Lys Val Lys Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly Asn Asp Thr Asn
260 265 270
Phe Ile Asp Ser Leu Trp Gln Lys Lys Phe Ser Arg Asp Ala Tyr Asp
275 280 285
Asn Leu Gln Asn Ile Ala Arg Ile Leu Asn Glu Ala Lys Thr Ile Val
290 295 300
Gly Thr Thr Thr Pro Leu Gln Tyr Met Lys Asn Ile Phe Ile Arg Lys
305 310 315 320

Tyr Phe Leu Ser Glu Asp Ala Ser Gly Lys Ile Ser Val Asn Lys Ala
325 330 335
Ala Phe Lys Glu Phe Tyr Arg Val Leu Thr Arg Gly Phe Thr Glu Leu
340 345 350
Glu Phe Val Asn Pro Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr
370 375 380
Thr Ile Asn Glu Gly Phe Asn Leu Glu Gly Ala Asn Ser Asn Gly Gln
385 390 395 400
Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu Lys Asn Phe Thr
405 410 415
Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Pro
420 425 430
Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys Ala Leu Asn Tyr
435 440 445
Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu
450 455 460
Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu Ile Thr Ala Asp
465 470 475 480
Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Ser Asp Leu Ile Gln
485 490 495
Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro Glu Asn Ile Ser
500 505 510
Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Pro Met Pro
515 520 525
Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr
530 535 540
Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Asp Ser
545 550 555 560
Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu Leu Lys Pro Asn
565 570 575
Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys Lys Ile Asn Lys
580 585 590
Ala Val Glu Ala Val Ile Phe Leu Ser Trp Ala Glu Glu Leu Val Tyr
595 600 605
Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met Asp Lys Ile Ala
610 615 620
Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly
625 630 635 640
Asn Met Val Ser Lys Gly Glu Phe Val Glu Ala Ile Leu Phe Thr Gly
645 650 655
Val Val Ala Leu Leu Glu Phe Ile Pro Glu Tyr Ser Leu Pro Val Phe
660 665 670
Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val
675 680 685
Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu
690 695 700
Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln
705 710 715 720
Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu Glu Asn Gln Ala
725 730 735
Glu Ala Thr Arg Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu
740 745 750
Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys
755 760 765
Leu Asn Arg Ser Ile Asn Arg Ala Met Ile Asn Ile Asn Lys Phe Leu
770 775 780
Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Ala
785 790 795 800
Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg Asp Val Leu Leu
805 810 815
Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Leu Gln Val Asp Arg
820 825 830
Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp Ile Pro Phe Gln
835 840 845
Leu Ser Lys Tyr Val Asn Asp Lys Lys Leu Leu Ser Thr Phe Thr Glu
850 855 860

Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser Ile Val Tyr Lys
865 870 875 880
Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala Lys Ile Asn Ile
885 890 895
Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn Gln Ile Lys Leu
900 905 910
Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu Lys Asn Ala Ile
915 920 925
Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Lys
930 935 940
Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn Glu Tyr Thr Ile
945 950 955 960
Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr
965 970 975
Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln Asn Ile Gln Arg
980 985 990
Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser Asp Tyr Ile Asn
995 1000 1005
Arg Trp Met Phe Val Thr Ile Thr Asn Asn Arg Leu Thr Lys Ser Lys
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Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu
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Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys Leu Asp Gly Cys
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Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe Asn Leu Phe Asp
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Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Ser Gln Ser
1075 1080 1085
Asn Pro Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Gln Tyr Asp
1090 1095 1100
Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn Lys Tyr Val Asp
1105 1110 1115 1120
Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg
1125 1130 1135
Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Thr Leu Tyr Met
1140 1145 1150
Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Glu Asp Asn
1155 1160 1165
Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1170 1175 1180
Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1185 1190 1195 1200
Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
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Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg Asn Lys Cys Lys
1220 1225 1230
Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Val Gly Phe
1235 1240 1245
His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn
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1265 1270 1275 1280
Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
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20 25 30
Val Lys Ala Phe Lys Ile His Asn Lys Val Trp Val Ile Pro Glu Arg
35 40 45

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Asp Ile Phe Thr Asn Pro Glu Glu Val Asp Leu Asn Pro Pro Pro Glu
     50                  55                  60
Ala Lys Gln Val Pro Ile Ser Tyr Tyr Asp Ser Ala Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Ile Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Gly Lys Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Ile Ile Gln Leu Asp Asp Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Ala Ile Ile Gly Pro Ser Ala Asn Ile
145                 150                 155                 160
Ile Glu Ser Gln Cys Ser Ser Phe Arg Asp Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Val Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Gln Asp Pro Ala Val Ala Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Thr Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ala Gly Leu
                245                 250                 255
Glu Val Ser Leu Glu Glu Leu Ile Thr Phe Gly Gly Asn Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Lys Lys Glu Phe Ser Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Ala Thr Gly Lys Phe Leu Val Asp Arg Leu
                325                 330                 335
Lys Phe Asp Glu Leu Tyr Lys Leu Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Asp Val Asn Tyr
    370                 375                 380
Thr Ile His Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Ile Glu Ile Asn Asn Lys Asn Phe Asp Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Glu Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Asn Phe Asn Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Thr Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asn Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Lys
545                 550                 555                 560
His Ser Asn Ser Arg Ile Ile Leu Thr Asn Ser Ala Lys Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Ile Val Tyr Thr Phe Phe Ser Ser Lys Tyr Ile Lys
            580                 585                 590
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Ala Ile Asn Lys Ala Val Glu Ala Val Thr Phe Val Asn Trp Ile Glu
595 600 605
Asn Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Ser Thr Met
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Val Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Ile Tyr Lys Gly Glu Phe Val Glu Ala Ile
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Ile Val Pro Glu Ile Ala
660 665 670
Leu Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Val Ser Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Ile
705 710 715 720
Val Asn Thr Gln Ile Asn Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
805 810 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830
Gln Val Asn Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Ala Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
850 855 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Thr Asn Ala Ser Ile Leu Ser
865 870 875 880
Ile Val Tyr Lys Asp Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
885 890 895
Glu Ile Tyr Asn Gly Asp Lys Val Tyr Tyr Asn Ser Ile Asp Lys Asn
900 905 910
Gln Ile Arg Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
915 920 925
Lys Lys Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
965 970 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Phe Gln Asp Thr Gln Glu
980 985 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
995 1000 1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Ile
1010 1015 1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025 1030 1035 1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
1045 1050 1055
Leu Asp Gly Cys Arg Asp Pro His Arg Tyr Ile Val Ile Lys Tyr Phe
1060 1065 1070
Asn Leu Phe Asp Lys Glu Leu Ser Glu Lys Glu Ile Lys Asp Leu Tyr
1075 1080 1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
1090 1095 1100
Leu Gln Tyr Asp Lys Ser Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105 1110 1115 1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
1125 1130 1135

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Lys Gly Pro Arg Asp Asn Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Met Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Arg Glu Arg Pro Leu
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Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Glu Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Glu His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
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Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Glu Val Asn Tyr
370 375 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
435 440 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560
His Gly Lys Ser Arg Ile Val Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575
Leu Asn Pro Ser Ser Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Arg
580 585 590
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Gly Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Gly Asp
755 760 765
Leu Ser Ser Lys Leu Asn Asp Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860

Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865 870 875 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
885 890 895
Glu Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
900 905 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Ile Ile Leu
915 920 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Lys Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val
965 970 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln
980 985 990
Asn Ile Gln Arg Val Val Phe Lys Tyr Ser Gln Met Val Ala Ile Ser
995 1000 1005
Asp Tyr Ile Asn Arg Trp Ile Phe Ile Thr Ile Thr Asn Asn Arg Leu
1010 1015 1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025 1030 1035 1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
1045 1050 1055
Leu Asp Gly Cys Arg Asp Pro Gln Arg Tyr Ile Trp Ile Lys Tyr Phe
1060 1065 1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
1075 1080 1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr
1090 1095 1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105 1110 1115 1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
1125 1130 1135
Lys Gly Pro Arg Gly Ser Ile Val Thr Thr Asn Ile Tyr Leu Asn Ser
1140 1145 1150
Ser Leu Tyr Met Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
1155 1160 1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
1170 1175 1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185 1190 1195 1200
Gly Val Glu Lys Ile Leu Ser Val Leu Glu Ile Pro Asp Val Gly Asn
1205 1210 1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Arg
1220 1225 1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Asp Lys Leu Val Ala Ser
1250 1255 1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Phe Gly Cys
1265 1270 1275 1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Pro Leu
1285 1290 1295

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Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg
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Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
35 40 45

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Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
    50                  55                  60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
65                  70                  75                  80
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
                85                  90                  95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
            100                 105                 110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
        115                 120                 125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
    130                 135                 140
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
145                 150                 155                 160
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
                165                 170                 175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
            180                 185                 190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
        195                 200                 205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
    210                 215                 220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225                 230                 235                 240
Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
                245                 250                 255
Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe
            260                 265                 270
Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile
        275                 280                 285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
    290                 295                 300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
305                 310                 315                 320
Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
                325                 330                 335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu
            340                 345                 350
Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys
        355                 360                 365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys
    370                 375                 380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile
385                 390                 395                 400
Ser Asp Lys Asp Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile
                405                 410                 415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr
            420                 425                 430
Lys Ile Gln Met Cys Lys Ser Val Lys Ala Pro Gly Ile Cys Ile Asp
        435                 440                 445
Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser
    450                 455                 460
Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asn Thr Gln Ser Asn
465                 470                 475                 480
Tyr Ile Glu Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp
                485                 490                 495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr
            500                 505                 510
Asp Phe Asn Val Asp Val Pro Ala Tyr Glu Lys Gln Pro Ala Ile Lys
        515                 520                 525
Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln
    530                 535                 540
Thr Phe Pro Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp
545                 550                 555                 560
Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp
                565                 570                 575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly
            580                 585                 590
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Trp Val Lys Gln Ile Val Asn Asp Phe Val Ile Glu Ala Asn Lys Ser
595 600 605
Asn Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile
610 615 620
Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu
625 630 635 640
Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro
645 650 655
Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile
660 665 670
Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys
675 680 685
Arg Asn Glu Lys Trp Ser Asp Met Tyr Gly Leu Ile Val Ala Gln Trp
690 695 700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr
705 710 715 720
Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
725 730 735
Arg Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp
740 745 750
Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
755 760 765
Asp Asn Ile Asn Asn Phe Ile Asn Gly Cys Ser Val Ser Tyr Leu Met
770 775 780
Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
785 790 795 800
Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
805 810 815
Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asn Lys Tyr Leu
820 825 830
Lys Thr Ile Met Pro Phe Asp Leu Ser Ile Tyr Thr Asn Asp Thr Ile
835 840 845
Leu Ile Glu Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
850 855 860
Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly
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Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys
885 890 895
Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr
900 905 910
Gln Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val
915 920 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
930 935 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser
945 950 955 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile
965 970 975
Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg
980 985 990
Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
995 1000 1005
Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
1010 1015 1020
Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile
1025 1030 1035 1040
Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met
1045 1050 1055
Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu
1060 1065 1070
Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
1075 1080 1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
1090 1095 1100
Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu
1105 1110 1115 1120
Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr
1125 1130 1135

Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
1155 1160 1165
Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Ile Tyr Lys
1170 1175 1180
Tyr Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp
1185 1190 1195 1200
Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1205 1210 1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr
1220 1225 1230
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile
1235 1240 1245
Val Phe Lys Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu
1250 1255 1260
Lys Glu Val Lys Arg Lys Pro Tyr Asn Ser Lys Leu Gly Cys Asn Trp
1265 1270 1275 1280
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
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Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
35 40 45
Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
50 55 60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
65 70 75 80
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
85 90 95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
100 105 110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
115 120 125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
130 135 140
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
145 150 155 160
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
165 170 175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
180 185 190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
195 200 205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
210 215 220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225 230 235 240
Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
245 250 255
Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe
260 265 270
Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile
275 280 285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
290 295 300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
305 310 315 320

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Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
                325                 330                 335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu
            340                 345                 350
Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys
        355                 360                 365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys
    370                 375                 380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile
385                 390                 395                 400
Ser Asp Lys Asn Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile
                405                 410                 415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr
            420                 425                 430
Lys Ile Gln Met Cys Lys Ser Val Arg Ala Pro Gly Ile Cys Ile Asp
        435                 440                 445
Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser
    450                 455                 460
Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asp Thr Gln Ser Asn
465                 470                 475                 480
Tyr Ile Glu Asn Arg Ser Ser Ile Asp Glu Leu Ile Leu Asp Thr Asn
                485                 490                 495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr
            500                 505                 510
Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys
        515                 520                 525
Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln
    530                 535                 540
Thr Phe Pro Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp
545                 550                 555                 560
Asp Ala Leu Leu Phe Ser Lys Lys Val Tyr Ser Phe Phe Ser Met Asp
                565                 570                 575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly
            580                 585                 590
Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser
        595                 600                 605
Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile
    610                 615                 620
Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu
625                 630                 635                 640
Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro
                645                 650                 655
Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile
            660                 665                 670
Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys
        675                 680                 685
Arg Asp Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp
    690                 695                 700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr
705                 710                 715                 720
Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
                725                 730                 735
Lys Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp
            740                 745                 750
Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
        755                 760                 765
Asp Asn Ile Asn Asn Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met
    770                 775                 780
Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
785                 790                 795                 800
Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
                805                 810                 815
Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asp Lys His Leu
            820                 825                 830
Lys Thr Ile Ile Pro Phe Asp Leu Ser Lys Tyr Thr Asn Asn Thr Ile
        835                 840                 845
Leu Ile Glu Ile Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
    850                 855                 860
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Ile Leu Asn Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly
865 870 875 880
Tyr Gly Ala Asn Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys
885 890 895
Asn Gln Phe Lys Leu Thr Ser Ser Thr Asn Ser Glu Ile Arg Val Thr
900 905 910
Gln Asn Gln Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val
915 920 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
930 935 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Ile Lys Asn Asn Ser
945 950 955 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Thr
965 970 975
Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Ser Ile Arg
980 985 990
Lys Asp Val Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
995 1000 1005
Asn Asn Ser Asp Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
1010 1015 1020
Asn Ile Asp Ile Lys Asp Ile Gly Glu Val Ile Ala Asn Gly Glu Ile
1025 1030 1035 1040
Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met
1045 1050 1055
Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Lys
1060 1065 1070
Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
1075 1080 1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
1090 1095 1100
Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Ser Val Gly Glu
1105 1110 1115 1120
Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr
1125 1130 1135
Arg Asn Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
1155 1160 1165
Leu Asp Phe Phe Asn Ser Asn Arg Glu Trp Arg Val Tyr Ala Tyr Lys
1170 1175 1180
Asp Phe Lys Glu Glu Glu Lys Lys Leu Phe Leu Ala Asn Ile Tyr Asp
1185 1190 1195 1200
Ser Asn Glu Phe Tyr Lys Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1205 1210 1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr
1220 1225 1230
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Thr
1235 1240 1245
Val Phe Lys Asn Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu
1250 1255 1260
Lys Glu Val Lys Arg Lys Pro Tyr Asn Ser Asp Leu Gly Cys Asn Trp
1265 1270 1275 1280
Lys Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
1285 1290

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<213> Clostridium botulinum B3

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Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
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Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg
20 25 30
Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
35 40 45

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Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
    50                  55                  60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
65                  70                  75                  80
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
                85                  90                  95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
            100                 105                 110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
        115                 120                 125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
    130                 135                 140
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
145                 150                 155                 160
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
                165                 170                 175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
            180                 185                 190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
        195                 200                 205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
    210                 215                 220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225                 230                 235                 240
Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
                245                 250                 255
Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe
            260                 265                 270
Gly Gly Gln Asp Pro Arg Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile
        275                 280                 285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
    290                 295                 300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
305                 310                 315                 320
Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
                325                 330                 335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu
            340                 345                 350
Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys
        355                 360                 365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys
    370                 375                 380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile
385                 390                 395                 400
Ser Asp Lys Asn Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile
                405                 410                 415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr
            420                 425                 430
Lys Ile Gln Met Cys Lys Ser Val Arg Ala Pro Gly Ile Cys Ile Asp
        435                 440                 445
Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser
    450                 455                 460
Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asp Thr Gln Ser Asn
465                 470                 475                 480
Tyr Ile Glu Asn Arg Ser Ser Ile Asp Glu Leu Ile Leu Asp Thr Asn
                485                 490                 495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr
            500                 505                 510
Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys
        515                 520                 525
Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln
    530                 535                 540
Thr Phe Pro Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp
545                 550                 555                 560
Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp
                565                 570                 575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly
            580                 585                 590
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Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser
595 600 605
Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile
610 615 620
Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu
625 630 635 640
Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro
645 650 655
Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile
660 665 670
Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys
675 680 685
Arg Asp Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp
690 695 700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr
705 710 715 720
Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
725 730 735
Lys Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp
740 745 750
Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
755 760 765
Asp Asn Ile Asn Asn Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met
770 775 780
Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
785 790 795 800
Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
805 810 815
Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asp Lys His Leu
820 825 830
Lys Thr Ile Ile Pro Phe Asp Leu Ser Met Tyr Thr Asn Asn Thr Ile
835 840 845
Leu Ile Glu Ile Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
850 855 860
Ile Leu Asn Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly
865 870 875 880
Tyr Gly Ala Lys Val Glu Val Tyr Asn Gly Val Glu Leu Asn Asp Lys
885 890 895
Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr
900 905 910
Gln Asn Gln Asp Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val
915 920 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
930 935 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Ile Lys Asn Asn Ser
945 950 955 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Lys Ile Ile Trp Thr Leu Thr
965 970 975
Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Ser Ile Arg
980 985 990
Lys Asp Val Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
995 1000 1005
Asn Asn Ser Asp Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
1010 1015 1020
Asn Ile Asp Ile Lys Asp Ile Gly Glu Val Ile Ala Asn Gly Glu Ile
1025 1030 1035 1040
Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met
1045 1050 1055
Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Lys
1060 1065 1070
Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
1075 1080 1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
1090 1095 1100
Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Ser Val Gly Glu
1105 1110 1115 1120
Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr
1125 1130 1135

Arg Asn Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
1155 1160 1165
Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Ala Tyr Lys
1170 1175 1180
Asp Phe Lys Lys Lys Glu Glu Lys Leu Phe Leu Ala Asn Ile Tyr Asp
1185 1190 1195 1200
Ser Asn Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1205 1210 1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr
1220 1225 1230
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile
1235 1240 1245
Val Phe Lys Asp Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu
1250 1255 1260
Lys Glu Val Lys Arg Lys Pro Tyr Asn Pro Asn Leu Gly Cys Asn Trp
1265 1270 1275 1280
Gln Phe Ile Pro Lys Asp Glu Gly Trp Ile Glu
1285 1290

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Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
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Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg
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Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
35 40 45
Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
50 55 60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
65 70 75 80
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
85 90 95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
100 105 110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
115 120 125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
130 135 140
Pro Gly Glu Val Glu Gln Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
145 150 155 160
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
165 170 175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
180 185 190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
195 200 205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
210 215 220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225 230 235 240
Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
245 250 255
Phe Met Gln Ser Thr Asp Thr Ile Gln Ala Glu Glu Leu Tyr Thr Phe
260 265 270
Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr Asp Lys Ser Ile
275 280 285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
290 295 300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
305 310 315 320

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Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
                325                 330                 335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asn Lys Leu Tyr Lys Ser Leu
            340                 345                 350
Met Phe Gly Phe Thr Glu Ile Asn Ile Ala Glu Asn Tyr Lys Ile Lys
        355                 360                 365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys
    370                 375                 380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile
385                 390                 395                 400
Ser Asp Lys Asn Met Gly Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile
                405                 410                 415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr
            420                 425                 430
Lys Ile Gln Met Cys Lys Ser Val Lys Val Pro Gly Ile Cys Ile Asp
        435                 440                 445
Val Asp Asn Glu Asn Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser
    450                 455                 460
Asp Asp Leu Ser Lys Asn Glu Arg Val Glu Tyr Asn Thr Gln Asn Asn
465                 470                 475                 480
Tyr Ile Gly Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp
                485                 490                 495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr
            500                 505                 510
Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys
        515                 520                 525
Lys Val Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln
    530                 535                 540
Thr Phe Pro Leu Asn Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp
545                 550                 555                 560
Asp Ala Leu Leu Val Ser Ser Lys Val Tyr Ser Phe Phe Ser Met Asp
                565                 570                 575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly
            580                 585                 590
Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser
        595                 600                 605
Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile
    610                 615                 620
Gly Leu Ala Leu Asn Val Gly Asp Glu Thr Ala Lys Gly Asn Phe Glu
625                 630                 635                 640
Ser Ala Phe Glu Ile Ala Gly Ser Ser Ile Leu Leu Glu Phe Ile Pro
                645                 650                 655
Glu Leu Leu Ile Pro Val Val Gly Val Phe Leu Leu Glu Ser Tyr Ile
            660                 665                 670
Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys
        675                 680                 685
Arg Val Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp
    690                 695                 700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr
705                 710                 715                 720
Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
                725                 730                 735
Lys Tyr Asn Ile Tyr Ser Glu Glu Glu Lys Ser Asn Ile Asn Ile Asn
            740                 745                 750
Phe Asn Asp Ile Asn Ser Lys Leu Asn Asp Gly Ile Asn Gln Ala Met
        755                 760                 765
Asp Asn Ile Asn Asp Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met
    770                 775                 780
Lys Lys Met Ile Pro Leu Ala Val Lys Lys Leu Leu Asp Phe Asp Asn
785                 790                 795                 800
Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
                805                 810                 815
Leu Ile Gly Ser Val Glu Asp Glu Lys Ser Lys Val Asp Lys Tyr Leu
            820                 825                 830
Lys Thr Ile Ile Pro Phe Asp Leu Ser Thr Tyr Thr Asn Asn Glu Ile
        835                 840                 845
Leu Ile Lys Ile Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
    850                 855                 860
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Ile Leu Asn Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly
865 870 875 880
Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Lys Leu Asn Asp Lys
885 890 895
Asn Gln Phe Lys Leu Thr Ser Ser Ala Asp Ser Lys Ile Arg Val Thr
900 905 910
Gln Asn Gln Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val
915 920 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Arg Asn Asp Asp Ile Gln Asn
930 935 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser
945 950 955 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile
965 970 975
Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg
980 985 990
Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
995 1000 1005
Asn Asn Leu Asp Asn Ala Lys Ile Tyr Ile Asn Gly Thr Leu Glu Ser
1010 1015 1020
Asn Met Asp Ile Lys Asp Ile Gly Glu Val Ile Val Asn Gly Glu Ile
1025 1030 1035 1040
Thr Phe Lys Leu Asp Gly Asp Val Asp Arg Thr Gln Phe Ile Trp Met
1045 1050 1055
Lys Tyr Phe Ser Ile Phe Asn Thr Gln Leu Asn Gln Ser Asn Ile Lys
1060 1065 1070
Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
1075 1080 1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
1090 1095 1100
Asn Lys Asn Ser Tyr Ile Lys Leu Val Lys Asp Ser Ser Val Gly Glu
1105 1110 1115 1120
Ile Leu Ile Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr
1125 1130 1135
Arg Asn Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile His
1155 1160 1165
Leu Asp Phe Val Asn Ser Asn Glu Glu Trp Arg Val Tyr Ala Tyr Lys
1170 1175 1180
Asn Phe Lys Glu Gln Glu Gln Lys Leu Phe Leu Ser Ile Ile Tyr Asp
1185 1190 1195 1200
Ser Asn Glu Phe Tyr Lys Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1205 1210 1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr
1220 1225 1230
Asp Asp Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Val
1235 1240 1245
Leu Arg Lys Lys Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu
1250 1255 1260
Lys Glu Val Lys Arg Lys Pro Tyr Lys Ser Asn Leu Gly Cys Asn Trp
1265 1270 1275 1280
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
1285 1290

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Asn Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Met Gly Arg
20 25 30
Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
35 40 45

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Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
    50                  55                  60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
65                  70                  75                  80
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
                85                  90                  95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
            100                 105                 110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
        115                 120                 125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
    130                 135                 140
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
145                 150                 155                 160
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
                165                 170                 175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
            180                 185                 190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
        195                 200                 205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
    210                 215                 220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225                 230                 235                 240
Gly Ile Lys Val Asn Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
                245                 250                 255
Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe
            260                 265                 270
Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr Asp Lys Ser Ile
        275                 280                 285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
    290                 295                 300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
305                 310                 315                 320
Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
                325                 330                 335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu
            340                 345                 350
Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys
        355                 360                 365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys
    370                 375                 380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile
385                 390                 395                 400
Ser Asp Lys Asn Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile
                405                 410                 415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr
            420                 425                 430
Lys Ile Gln Met Cys Lys Ser Val Lys Ala Pro Gly Ile Cys Ile Asp
        435                 440                 445
Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser
    450                 455                 460
Asp Asp Leu Ser Lys Asn Glu Arg Ile Ala Tyr Asn Thr Gln Asn Asn
465                 470                 475                 480
Tyr Ile Glu Asn Asp Phe Ser Ile Asn Glu Leu Ile Leu Asp Thr Asp
                485                 490                 495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr
            500                 505                 510
Asp Phe Asn Val Tyr Val Pro Val Tyr Lys Lys Gln Pro Ala Ile Lys
        515                 520                 525
Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln
    530                 535                 540
Thr Phe Pro Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp
545                 550                 555                 560
Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp
                565                 570                 575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly
            580                 585                 590
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Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser
        595                 600                 605
Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile
    610                 615                 620
Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu
625                 630                 635                 640
Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro
                645                 650                 655
Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile
            660                 665                 670
Asp Asn Lys Asn Lys Ile Ile Glu Thr Ile Asn Ser Ala Leu Thr Lys
        675                 680                 685
Arg Asp Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp
    690                 695                 700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr
705                 710                 715                 720
Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
                725                 730                 735
Lys Tyr Asn Ile Tyr Ser Glu Lys Glu Arg Ser Asn Ile Asn Ile Asp
            740                 745                 750
Phe Asn Asp Val Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
        755                 760                 765
Asp Asn Ile Asn Asn Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met
    770                 775                 780
Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
785                 790                 795                 800
Thr Leu Arg Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
                805                 810                 815
Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asp Lys Tyr Leu
            820                 825                 830
Lys Thr Ser Ile Pro Phe Asp Leu Ser Thr Tyr Thr Asn Asn Thr Ile
        835                 840                 845
Leu Ile Glu Ile Phe Asn Lys Tyr Asn Ser Asp Ile Leu Asn Asn Ile
    850                 855                 860
Ile Leu Asn Leu Arg Tyr Arg Asp Asn Lys Leu Ile Asp Leu Ser Gly
865                 870                 875                 880
Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Lys Leu Asn Asp Lys
                885                 890                 895
Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Ile
            900                 905                 910
Gln Asn Gln Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val
        915                 920                 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
    930                 935                 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser
945                 950                 955                 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Met Ile Ile Trp Thr Leu Ile
                965                 970                 975
Asp Ile Asn Gly Lys Ile Lys Ser Val Phe Phe Glu Tyr Ser Ile Lys
            980                 985                 990
Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
        995                 1000                1005
Asn Asn Ser Asp Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
    1010                1015                1020
His Ile Asp Ile Arg Asp Ile Arg Glu Val Ile Ala Asn Asp Glu Ile
1025                1030                1035                1040
Ile Phe Lys Leu Asp Gly Asn Ile Asp Arg Thr Gln Phe Ile Trp Met
                1045                1050                1055
Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu
            1060                1065                1070
Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
        1075                1080                1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
    1090                1095                1100
Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Ser Val Gly Glu
1105                1110                1115                1120
Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr
                1125                1130                1135
```

Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
1155 1160 1165
Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Met Tyr Lys
1170 1175 1180
Tyr Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp
1185 1190 1195 1200
Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1205 1210 1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr
1220 1225 1230
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile
1235 1240 1245
Val Phe Lys Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu
1250 1255 1260
Lys Glu Val Lys Arg Lys Pro Tyr Asn Ser Lys Leu Gly Cys Asn Trp
1265 1270 1275 1280
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
1285 1290

<210> 11
<211> 1291
<212> PRT
<213> Clostridium botulinum C1-1

<400> 11
Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn
1 5 10 15
Lys Asn Ile Leu Tyr Leu Asp Thr His Leu Asn Thr Leu Ala Asn Glu
20 25 30
Pro Glu Lys Ala Phe Arg Ile Thr Gly Asn Ile Trp Val Ile Pro Asp
35 40 45
Arg Phe Ser Arg Asn Ser Asn Pro Asn Leu Asn Lys Pro Pro Arg Val
50 55 60
Thr Ser Pro Lys Ser Gly Tyr Tyr Asp Pro Asn Tyr Leu Ser Thr Asp
65 70 75 80
Ser Asp Lys Asp Thr Phe Leu Lys Glu Ile Ile Lys Leu Phe Lys Arg
85 90 95
Ile Asn Ser Arg Glu Ile Gly Glu Glu Leu Ile Tyr Arg Leu Ser Thr
100 105 110
Asp Ile Pro Phe Pro Gly Asn Asn Asn Thr Pro Ile Asn Thr Phe Asp
115 120 125
Phe Asp Val Asp Phe Asn Ser Val Asp Val Lys Thr Arg Gln Gly Asn
130 135 140
Asn Trp Val Lys Thr Gly Ser Ile Asn Pro Ser Val Ile Ile Thr Gly
145 150 155 160
Pro Arg Glu Asn Ile Ile Asp Pro Glu Thr Ser Thr Phe Lys Leu Thr
165 170 175
Asn Asn Thr Phe Ala Ala Gln Glu Gly Phe Gly Ala Leu Ser Ile Ile
180 185 190
Ser Ile Ser Pro Arg Phe Met Leu Thr Tyr Ser Asn Ala Thr Asn Asp
195 200 205
Val Gly Glu Gly Arg Phe Ser Lys Ser Glu Phe Cys Met Asp Pro Ile
210 215 220
Leu Ile Leu Met His Glu Leu Asn His Ala Met His Asn Leu Tyr Gly
225 230 235 240
Ile Ala Ile Pro Asn Asp Gln Thr Ile Ser Ser Val Thr Ser Asn Ile
245 250 255
Phe Tyr Ser Gln Tyr Asn Val Lys Leu Glu Tyr Ala Glu Ile Tyr Ala
260 265 270
Phe Gly Gly Pro Thr Ile Asp Leu Ile Pro Lys Ser Ala Arg Lys Tyr
275 280 285
Phe Glu Glu Lys Ala Leu Asp Tyr Tyr Arg Ser Ile Ala Lys Arg Leu
290 295 300
Asn Ser Ile Thr Thr Ala Asn Pro Ser Ser Phe Asn Lys Tyr Ile Gly
305 310 315 320

```
Glu Tyr Lys Gln Lys Leu Ile Arg Lys Tyr Arg Phe Val Val Glu Ser
                325                 330                 335
Ser Gly Glu Val Thr Val Asn Arg Asn Lys Phe Val Glu Leu Tyr Asn
            340                 345                 350
Glu Leu Thr Gln Ile Phe Thr Glu Phe Asn Tyr Ala Lys Ile Tyr Asn
        355                 360                 365
Val Gln Asn Arg Lys Ile Tyr Leu Ser Asn Val Tyr Thr Pro Val Thr
    370                 375                 380
Ala Asn Ile Leu Asp Asp Asn Val Tyr Asp Ile Gln Asn Gly Phe Asn
385                 390                 395                 400
Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu Ser
                405                 410                 415
Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr Leu
            420                 425                 430
Phe Thr Lys Phe Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn
        435                 440                 445
Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro
    450                 455                 460
Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys
465                 470                 475                 480
Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser
                485                 490                 495
Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu
            500                 505                 510
Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly
        515                 520                 525
Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu
    530                 535                 540
Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu
545                 550                 555                 560
Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala
                565                 570                 575
Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly
            580                 585                 590
Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp
        595                 600                 605
Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp
    610                 615                 620
Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn
625                 630                 635                 640
Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val
                645                 650                 655
Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly
            660                 665                 670
Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys
        675                 680                 685
Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser
    690                 695                 700
Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe
705                 710                 715                 720
Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly
                725                 730                 735
Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser
            740                 745                 750
Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu
        755                 760                 765
Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg
    770                 775                 780
Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile
785                 790                 795                 800
Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn
                805                 810                 815
Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu
            820                 825                 830
Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile
        835                 840                 845
Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr
    850                 855                 860
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Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys
865 870 875 880
Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu
885 890 895
Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly
900 905 910
Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn
915 920 925
Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile
930 935 940
Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp
945 950 955 960
Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe
965 970 975
Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn
980 985 990
Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe
995 1000 1005
Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile
1010 1015 1020
Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile
1025 1030 1035 1040
Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr
1045 1050 1055
Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp
1060 1065 1070
Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu
1075 1080 1085
Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn
1090 1095 1100
Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu
1105 1110 1115 1120
Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg
1125 1130 1135
Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg
1140 1145 1150
Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu
1155 1160 1165
Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys
1170 1175 1180
Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala
1185 1190 1195 1200
Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe
1205 1210 1215
Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe
1220 1225 1230
Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly
1235 1240 1245
Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu
1250 1255 1260
Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr
1265 1270 1275 1280
Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
1285 1290

<210> 12
<211> 1280
<212> PRT
<213> Clostridium botulinum C1-2

<400> 12
Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn
1 5 10 15
Lys Asn Ile Leu Tyr Leu Asp Thr His Leu Asn Thr Leu Ala Asn Glu
20 25 30
Pro Glu Lys Ala Phe Arg Ile Ile Gly Asn Ile Trp Val Ile Pro Asp
35 40 45

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Arg Phe Ser Arg Asp Ser Asn Pro Asn Leu Asn Lys Pro Pro Arg Val
    50                  55                  60
Thr Ser Pro Lys Ser Gly Tyr Tyr Asp Pro Asn Tyr Leu Ser Thr Asp
65                  70                  75                  80
Ser Glu Lys Asp Thr Phe Leu Lys Glu Ile Ile Lys Leu Phe Lys Arg
                85                  90                  95
Ile Asn Ser Arg Glu Ile Gly Glu Glu Leu Ile Tyr Arg Leu Ala Thr
            100                 105                 110
Asp Ile Pro Phe Pro Gly Asn Asn Asn Thr Pro Ile Asn Thr Phe Asp
        115                 120                 125
Phe Asp Val Asp Phe Asn Ser Val Asp Val Lys Thr Arg Gln Gly Asn
    130                 135                 140
Asn Trp Val Lys Thr Gly Ser Ile Asn Pro Ser Val Ile Ile Thr Gly
145                 150                 155                 160
Pro Arg Glu Asn Ile Ile Asp Pro Glu Thr Ser Thr Phe Lys Leu Thr
                165                 170                 175
Asn Asn Thr Phe Ala Ala Gln Glu Gly Phe Gly Ala Leu Ser Ile Ile
            180                 185                 190
Ser Ile Ser Pro Arg Phe Met Leu Thr Tyr Ser Asn Ala Thr Asn Asn
        195                 200                 205
Val Gly Glu Gly Arg Phe Ser Lys Ser Glu Phe Cys Met Asp Pro Ile
    210                 215                 220
Leu Ile Leu Met His Glu Leu Asn His Thr Met His Asn Leu Tyr Gly
225                 230                 235                 240
Ile Ala Ile Pro Asn Asp Gln Arg Ile Ser Ser Val Thr Ser Asn Ile
                245                 250                 255
Phe Tyr Ser Gln Tyr Lys Val Lys Leu Glu Tyr Ala Glu Ile Tyr Ala
            260                 265                 270
Phe Gly Gly Pro Thr Ile Asp Leu Ile Pro Lys Ser Gly Arg Lys Tyr
        275                 280                 285
Phe Glu Glu Lys Ala Leu Asp Tyr Tyr Arg Ser Ile Ala Lys Arg Leu
    290                 295                 300
Asn Ser Ile Thr Thr Ala Asn Pro Ser Ser Phe Asn Lys Tyr Ile Gly
305                 310                 315                 320
Glu Tyr Lys Gln Lys Leu Ile Arg Lys Tyr Arg Phe Val Val Glu Ser
                325                 330                 335
Ser Gly Glu Val Ala Val Asp Arg Asn Lys Phe Ala Glu Leu Tyr Lys
            340                 345                 350
Glu Leu Thr Gln Ile Phe Thr Glu Phe Asn Tyr Ala Lys Ile Tyr Asn
        355                 360                 365
Val Gln Asn Arg Lys Ile Tyr Leu Ser Asn Val Tyr Thr Pro Val Thr
    370                 375                 380
Ala Asn Ile Leu Asp Asp Asn Val Tyr Asp Ile Gln Asn Gly Phe Asn
385                 390                 395                 400
Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu Ser
                405                 410                 415
Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr Leu
            420                 425                 430
Phe Thr Lys Phe Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn
        435                 440                 445
Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro
    450                 455                 460
Phe Ile Gly Asp Ile Ser Asp Ile Lys Thr Asp Ile Phe Leu Ser Lys
465                 470                 475                 480
Asp Ile Asn Val Glu Thr Glu Val Ile Asp Tyr Pro Asp Asn Val Ser
                485                 490                 495
Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu
            500                 505                 510
Asp Leu Leu Tyr Pro Ile Ile Glu Gly Glu Ser Gln Val Leu Pro Gly
        515                 520                 525
Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu
    530                 535                 540
Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu
545                 550                 555                 560
Asp Phe Thr Phe Thr Thr Ser Ile Glu Glu Ala Leu Asp Asn Ser Gly
                565                 570                 575
Lys Val Tyr Thr Tyr Phe Pro Lys Leu Ala Asp Lys Val Asn Thr Gly
            580                 585                 590
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Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp
595 600 605
Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp
610 615 620
Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn
625 630 635 640
Ser Val Arg Arg Glu Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val
645 650 655
Thr Ile Leu Leu Glu Ala Phe Gln Glu Phe Thr Ile Pro Ala Leu Gly
660 665 670
Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys
675 680 685
Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser
690 695 700
Tyr Glu Trp Met Ile Gly Thr Trp Leu Ser Arg Ile Thr Thr Gln Phe
705 710 715 720
Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Asp
725 730 735
Ala Ile Lys Asp Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser
740 745 750
Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu
755 760 765
Asp Ile Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg
770 775 780
Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile
785 790 795 800
Asp Glu Leu Asn Lys Phe Asp Leu Lys Thr Lys Thr Glu Leu Ile Asn
805 810 815
Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu
820 825 830
Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Ile Pro Phe Asn Ile
835 840 845
Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr
850 855 860
Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys
865 870 875 880
Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Leu Glu
885 890 895
Gly Asp Val Gln Val Asn Thr Ile Tyr Thr Asn Asp Phe Lys Leu Ser
900 905 910
Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn Ile Leu Tyr
915 920 925
Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser
930 935 940
Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile
945 950 955 960
Lys Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu
965 970 975
Trp Ile Leu Gln Asp Ile Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp
980 985 990
Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe
995 1000 1005
Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu Tyr Ile Asn
1010 1015 1020
Gly Glu Leu Lys Gln Ser Glu Arg Ile Glu Asp Leu Asn Glu Val Lys
1025 1030 1035 1040
Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn
1045 1050 1055
Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser
1060 1065 1070
Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn Val
1075 1080 1085
Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu Tyr Tyr
1090 1095 1100
Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro Lys Ser Asn
1105 1110 1115 1120
Ile Leu Val Leu Val Gln Tyr Pro Asp Arg Ser Lys Leu Tyr Thr Gly
1125 1130 1135

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Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro Tyr Ser Arg
            1140                1145                1150
Ile Leu Asn Gly Asp Asn Ile Met Phe His Met Leu Tyr Asn Ser Gly
        1155                1160                1165
Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala Ile Glu Gly
    1170                1175                1180
Arg Glu Cys Ser Lys Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn
1185                1190                1195                1200
Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser
                1205                1210                1215
Gln Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Met Lys Asn Thr
            1220                1225                1230
Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Glu Asn
        1235                1240                1245
Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser
    1250                1255                1260
Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu
1265                1270                1275                1280


<210> 13
<211> 1276
<212> PRT
<213> Clostridium botulinum D1

<400> 13
Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp
 1               5                  10                  15
Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile Thr Thr
            20                  25                  30
Pro Val Lys Ala Phe Met Ile Thr Gln Asn Ile Trp Val Ile Pro Glu
        35                  40                  45
Arg Phe Ser Ser Asp Thr Asn Pro Ser Leu Ser Lys Pro Pro Arg Pro
    50                  55                  60
Thr Ser Lys Tyr Gln Ser Tyr Tyr Asp Pro Ser Tyr Leu Ser Thr Asp
65                  70                  75                  80
Glu Gln Lys Asp Thr Phe Leu Lys Gly Ile Ile Lys Leu Phe Lys Arg
                85                  90                  95
Ile Asn Glu Arg Asp Ile Gly Lys Lys Leu Ile Asn Tyr Leu Val Val
            100                 105                 110
Gly Ser Pro Phe Met Gly Asp Ser Ser Thr Pro Glu Asp Thr Phe Asp
        115                 120                 125
Phe Thr Arg His Thr Thr Asn Ile Ala Val Glu Lys Phe Glu Asn Gly
    130                 135                 140
Ser Trp Lys Val Thr Asn Ile Ile Thr Pro Ser Val Leu Ile Phe Gly
145                 150                 155                 160
Pro Leu Pro Asn Ile Leu Asp Tyr Thr Ala Ser Leu Thr Leu Gln Gly
                165                 170                 175
Gln Gln Ser Asn Pro Ser Phe Glu Gly Phe Gly Thr Leu Ser Ile Leu
            180                 185                 190
Lys Val Ala Pro Glu Phe Leu Leu Thr Phe Ser Asp Val Thr Ser Asn
        195                 200                 205
Gln Ser Ser Ala Val Leu Gly Lys Ser Ile Phe Cys Met Asp Pro Val
    210                 215                 220
Ile Ala Leu Met His Glu Leu Thr His Ser Leu His Gln Leu Tyr Gly
225                 230                 235                 240
Ile Asn Ile Pro Ser Asp Lys Arg Ile Arg Pro Gln Val Ser Glu Gly
                245                 250                 255
Phe Phe Ser Gln Asp Gly Pro Asn Val Gln Phe Glu Glu Leu Tyr Thr
            260                 265                 270
Phe Gly Gly Leu Asp Val Glu Ile Ile Pro Gln Ile Glu Arg Ser Gln
        275                 280                 285
Leu Arg Glu Lys Ala Leu Gly His Tyr Lys Asp Ile Ala Lys Arg Leu
    290                 295                 300
Asn Asn Ile Asn Lys Thr Ile Pro Ser Ser Trp Ile Ser Asn Ile Asp
305                 310                 315                 320
Lys Tyr Lys Lys Ile Phe Ser Glu Lys Tyr Asn Phe Asp Lys Asp Asn
                325                 330                 335
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Thr Gly Asn Phe Val Val Asn Ile Asp Lys Phe Asn Ser Leu Tyr Ser
            340                 345                 350
Asp Leu Thr Asn Val Met Ser Glu Val Val Tyr Ser Ser Gln Tyr Asn
        355                 360                 365
Val Lys Asn Arg Thr His Tyr Phe Ser Arg His Tyr Leu Pro Val Phe
    370                 375                 380
Ala Asn Ile Leu Asp Asp Asn Ile Tyr Thr Ile Arg Asp Gly Phe Asn
385                 390                 395                 400
Leu Thr Asn Lys Gly Phe Asn Ile Glu Asn Ser Gly Gln Asn Ile Glu
                405                 410                 415
Arg Asn Pro Ala Leu Gln Lys Leu Ser Ser Glu Ser Val Val Asp Leu
            420                 425                 430
Phe Thr Lys Val Cys Leu Arg Leu Thr Lys Asn Ser Arg Asp Asp Ser
        435                 440                 445
Thr Cys Ile Lys Val Lys Asn Asn Arg Leu Pro Tyr Val Ala Asp Lys
    450                 455                 460
Asp Ser Ile Ser Gln Glu Ile Phe Glu Asn Lys Ile Ile Thr Asp Glu
465                 470                 475                 480
Thr Asn Val Gln Asn Tyr Ser Asp Lys Phe Ser Leu Asp Glu Ser Ile
                485                 490                 495
Leu Asp Gly Gln Val Pro Ile Asn Pro Glu Ile Val Asp Pro Leu Leu
            500                 505                 510
Pro Asn Val Asn Met Glu Pro Leu Asn Leu Pro Gly Glu Glu Ile Val
        515                 520                 525
Phe Tyr Asp Asp Ile Thr Lys Tyr Val Asp Tyr Leu Asn Ser Tyr Tyr
    530                 535                 540
Tyr Leu Glu Ser Gln Lys Leu Ser Asn Asn Val Glu Asn Ile Thr Leu
545                 550                 555                 560
Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys Ile Tyr Thr
                565                 570                 575
Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val Gln Ala Gly
            580                 585                 590
Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe Thr Thr Asn
        595                 600                 605
Ile Met Lys Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Val Ile
    610                 615                 620
Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser Ala Leu Arg
625                 630                 635                 640
Gly Asn Phe Asn Gln Ala Phe Ala Thr Ala Gly Val Ala Phe Leu Leu
                645                 650                 655
Glu Gly Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Val Phe Thr Phe
            660                 665                 670
Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr Ile Glu Asn
        675                 680                 685
Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr Gln Trp Met
    690                 695                 700
Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Gln Phe Asn His Ile Asn
705                 710                 715                 720
Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala Ile Lys Ala
                725                 730                 735
Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn
            740                 745                 750
Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile
        755                 760                 765
Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val
    770                 775                 780
Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn
785                 790                 795                 800
Lys Phe Asp Leu Arg Thr Lys Thr Glu Leu Ile Asn Leu Ile Asp Ser
                805                 810                 815
His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys Ala Lys Val
            820                 825                 830
Asn Glu Ser Phe Glu Asn Thr Met Pro Phe Asn Ile Phe Ser Tyr Thr
        835                 840                 845
Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Ser Ile
    850                 855                 860
Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys Asn Ala Leu Val
865                 870                 875                 880
```

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Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Val Gly Asp Asn Val Gln
                885                 890                 895
Leu Asn Thr Ile Tyr Thr Asn Asp Phe Lys Leu Ser Ser Ser Gly Asp
            900                 905                 910
Lys Ile Ile Val Asn Leu Asn Asn Asn Ile Leu Tyr Ser Ala Ile Tyr
        915                 920                 925
Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser Lys Asp Leu Thr
    930                 935                 940
Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile Glu Gln Asn Ser
945                 950                 955                 960
Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu Trp Ile Leu Gln
                965                 970                 975
Asp Val Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp Tyr Ser Glu Ser
            980                 985                 990
Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe Val Thr Ile Thr
        995                 1000                1005
Asn Asn Ile Met Gly Tyr Met Lys Leu Tyr Ile Asn Gly Glu Leu Lys
    1010                1015                1020
Gln Ser Gln Lys Ile Glu Asp Leu Asp Glu Val Lys Leu Asp Lys Thr
1025                1030                1035                1040
Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn Gln Met Leu Trp
                1045                1050                1055
Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser Asn Glu Asp Ile
            1060                1065                1070
Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn Val Ile Lys Asp Tyr
        1075                1080                1085
Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu Tyr Tyr Ile Ile Asn Asp
    1090                1095                1100
Asn Tyr Ile Asp Arg Tyr Ile Ala Pro Glu Ser Asn Val Leu Val Leu
1105                1110                1115                1120
Val Gln Tyr Pro Asp Arg Ser Lys Leu Tyr Thr Gly Asn Pro Ile Thr
                1125                1130                1135
Ile Lys Ser Val Ser Asp Lys Asn Pro Tyr Ser Arg Ile Leu Asn Gly
            1140                1145                1150
Asp Asn Ile Ile Leu His Met Leu Tyr Asn Ser Arg Lys Tyr Met Ile
        1155                1160                1165
Ile Arg Asp Thr Asp Thr Ile Tyr Ala Thr Gln Gly Gly Glu Cys Ser
    1170                1175                1180
Gln Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn Leu Gly Asn Tyr
1185                1190                1195                1200
Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser Lys Asn Lys Tyr
                1205                1210                1215
Cys Ser Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr Met Leu Leu Ala
            1220                1225                1230
Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Lys Asn Ala Tyr Thr Pro
        1235                1240                1245
Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser Thr Ser Ser Phe
    1250                1255                1260
Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu
1265                1270                1275


<210> 14
<211> 1285
<212> PRT
<213> Clostridium botulinum D2

<400> 14
Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp
 1                5                  10                  15
Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile Thr Thr
            20                  25                  30
Pro Val Lys Ala Phe Met Ile Thr Gln Asn Ile Trp Val Ile Pro Glu
        35                  40                  45
Arg Phe Ser Ser Asp Thr Asn Pro Ser Leu Ser Lys Pro Pro Arg Pro
    50                  55                  60
Thr Ser Lys Tyr Gln Ser Tyr Tyr Asp Pro Ser Tyr Leu Ser Thr Asp
65                  70                  75                  80
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Glu Gln Lys Asp Thr Phe Leu Lys Gly Ile Ile Lys Leu Phe Lys Arg
                85                  90                  95
Ile Asn Glu Arg Asp Ile Gly Lys Lys Leu Ile Asn Tyr Leu Val Val
            100                 105                 110
Gly Ser Pro Phe Met Gly Asp Ser Ser Thr Pro Glu Asp Thr Phe Asp
        115                 120                 125
Phe Thr Arg His Thr Thr Asn Ile Ala Val Glu Lys Phe Glu Asn Gly
    130                 135                 140
Ser Trp Lys Val Thr Asn Ile Ile Thr Pro Ser Val Leu Ile Phe Gly
145                 150                 155                 160
Pro Leu Pro Asn Ile Leu Asp Tyr Thr Ala Ser Leu Thr Leu Gln Gly
                165                 170                 175
Gln Gln Ser Asn Pro Ser Phe Glu Gly Phe Gly Thr Leu Ser Ile Leu
            180                 185                 190
Lys Val Ala Pro Glu Phe Leu Leu Thr Phe Ser Asp Val Thr Ser Asn
        195                 200                 205
Gln Ser Ser Ala Val Leu Gly Lys Ser Ile Phe Cys Met Asp Pro Val
    210                 215                 220
Ile Ala Leu Met His Glu Leu Thr His Ser Leu His Gln Leu Tyr Gly
225                 230                 235                 240
Ile Asn Ile Pro Ser Asp Lys Arg Ile Arg Pro Gln Val Ser Glu Gly
                245                 250                 255
Phe Phe Ser Gln Asp Gly Pro Asn Val Gln Phe Glu Glu Leu Tyr Thr
            260                 265                 270
Phe Gly Gly Ser Asp Val Glu Ile Ile Pro Gln Ile Glu Arg Leu Gln
        275                 280                 285
Leu Arg Glu Lys Ala Leu Gly His Tyr Lys Asp Ile Ala Lys Arg Leu
    290                 295                 300
Asn Asn Ile Asn Lys Thr Ile Pro Ser Ser Trp Ser Ser Asn Ile Asp
305                 310                 315                 320
Lys Tyr Lys Lys Ile Phe Ser Glu Lys Tyr Asn Phe Asp Lys Asp Asn
                325                 330                 335
Thr Gly Asn Phe Val Val Asn Ile Asp Lys Phe Asn Ser Leu Tyr Ser
            340                 345                 350
Asp Leu Thr Asn Val Met Ser Glu Val Val Tyr Ser Ser Gln Tyr Asn
        355                 360                 365
Val Lys Asn Arg Thr His Tyr Phe Ser Lys His Tyr Leu Pro Val Phe
    370                 375                 380
Ala Asn Ile Leu Asp Asp Asn Ile Tyr Thr Ile Ile Asn Gly Phe Asn
385                 390                 395                 400
Leu Thr Thr Lys Gly Phe Asn Ile Glu Asn Ser Gly Gln Asn Ile Glu
                405                 410                 415
Arg Asn Pro Ala Leu Gln Lys Leu Ser Ser Glu Ser Val Val Asp Leu
            420                 425                 430
Phe Thr Lys Val Cys Leu Arg Leu Thr Arg Asn Ser Arg Asp Asp Ser
        435                 440                 445
Thr Cys Ile Gln Val Lys Asn Asn Thr Leu Pro Tyr Val Ala Asp Lys
    450                 455                 460
Asp Ser Ile Ser Gln Glu Ile Phe Glu Ser Gln Ile Ile Thr Asp Glu
465                 470                 475                 480
Thr Asn Val Glu Asn Tyr Ser Asp Asn Phe Ser Leu Asp Glu Ser Ile
                485                 490                 495
Leu Asp Ala Lys Val Pro Thr Asn Pro Glu Ala Val Asp Pro Leu Leu
            500                 505                 510
Pro Asn Val Asn Met Glu Pro Leu Asn Val Pro Gly Glu Glu Glu Val
        515                 520                 525
Phe Tyr Asp Asp Ile Thr Lys Asp Val Asp Tyr Leu Asn Ser Tyr Tyr
    530                 535                 540
Tyr Leu Glu Ala Gln Lys Leu Ser Asn Asn Val Glu Asn Ile Thr Leu
545                 550                 555                 560
Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys Ile Tyr Thr
                565                 570                 575
Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val Gln Ala Gly
            580                 585                 590
Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe Thr Thr Asn
        595                 600                 605
Ile Met Lys Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Ala Ile
    610                 615                 620
```

Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser Ala Leu Arg
625 630 635 640
Gly Asn Phe Lys Gln Ala Phe Ala Thr Ala Gly Val Ala Phe Leu Leu
645 650 655
Glu Gly Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Val Phe Thr Phe
660 665 670
Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr Ile Glu Asn
675 680 685
Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr Gln Trp Met
690 695 700
Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Arg Phe Asn His Ile Ser
705 710 715 720
Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala Ile Lys Ala
725 730 735
Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn
740 745 750
Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile
755 760 765
Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val
770 775 780
Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn
785 790 795 800
Lys Phe Asp Leu Lys Thr Lys Thr Glu Leu Ile Asn Leu Ile Asp Ser
805 810 815
His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys Ala Lys Val
820 825 830
Asn Glu Ser Phe Glu Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr
835 840 845
Asn Asn Ser Leu Leu Lys Asp Met Ile Asn Glu Tyr Phe Asn Ser Ile
850 855 860
Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys Asn Thr Leu Met
865 870 875 880
Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Val Glu Gly Asn Val Gln
885 890 895
Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Asp
900 905 910
Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn
915 920 925
Ala Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys
930 935 940
Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn
945 950 955 960
Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr
965 970 975
Leu Lys Gln Asn Glu Asn Ser Glu Gln Asp Ile Asn Phe Ser Tyr Asp
980 985 990
Ile Ser Lys Asn Ala Ala Gly Tyr Asn Lys Trp Phe Phe Val Thr Ile
995 1000 1005
Thr Thr Asn Met Met Gly Asn Met Met Ile Tyr Ile Asn Gly Lys Leu
1010 1015 1020
Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys
1025 1030 1035 1040
Thr Ile Thr Phe Gln Met Asn Lys Ile Pro Asn Thr Gly Leu Ile Thr
1045 1050 1055
Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe
1060 1065 1070
Ala Lys Glu Leu Asp Asp Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu
1075 1080 1085
Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr
1090 1095 1100
Asp Lys Glu Tyr Tyr Met Ile Asn Val Asn Tyr Met Asn Arg Tyr Met
1105 1110 1115 1120
Ser Lys Lys Gly Asn Gly Ile Val Phe Asn Thr Arg Lys Asn Asn Asn
1125 1130 1135
Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn
1140 1145 1150
Thr Asn Asp Thr Arg Val Arg Gly Glu Asn Val Leu Tyr Phe Asn Thr
1155 1160 1165

Thr Ile Asp Asn Lys Gln Tyr Ser Leu Gly Met Tyr Lys Pro Ser Arg
1170 1175 1180
Asn Leu Gly Thr Asp Leu Val Pro Leu Gly Ala Leu Asp Gln Pro Met
1185 1190 1195 1200
Asp Glu Ile Arg Lys Tyr Gly Ser Phe Ile Ile Gln Pro Cys Asn Thr
1205 1210 1215
Phe Asp Tyr Tyr Ala Ser Gln Leu Phe Leu Ser Ser Asn Ala Thr Thr
1220 1225 1230
Asn Arg Leu Gly Ile Leu Ser Ile Gly Ser Tyr Ser Phe Lys Leu Gly
1235 1240 1245
Asp Asp Tyr Trp Phe Asn His Glu Tyr Leu Ile Pro Val Ile Lys Ile
1250 1255 1260
Glu His Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Val Phe
1265 1270 1275 1280
Val Pro Ala Ser Glu
1285

<210> 15
<211> 1252
<212> PRT
<213> Clostridium botulinum E1

<400> 15
Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
1 5 10 15
Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser
20 25 30
Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
35 40 45
Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
50 55 60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
65 70 75 80
Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
85 90 95
Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100 105 110
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115 120 125
Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu
130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190
Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
195 200 205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210 215 220
Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
225 230 235 240
Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
245 250 255
Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
260 265 270
Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
275 280 285
Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
290 295 300
Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305 310 315 320
Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
325 330 335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
340 345 350

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Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
        355                 360                 365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
    370                 375                 380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr
385                 390                 395                 400
Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val
                405                 410                 415
Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly
            420                 425                 430
Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile
        435                 440                 445
Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr
    450                 455                 460
Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala
465                 470                 475                 480
Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
                485                 490                 495
Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His
            500                 505                 510
Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
        515                 520                 525
Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala
    530                 535                 540
Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile
545                 550                 555                 560
Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile
                565                 570                 575
Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr
            580                 585                 590
Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu
        595                 600                 605
Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala
    610                 615                 620
Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu
625                 630                 635                 640
Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
                645                 650                 655
Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
            660                 665                 670
Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
        675                 680                 685
Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met
    690                 695                 700
Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile Ile Glu
705                 710                 715                 720
Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn
                725                 730                 735
Lys Tyr Asp Ile Lys Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
            740                 745                 750
Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser
        755                 760                 765
Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu
    770                 775                 780
Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His
785                 790                 795                 800
Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr
                805                 810                 815
Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp
            820                 825                 830
Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys
        835                 840                 845
Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp
    850                 855                 860
Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys
865                 870                 875                 880
Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser
                885                 890                 895
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Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr
            900                 905                 910
Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn
        915                 920                 925
Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg
    930                 935                 940
Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile
945                 950                 955                 960
Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn
                965                 970                 975
Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe
            980                 985                 990
Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
        995                 1000                1005
Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His
    1010                1015                1020
Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg
1025                1030                1035                1040
Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu
                1045                1050                1055
Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu
            1060                1065                1070
Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu
        1075                1080                1085
Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser
    1090                1095                1100
Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg
1105                1110                1115                1120
Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser
                1125                1130                1135
Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe
            1140                1145                1150
Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr
        1155                1160                1165
Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe
    1170                1175                1180
Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn
1185                1190                1195                1200
Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala
                1205                1210                1215
Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His
            1220                1225                1230
Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly
        1235                1240                1245
Trp Gln Glu Lys
    1250


<210> 16
<211> 1252
<212> PRT
<213> Clostridium botulinum E2

<400> 16
Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
 1               5                  10                  15
Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser
            20                  25                  30
Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
        35                  40                  45
Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
    50                  55                  60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
65                  70                  75                  80
Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
                85                  90                  95
Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
            100                 105                 110
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Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115 120 125
Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ile Gln Asp Ile Leu
130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190
Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
195 200 205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210 215 220
Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
225 230 235 240
Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
245 250 255
Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
260 265 270
Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
275 280 285
Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
290 295 300
Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305 310 315 320
Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
325 330 335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
340 345 350
Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
355 360 365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
370 375 380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr
385 390 395 400
Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val
405 410 415
Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly
420 425 430
Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile
435 440 445
Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr
450 455 460
Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala
465 470 475 480
Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
485 490 495
Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His
500 505 510
Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
515 520 525
Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala
530 535 540
Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile
545 550 555 560
Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile
565 570 575
Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr
580 585 590
Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu
595 600 605
Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala
610 615 620
Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu
625 630 635 640
Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
645 650 655

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Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
            660                 665                 670
Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
        675                 680                 685
Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met
    690                 695                 700
Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile Ile Glu
705                 710                 715                 720
Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn
                725                 730                 735
Lys Tyr Asp Ile Lys Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
            740                 745                 750
Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser
        755                 760                 765
Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu
    770                 775                 780
Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His
785                 790                 795                 800
Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr
                805                 810                 815
Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp
            820                 825                 830
Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys
        835                 840                 845
Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp
    850                 855                 860
Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys
865                 870                 875                 880
Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser
                885                 890                 895
Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr
            900                 905                 910
Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn
        915                 920                 925
Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg
    930                 935                 940
Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile
945                 950                 955                 960
Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn
                965                 970                 975
Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe
            980                 985                 990
Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
        995                 1000                1005
Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His
    1010                1015                1020
Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg
1025                1030                1035                1040
Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu
                1045                1050                1055
Thr Glu Ile Gln Thr Leu Tyr Asn Asn Glu Pro Asn Ala Asn Ile Leu
            1060                1065                1070
Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu
        1075                1080                1085
Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Thr Asp Ser
    1090                1095                1100
Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg
1105                1110                1115                1120
Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser
                1125                1130                1135
Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe
            1140                1145                1150
Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Asn Thr
        1155                1160                1165
Thr Asn Lys Glu Lys Thr Ile Lys Ser Ser Ser Ser Gly Asn Arg Phe
    1170                1175                1180
Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn
1185                1190                1195                1200
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Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Met Leu Gly Phe Lys Asp
1205 1210 1215
Asn Thr Leu Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp Asn
1220 1225 1230
Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly
1235 1240 1245
Trp Gln Glu Lys
1250

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<211> 1252
<212> PRT
<213> Clostridium botulinum E3

<400> 17
Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
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Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser
20 25 30
Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
35 40 45
Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
50 55 60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
65 70 75 80
Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
85 90 95
Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100 105 110
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115 120 125
Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln His Ile Leu
130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190
Arg Phe Asn Asp Asn Ser Ile Asn Glu Phe Ile Gln Asp Pro Ala Leu
195 200 205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210 215 220
Lys Gly Ile Thr Thr Thr Cys Ile Ile Thr Gln Gln Gln Asn Pro Leu
225 230 235 240
Ile Thr Asn Arg Lys Gly Ile Asn Ile Glu Glu Phe Leu Thr Phe Gly
245 250 255
Gly Asn Asp Leu Asn Ile Ile Thr Val Ala Gln Tyr Asn Asp Ile Tyr
260 265 270
Thr Asn Leu Leu Asn Asp Tyr Arg Lys Ile Ala Ser Lys Leu Ser Lys
275 280 285
Val Gln Val Ser Asn Pro Gln Leu Asn Pro Tyr Lys Asp Ile Phe Gln
290 295 300
Glu Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305 310 315 320
Ile Asn Lys Phe Asp Asp Ile Leu Lys Lys Leu Tyr Ser Phe Thr Glu
325 330 335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Glu Thr Tyr Ile
340 345 350
Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
355 360 365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
370 375 380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Lys Pro Ile Thr
385 390 395 400
Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val
405 410 415

Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly
420 425 430
Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile
435 440 445
Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr
450 455 460
Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala
465 470 475 480
Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
485 490 495
Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His
500 505 510
Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
515 520 525
Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala
530 535 540
Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile
545 550 555 560
Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile
565 570 575
Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr
580 585 590
Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu
595 600 605
Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala
610 615 620
Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu
625 630 635 640
Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
645 650 655
Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
660 665 670
Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
675 680 685
Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met
690 695 700
Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile Ile Glu
705 710 715 720
Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn
725 730 735
Lys Tyr Asp Ile Lys Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
740 745 750
Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser
755 760 765
Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu
770 775 780
Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His
785 790 795 800
Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr
805 810 815
Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp
820 825 830
Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys
835 840 845
Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp
850 855 860
Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys
865 870 875 880
Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser
885 890 895
Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr
900 905 910
Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn
915 920 925
Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg
930 935 940
Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile
945 950 955 960

Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn
965 970 975
Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe
980 985 990
Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
995 1000 1005
Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His
1010 1015 1020
Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg
1025 1030 1035 1040
Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu
1045 1050 1055
Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu
1060 1065 1070
Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu
1075 1080 1085
Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser
1090 1095 1100
Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg
1105 1110 1115 1120
Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser
1125 1130 1135
Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe
1140 1145 1150
Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr
1155 1160 1165
Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe
1170 1175 1180
Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn
1185 1190 1195 1200
Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala
1205 1210 1215
Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His
1220 1225 1230
Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly
1235 1240 1245
Trp Gln Glu Lys
1250

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<212> PRT
<213> Clostridium botulinum F1

<400> 18
Met Pro Val Ala Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp
1 5 10 15
Asp Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys Ser Lys Lys
20 25 30
Tyr Tyr Lys Ala Phe Glu Ile Met Arg Asn Val Trp Ile Ile Pro Glu
35 40 45
Arg Asn Thr Ile Gly Thr Asn Pro Ser Asp Phe Asp Pro Pro Ala Ser
50 55 60
Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
65 70 75 80
Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys Leu Phe Lys
85 90 95
Arg Ile Asn Ser Asn Pro Ala Gly Lys Val Leu Leu Gln Glu Ile Ser
100 105 110
Tyr Ala Lys Pro Tyr Leu Gly Asn Asp His Thr Pro Ile Asp Glu Phe
115 120 125
Ser Pro Val Thr Arg Thr Thr Ser Val Asn Ile Lys Leu Ser Thr Asn
130 135 140
Val Glu Ser Ser Met Leu Leu Asn Leu Leu Val Leu Gly Ala Gly Pro
145 150 155 160
Asp Ile Phe Glu Ser Cys Cys Tyr Pro Val Arg Lys Leu Ile Asp Pro
165 170 175

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Asp Val Val Tyr Asp Pro Ser Asn Tyr Gly Phe Gly Ser Ile Asn Ile
            180                 185                 190
Val Thr Phe Ser Pro Glu Tyr Glu Tyr Thr Phe Asn Asp Ile Ser Gly
        195                 200                 205
Gly His Asn Ser Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser
    210                 215                 220
Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Arg
225                 230                 235                 240
Gly Val Thr Tyr Glu Glu Thr Ile Glu Val Lys Gln Ala Pro Leu Met
                245                 250                 255
Ile Ala Glu Lys Pro Ile Arg Leu Glu Glu Phe Leu Thr Phe Gly Gly
            260                 265                 270
Gln Asp Leu Asn Ile Ile Thr Ser Ala Met Lys Glu Lys Ile Tyr Asn
        275                 280                 285
Asn Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Ser Glu Val
    290                 295                 300
Asn Ser Ala Pro Pro Glu Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe
305                 310                 315                 320
Gln Trp Lys Tyr Gly Leu Asp Lys Asn Ala Asp Gly Ser Tyr Thr Val
                325                 330                 335
Asn Glu Asn Lys Phe Asn Glu Ile Tyr Lys Lys Leu Tyr Ser Phe Thr
            340                 345                 350
Glu Ser Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr
        355                 360                 365
Phe Ile Lys Tyr Glu Phe Leu Lys Val Pro Asn Leu Leu Asp Asp Asp
    370                 375                 380
Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn
385                 390                 395                 400
Asn Arg Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile
                405                 410                 415
Pro Asp Lys Gly Leu Val Glu Lys Ile Val Lys Phe Cys Lys Ser Val
            420                 425                 430
Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu Cys Ile Arg Val
        435                 440                 445
Asn Asn Ser Glu Leu Phe Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu
    450                 455                 460
Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn
465                 470                 475                 480
Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser
                485                 490                 495
Gln Thr Ile Pro Gln Ile Ser Asn Arg Thr Leu Asn Thr Leu Val Gln
            500                 505                 510
Asp Asn Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile
        515                 520                 525
Glu Glu Tyr Asp Val Val Asp Phe Asn Val Phe Phe Tyr Leu His Ala
    530                 535                 540
Gln Lys Val Pro Glu Gly Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile
545                 550                 555                 560
Asp Thr Ala Leu Leu Glu Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu
                565                 570                 575
Phe Ile Asp Thr Ile Asn Lys Pro Val Asn Ala Ala Leu Phe Ile Asp
            580                 585                 590
Trp Ile Ser Lys Val Ile Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys
        595                 600                 605
Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Val
    610                 615                 620
Gly Leu Ala Leu Asn Ile Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu
625                 630                 635                 640
Glu Ala Phe Glu Leu Leu Gly Val Gly Ile Leu Leu Glu Phe Val Pro
                645                 650                 655
Glu Leu Thr Ile Pro Val Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile
            660                 665                 670
Asp Ser Tyr Glu Asn Lys Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser
        675                 680                 685
Leu Ile Glu Arg Glu Ala Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val
    690                 695                 700
Ser Asn Trp Leu Thr Arg Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu
705                 710                 715                 720
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Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asp Ala Ile Lys Thr Ala
                725                 730                 735
Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu
            740                 745                 750
Glu Ser Glu Tyr Asn Ile Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys
        755                 760                 765
Val Ser Leu Ala Met Lys Asn Ile Glu Arg Phe Met Thr Glu Ser Ser
    770                 775                 780
Ile Ser Tyr Leu Met Lys Leu Ile Asn Glu Ala Lys Val Gly Lys Leu
785                 790                 795                 800
Lys Lys Tyr Asp Asn His Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu
                805                 810                 815
Asp His Arg Ser Ile Leu Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu
            820                 825                 830
Val Thr Ser Thr Leu Asn Ser Ser Ile Pro Phe Glu Leu Ser Ser Tyr
        835                 840                 845
Thr Asn Asp Lys Ile Leu Ile Ile Tyr Phe Asn Arg Leu Tyr Lys Lys
    850                 855                 860
Ile Lys Asp Ser Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys Phe
865                 870                 875                 880
Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asn Val
                885                 890                 895
Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Asn Ser Arg
            900                 905                 910
Leu Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn Ser
        915                 920                 925
Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Lys His
    930                 935                 940
Tyr Lys Pro Met Asn His Asn Arg Glu Tyr Thr Ile Ile Asn Cys Met
945                 950                 955                 960
Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Arg Thr Val Arg Asp
                965                 970                 975
Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr Ser Gly Asn Lys Glu Asn
            980                 985                 990
Leu Ile Phe Arg Tyr Glu Glu Leu Asn Arg Ile Ser Asn Tyr Ile Asn
        995                 1000                1005
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
    1010                1015                1020
Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu Lys Ser Ile Ser Asn Leu
1025                1030                1035                1040
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
                1045                1050                1055
Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asn Thr
            1060                1065                1070
Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asn Glu Pro Asp
        1075                1080                1085
Pro Ser Ile Leu Lys Asn Tyr Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
    1090                1095                1100
Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys Asp Lys Tyr Ile Thr Leu
1105                1110                1115                1120
Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln Arg Gly Val Thr Glu Gly
                1125                1130                1135
Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu Gly Val Glu Val Ile Ile
            1140                1145                1150
Arg Lys Asn Gly Pro Ile Asp Ile Ser Asn Thr Asp Asn Phe Val Arg
        1155                1160                1165
Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Gly Val Glu Tyr
    1170                1175                1180
Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys Glu Lys Ile Ile Arg Thr
1185                1190                1195                1200
Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile Ile Val Met Asp Ser Ile
                1205                1210                1215
Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly Ser Asn Ile
            1220                1225                1230
Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp Tyr
        1235                1240                1245
Tyr Asn Asn Ile Arg Arg Asn Thr Ser Ser Asn Gly Cys Phe Trp Ser
    1250                1255                1260
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Ser Ile Ser Lys Glu Asn Gly Trp Lys Glu
1265 1270

<210> 19
<211> 1280
<212> PRT
<213> Clostridium botulinum F2

<400> 19

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 1               5                  10                  15
Glu Thr Ile Leu Tyr Met Gln Lys Pro Tyr Glu Glu Arg Ser Arg Lys
            20                  25                  30
Tyr Tyr Lys Ala Phe Glu Ile Met Pro Asn Val Trp Ile Met Pro Glu
        35                  40                  45
Arg Asp Thr Ile Gly Thr Lys Pro Asp Glu Phe Gln Val Pro Asp Ser
    50                  55                  60
Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
65                  70                  75                  80
Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Met Ile Lys Leu Phe Asn
                85                  90                  95
Arg Ile Asn Ser Asn Pro Thr Gly Lys Val Leu Leu Glu Glu Val Ser
            100                 105                 110
Asn Ala Arg Pro Tyr Leu Gly Asp Asp Asp Thr Leu Ile Asn Glu Phe
        115                 120                 125
Leu Pro Val Asn Val Thr Thr Ser Val Asn Ile Lys Phe Ser Thr Asp
    130                 135                 140
Val Glu Ser Ser Ile Ile Ser Asn Leu Leu Val Leu Gly Ala Gly Pro
145                 150                 155                 160
Asp Ile Phe Lys Ala Tyr Cys Thr Pro Leu Val Arg Phe Asn Lys Ser
                165                 170                 175
Asp Lys Leu Ile Glu Pro Ser Asn His Gly Phe Gly Ser Ile Asn Ile
            180                 185                 190
Leu Thr Phe Ser Pro Glu Tyr Glu His Ile Phe Asn Asp Ile Ser Gly
        195                 200                 205
Gly Asn His Asn Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser
    210                 215                 220
Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Lys
225                 230                 235                 240
Ala Val Thr His Lys Glu Ser Leu Val Ala Glu Arg Gly Pro Leu Met
                245                 250                 255
Ile Ala Glu Lys Pro Ile Arg Leu Glu Glu Phe Leu Thr Phe Gly Gly
            260                 265                 270
Glu Asp Leu Asn Ile Ile Pro Ser Ala Met Lys Glu Lys Ile Tyr Asn
        275                 280                 285
Asp Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Arg Glu Val
    290                 295                 300
Asn Thr Ala Pro Pro Gly Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe
305                 310                 315                 320
Gln Trp Lys Tyr Gly Leu Asp Arg Asn Ala Asp Gly Ser Tyr Thr Val
                325                 330                 335
Asn Arg Asn Lys Phe Asn Glu Ile Tyr Lys Lys Leu Tyr Ser Phe Thr
            340                 345                 350
Glu Ile Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr
        355                 360                 365
Phe Ile Lys Tyr Gly Phe Val Lys Val Pro Asn Leu Leu Asp Asp Asp
    370                 375                 380
Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn
385                 390                 395                 400
Asn Arg Gly Gln Asn Ile Asn Leu Asn Pro Lys Ile Ile Asp Ser Ile
                405                 410                 415
Pro Asp Lys Gly Leu Val Glu Lys Ile Ile Lys Phe Cys Lys Ser Ile
            420                 425                 430
Ile Pro Arg Lys Gly Thr Lys Gln Ser Pro Ser Leu Cys Ile Arg Val
        435                 440                 445
Asn Asn Arg Glu Leu Phe Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu
    450                 455                 460
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Ser Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn
465                 470                 475                 480
Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser
                485                 490                 495
Glu Thr Ile Pro Gln Ile Ser Asn Arg Thr Leu Asn Thr Leu Val Gln
            500                 505                 510
Asp Asn Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile
        515                 520                 525
Glu Glu Tyr Asp Val Val Asp Phe Asn Val Phe Phe Tyr Leu His Ala
    530                 535                 540
Gln Lys Val Pro Glu Gly Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile
545                 550                 555                 560
Asp Thr Ala Leu Leu Glu Glu Ser Lys Val Tyr Thr Phe Phe Ser Ser
                565                 570                 575
Glu Phe Ile Asp Thr Ile Asn Lys Pro Val Asn Ala Ala Leu Phe Ile
            580                 585                 590
Asp Trp Ile Ser Lys Val Ile Arg Asp Phe Thr Thr Glu Ala Thr Gln
        595                 600                 605
Lys Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr
    610                 615                 620
Val Gly Leu Ala Leu Asn Ile Val Ile Glu Ala Glu Lys Gly Asn Phe
625                 630                 635                 640
Glu Glu Ala Phe Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Val
                645                 650                 655
Pro Glu Leu Thr Ile Pro Val Ile Leu Val Phe Thr Ile Lys Ser Tyr
            660                 665                 670
Ile Asp Ser Tyr Glu Asn Lys Asn Lys Ala Ile Lys Ala Ile Asn Asn
        675                 680                 685
Ser Leu Ile Glu Arg Glu Ala Lys Trp Lys Glu Ile Tyr Ser Trp Ile
    690                 695                 700
Val Ser Asn Trp Leu Thr Arg Ile Asn Thr Gln Phe Asn Lys Arg Lys
705                 710                 715                 720
Glu Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asp Ala Ile Lys Thr
                725                 730                 735
Ala Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr Ser Asp Glu Lys Asn Arg
            740                 745                 750
Leu Glu Ser Lys Tyr Asn Ile Asn Asn Ile Glu Glu Glu Leu Asn Lys
        755                 760                 765
Lys Val Ser Leu Ala Met Lys Asn Ile Glu Arg Phe Met Thr Glu Ser
    770                 775                 780
Ser Ile Ser Tyr Leu Met Lys Leu Ile Asn Glu Ala Glu Val Gly Lys
785                 790                 795                 800
Leu Lys Glu Tyr Asp Lys His Val Lys Ser Asp Leu Leu Asp Tyr Ile
                805                 810                 815
Leu Tyr His Lys Leu Ile Leu Gly Glu Gln Thr Lys Glu Leu Ile Asp
            820                 825                 830
Leu Val Thr Ser Thr Leu Asn Ser Ser Ile Pro Phe Glu Leu Ser Ser
        835                 840                 845
Tyr Thr Asn Asp Lys Ile Leu Ile Ile Tyr Phe Asn Arg Leu Tyr Lys
    850                 855                 860
Lys Ile Lys Asp Ser Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys
865                 870                 875                 880
Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asn
                885                 890                 895
Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser Gly
            900                 905                 910
Arg Leu Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn
        915                 920                 925
Ser Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Thr Ile Pro Lys
    930                 935                 940
His Tyr Arg Pro Met Asn Arg Asn Arg Glu Tyr Thr Ile Ile Asn Cys
945                 950                 955                 960
Met Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Arg Thr Ile Arg
                965                 970                 975
Asp Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr Ser Gly Asn Lys Glu
            980                 985                 990
Lys Leu Ile Phe Arg Tyr Glu Glu Leu Ala Ser Ile Ser Asp Tyr Ile
        995                 1000                1005
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Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser
    1010                1015                1020
Arg Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu Lys Ser Ile Ser Asn
1025                1030                1035                1040
Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly
                1045                1050                1055
Cys Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asn
            1060                1065                1070
Thr Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asn Glu Pro
        1075                1080                1085
Asp Pro Ser Ile Leu Lys Asp Tyr Trp Gly Asn Tyr Leu Leu Tyr Asn
    1090                1095                1100
Lys Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys Asp Lys Tyr Ile Thr
1105                1110                1115                1120
Arg Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln Arg Gly Val Thr Gly
                1125                1130                1135
Gly Ile Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu Gly Val Glu Val
            1140                1145                1150
Ile Ile Arg Lys Asn Ala Pro Ile Asp Ile Ser Asn Thr Asp Asn Phe
        1155                1160                1165
Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp His Gly Val
    1170                1175                1180
Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Thr Lys Ser Glu Lys Ile
1185                1190                1195                1200
Ile Lys Leu Ile Arg Thr Ser Asn Pro Asn Asp Ser Leu Gly Gln Ile
                1205                1210                1215
Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn
            1220                1225                1230
Asn Asp Gly Ser Asn Ile Gly Leu Leu Gly Phe His Ser Asp Asp Leu
        1235                1240                1245
Val Ala Ser Ser Trp Tyr Tyr Asn His Ile Arg Arg Asn Thr Ser Ser
    1250                1255                1260
Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Lys Glu
1265                1270                1275                1280


<210> 20
<211> 1278
<212> PRT
<213> Clostridium botulinum F3

<400> 20
Met Pro Val Val Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp
 1               5                  10                  15
Asp Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys Ser Lys Lys
            20                  25                  30
Tyr Tyr Lys Ala Phe Glu Ile Met Arg Asn Val Trp Ile Ile Pro Glu
        35                  40                  45
Arg Asn Thr Ile Gly Thr Asp Pro Ser Asp Phe Asp Pro Pro Ala Ser
    50                  55                  60
Leu Glu Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
65                  70                  75                  80
Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys Leu Phe Lys
                85                  90                  95
Arg Ile Asn Ser Asn Pro Ala Gly Glu Val Leu Leu Gln Glu Ile Ser
            100                 105                 110
Tyr Ala Lys Pro Tyr Leu Gly Asn Glu His Thr Pro Ile Asn Glu Phe
        115                 120                 125
His Pro Val Thr Arg Thr Thr Ser Val Asn Ile Lys Ser Ser Thr Asn
    130                 135                 140
Val Lys Ser Ser Ile Ile Leu Asn Leu Leu Val Leu Gly Ala Gly Pro
145                 150                 155                 160
Asp Ile Phe Glu Asn Ser Ser Tyr Pro Val Arg Lys Leu Met Asp Ser
                165                 170                 175
Gly Gly Val Tyr Asp Pro Ser Asn Asp Gly Phe Gly Ser Ile Asn Ile
            180                 185                 190
Val Thr Phe Ser Pro Glu Tyr Glu Tyr Thr Phe Asn Asp Ile Ser Gly
        195                 200                 205
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Gly Tyr Asn Ser Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser
    210                 215                 220
Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Arg
225                 230                 235                 240
Gly Val Thr Tyr Lys Glu Thr Ile Lys Val Lys Gln Ala Pro Leu Met
                245                 250                 255
Ile Ala Glu Lys Pro Ile Arg Leu Glu Glu Phe Leu Thr Phe Gly Gly
            260                 265                 270
Gln Asp Leu Asn Ile Ile Thr Ser Ala Met Lys Glu Lys Ile Tyr Asn
        275                 280                 285
Asn Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Ser Arg Val
    290                 295                 300
Asn Ser Ala Pro Pro Glu Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe
305                 310                 315                 320
Gln Trp Lys Tyr Gly Leu Asp Lys Asn Ala Asp Gly Ser Tyr Thr Val
                325                 330                 335
Asn Glu Asn Lys Phe Asn Glu Ile Tyr Lys Lys Leu Tyr Ser Phe Thr
            340                 345                 350
Glu Ile Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr
        355                 360                 365
Phe Ile Lys Tyr Gly Phe Leu Lys Val Pro Asn Leu Leu Asp Asp Asp
    370                 375                 380
Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn
385                 390                 395                 400
Asn Arg Gly Gln Asn Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile
                405                 410                 415
Pro Asp Lys Gly Leu Val Glu Lys Ile Val Lys Phe Cys Lys Ser Val
            420                 425                 430
Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu Cys Ile Arg Val
        435                 440                 445
Asn Asn Arg Glu Leu Phe Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu
    450                 455                 460
Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn
465                 470                 475                 480
Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser
                485                 490                 495
Glu Thr Ile Pro Gln Ile Ser Asn Gln Thr Leu Asn Thr Leu Val Gln
            500                 505                 510
Asp Asp Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile
        515                 520                 525
Glu Glu His Asn Val Val Asp Leu Asn Val Phe Phe Tyr Leu His Ala
    530                 535                 540
Gln Lys Val Pro Glu Gly Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile
545                 550                 555                 560
Asp Thr Ala Leu Ser Glu Glu Ser Gln Val Tyr Thr Phe Phe Ser Ser
                565                 570                 575
Glu Phe Ile Asn Thr Ile Asn Lys Pro Val His Ala Ala Leu Phe Ile
            580                 585                 590
Ser Trp Ile Asn Gln Val Ile Arg Asp Phe Thr Thr Glu Ala Thr Gln
        595                 600                 605
Lys Ser Thr Phe Asp Lys Ile Ala Asp Ile Ser Leu Val Val Pro Tyr
    610                 615                 620
Val Gly Leu Ala Leu Asn Ile Gly Asn Glu Val Gln Lys Glu Asn Phe
625                 630                 635                 640
Lys Glu Ala Phe Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Val
                645                 650                 655
Pro Glu Leu Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe
            660                 665                 670
Ile Gly Ser Ser Glu Asn Lys Asn Lys Ile Ile Lys Ala Ile Asn Asn
        675                 680                 685
Ser Leu Met Glu Arg Glu Thr Lys Trp Lys Glu Ile Tyr Ser Trp Ile
    690                 695                 700
Val Ser Asn Trp Leu Thr Arg Ile Asn Thr Gln Phe Asn Lys Arg Lys
705                 710                 715                 720
Glu Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asp Ala Ile Lys Thr
                725                 730                 735
Val Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr Ser Asp Glu Arg Asn Arg
            740                 745                 750
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Leu Glu Ser Glu Tyr Asn Ile Asn Asn Ile Arg Glu Glu Leu Asn Lys
755 760 765
Lys Val Ser Leu Ala Met Glu Asn Ile Glu Arg Phe Ile Thr Glu Ser
770 775 780
Ser Ile Phe Tyr Leu Met Lys Leu Ile Asn Glu Ala Lys Val Ser Lys
785 790 795 800
Leu Arg Glu Tyr Asp Glu Gly Val Lys Glu Tyr Leu Leu Asp Tyr Ile
805 810 815
Ser Glu His Arg Ser Ile Leu Gly Asn Ser Val Gln Glu Leu Asn Asp
820 825 830
Leu Val Thr Ser Thr Leu Asn Asn Ser Ile Pro Phe Glu Leu Ser Ser
835 840 845
Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr Lys
850 855 860
Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys
865 870 875 880
Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asp
885 890 895
Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser Ser
900 905 910
Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn
915 920 925
Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Lys
930 935 940
Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp Cys
945 950 955 960
Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn Lys
965 970 975
Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu Val
980 985 990
Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys Trp
995 1000 1005
Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile Tyr
1010 1015 1020
Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly Asp
1025 1030 1035 1040
Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn Asp
1045 1050 1055
Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu Leu
1060 1065 1070
Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro Ser
1075 1080 1085
Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg Tyr
1090 1095 1100
Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn Ser
1105 1110 1115 1120
Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro Asn
1125 1130 1135
Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile Arg
1140 1145 1150
Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg Lys
1155 1160 1165
Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr Arg
1170 1175 1180
Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys Leu
1185 1190 1195 1200
Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val Met
1205 1210 1215
Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly
1220 1225 1230
Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser
1235 1240 1245
Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly Cys
1250 1255 1260
Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
1265 1270 1275

<210> 21
<211> 1297
<212> PRT
<213> Clostridium botulinum G

<220>
<221> VARIANT
<222> 7
<223> Identifty of amino acid is unknown

<400> 21

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Met Pro Val Asn Ile Lys Xaa Phe Asn Tyr Asn Asp Pro Ile Asn Asn
 1               5                  10                  15
Asp Asp Ile Ile Met Met Glu Pro Phe Asn Asp Pro Gly Pro Gly Thr
            20                  25                  30
Tyr Tyr Lys Ala Phe Arg Ile Ile Asp Arg Ile Trp Ile Val Pro Glu
        35                  40                  45
Arg Phe Thr Tyr Gly Phe Gln Pro Asp Gln Phe Asn Ala Ser Thr Gly
    50                  55                  60
Val Phe Ser Lys Asp Val Tyr Glu Tyr Tyr Asp Pro Thr Tyr Leu Lys
65                  70                  75                  80
Thr Asp Ala Glu Lys Asp Lys Phe Leu Lys Thr Met Ile Lys Leu Phe
                85                  90                  95
Asn Arg Ile Asn Ser Lys Pro Ser Gly Gln Arg Leu Leu Asp Met Ile
            100                 105                 110
Val Asp Ala Ile Pro Tyr Leu Gly Asn Ala Ser Thr Pro Pro Asp Lys
        115                 120                 125
Phe Ala Ala Asn Val Ala Asn Val Ser Ile Asn Lys Lys Ile Ile Gln
    130                 135                 140
Pro Gly Ala Glu Asp Gln Ile Lys Gly Leu Met Thr Asn Leu Ile Ile
145                 150                 155                 160
Phe Gly Pro Gly Pro Val Leu Ser Asp Asn Phe Thr Asp Ser Met Ile
                165                 170                 175
Met Asn Gly His Ser Pro Ile Ser Glu Gly Phe Gly Ala Arg Met Met
            180                 185                 190
Ile Arg Phe Cys Pro Ser Cys Leu Asn Val Phe Asn Asn Val Gln Glu
        195                 200                 205
Asn Lys Asp Thr Ser Ile Phe Ser Arg Arg Ala Tyr Phe Ala Asp Pro
    210                 215                 220
Ala Leu Thr Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
225                 230                 235                 240
Gly Ile Lys Ile Ser Asn Leu Pro Ile Thr Pro Asn Thr Lys Glu Phe
                245                 250                 255
Phe Met Gln His Ser Asp Pro Val Gln Ala Glu Glu Leu Tyr Thr Phe
            260                 265                 270
Gly Gly His Asp Pro Ser Val Ile Ser Pro Ser Thr Asp Met Asn Ile
        275                 280                 285
Tyr Asn Lys Ala Leu Gln Asn Phe Gln Asp Ile Ala Asn Arg Leu Asn
    290                 295                 300
Ile Val Ser Ser Ala Gln Gly Ser Gly Ile Asp Ile Ser Leu Tyr Lys
305                 310                 315                 320
Gln Ile Tyr Lys Asn Lys Tyr Asp Phe Val Glu Asp Pro Asn Gly Lys
                325                 330                 335
Tyr Ser Val Asp Lys Asp Lys Phe Asp Lys Leu Tyr Lys Ala Leu Met
            340                 345                 350
Phe Gly Phe Thr Glu Thr Asn Leu Ala Gly Glu Tyr Gly Ile Lys Thr
        355                 360                 365
Arg Tyr Ser Tyr Phe Ser Glu Tyr Leu Pro Pro Ile Lys Thr Glu Lys
    370                 375                 380
Leu Leu Asp Asn Thr Ile Tyr Thr Gln Asn Glu Gly Phe Asn Ile Ala
385                 390                 395                 400
Ser Lys Asn Leu Lys Thr Glu Phe Asn Gly Gln Asn Lys Ala Val Asn
                405                 410                 415
Lys Glu Ala Tyr Glu Glu Ile Ser Leu Glu His Leu Val Ile Tyr Arg
            420                 425                 430
Ile Ala Met Cys Lys Pro Val Met Tyr Lys Asn Thr Gly Lys Ser Glu
        435                 440                 445
Gln Cys Ile Ile Val Asn Asn Glu Asp Leu Phe Phe Ile Ala Asn Lys
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    450                 455                 460
Asp Ser Phe Ser Lys Asp Leu Ala Lys Ala Glu Thr Ile Ala Tyr Asn
465                 470                 475                 480
Thr Gln Asn Asn Thr Ile Glu Asn Asn Phe Ser Ile Asp Gln Leu Ile
                485                 490                 495
Leu Asp Asn Asp Leu Ser Ser Gly Ile Asp Leu Pro Asn Glu Asn Thr
            500                 505                 510
Glu Pro Phe Thr Asn Phe Asp Asp Ile Asp Ile Pro Val Tyr Ile Lys
        515                 520                 525
Gln Ser Ala Leu Lys Lys Ile Phe Val Asp Gly Asp Ser Leu Phe Glu
    530                 535                 540
Tyr Leu His Ala Gln Thr Phe Pro Ser Asn Ile Glu Asn Leu Gln Leu
545                 550                 555                 560
Thr Asn Ser Leu Asn Asp Ala Leu Arg Asn Asn Asn Lys Val Tyr Thr
                565                 570                 575
Phe Phe Ser Thr Asn Leu Val Glu Lys Ala Asn Thr Val Val Gly Ala
            580                 585                 590
Ser Leu Phe Val Asn Trp Val Lys Gly Val Ile Asp Asp Phe Thr Ser
        595                 600                 605
Glu Ser Thr Gln Lys Ser Thr Ile Asp Lys Val Ser Asp Val Ser Ile
    610                 615                 620
Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Val Gly Asn Glu Thr Ala
625                 630                 635                 640
Lys Glu Asn Phe Lys Asn Ala Phe Glu Ile Gly Gly Ala Ala Ile Leu
                645                 650                 655
Met Glu Phe Ile Pro Glu Leu Ile Val Pro Ile Val Gly Phe Phe Thr
            660                 665                 670
Leu Glu Ser Tyr Val Gly Asn Lys Gly His Ile Ile Met Thr Ile Ser
        675                 680                 685
Asn Ala Leu Lys Lys Arg Asp Gln Lys Trp Thr Asp Met Tyr Gly Leu
    690                 695                 700
Ile Val Ser Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile
705                 710                 715                 720
Lys Glu Arg Met Tyr Asn Ala Leu Asn Asn Gln Ser Gln Ala Ile Glu
                725                 730                 735
Lys Ile Ile Glu Asp Gln Tyr Asn Arg Tyr Ser Glu Glu Asp Lys Met
            740                 745                 750
Asn Ile Asn Ile Asp Phe Asn Asp Ile Asp Phe Lys Leu Asn Gln Ser
        755                 760                 765
Ile Asn Leu Ala Ile Asn Asn Ile Asp Asp Phe Ile Asn Gln Cys Ser
    770                 775                 780
Ile Ser Tyr Leu Met Asn Arg Met Ile Pro Leu Ala Val Lys Lys Leu
785                 790                 795                 800
Lys Asp Phe Asp Asp Asn Leu Lys Arg Asp Leu Leu Glu Tyr Ile Asp
                805                 810                 815
Thr Asn Glu Leu Tyr Leu Leu Asp Glu Val Asn Ile Leu Lys Ser Lys
            820                 825                 830
Val Asn Arg His Leu Lys Asp Ser Ile Pro Phe Asp Leu Ser Leu Tyr
        835                 840                 845
Thr Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
    850                 855                 860
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
865                 870                 875                 880
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
                885                 890                 895
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
            900                 905                 910
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
        915                 920                 925
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
    930                 935                 940
Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
945                 950                 955                 960
Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
                965                 970                 975
Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
            980                 985                 990
Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
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995 1000 1005
Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
1010 1015 1020
Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
1025 1030 1035 1040
Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
1045 1050 1055
Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
1060 1065 1070
Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
1075 1080 1085
Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
1090 1095 1100
Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
1105 1110 1115 1120
Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
1125 1130 1135
Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
1140 1145 1150
Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
1155 1160 1165
Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
1170 1175 1180
Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
1185 1190 1195 1200
Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
1205 1210 1215
Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
1220 1225 1230
Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
1235 1240 1245
Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
1250 1255 1260
Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
1265 1270 1275 1280
Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
1285 1290 1295
Glu

<210> 22
<211> 1315
<212> PRT
<213> Clostridium tetani

<400> 22
Met Pro Ile Thr Ile Asn Asn Phe Arg Tyr Ser Asp Pro Val Asn Asn
1 5 10 15
Asp Thr Ile Ile Met Met Glu Pro Pro Tyr Cys Lys Gly Leu Asp Ile
20 25 30
Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Val Pro Glu
35 40 45
Arg Tyr Glu Phe Gly Thr Lys Pro Glu Asp Phe Asn Pro Pro Ser Ser
50 55 60
Leu Ile Glu Gly Ala Ser Glu Tyr Tyr Asp Pro Asn Tyr Leu Arg Thr
65 70 75 80
Asp Ser Asp Lys Asp Arg Phe Leu Gln Thr Met Val Lys Leu Phe Asn
85 90 95
Arg Ile Lys Asn Asn Val Ala Gly Glu Ala Leu Leu Asp Lys Ile Ile
100 105 110
Asn Ala Ile Pro Tyr Leu Gly Asn Ser Tyr Ser Leu Leu Asp Lys Phe
115 120 125
Asp Thr Asn Ser Asn Ser Val Ser Phe Asn Leu Leu Glu Gln Asp Pro
130 135 140
Ser Gly Ala Thr Thr Lys Ser Ala Met Leu Thr Asn Leu Ile Ile Phe
145 150 155 160
Gly Pro Gly Pro Val Leu Asn Lys Asn Glu Val Arg Gly Ile Val Leu

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                    165                 170                 175
Arg Val Asp Asn Lys Asn Tyr Phe Pro Cys Arg Asp Gly Phe Gly Ser
                180                 185                 190
Ile Met Gln Met Ala Phe Cys Pro Glu Tyr Val Pro Thr Phe Asp Asn
        195                 200                 205
Val Ile Glu Asn Ile Thr Ser Leu Thr Ile Gly Lys Ser Lys Tyr Phe
    210                 215                 220
Gln Asp Pro Ala Leu Leu Leu Met His Glu Leu Ile His Val Leu His
225                 230                 235                 240
Gly Leu Tyr Gly Met Gln Val Ser Ser His Glu Ile Ile Pro Ser Lys
                245                 250                 255
Gln Glu Ile Tyr Met Gln His Thr Tyr Pro Ile Ser Ala Glu Glu Leu
            260                 265                 270
Phe Thr Phe Gly Gly Gln Asp Ala Asn Leu Ile Ser Ile Asp Ile Lys
        275                 280                 285
Asn Asp Leu Tyr Glu Lys Thr Leu Asn Asp Tyr Lys Ala Ile Ala Asn
    290                 295                 300
Lys Leu Ser Gln Val Thr Ser Cys Asn Asp Pro Asn Ile Asp Ile Asp
305                 310                 315                 320
Ser Tyr Lys Gln Ile Tyr Gln Gln Lys Tyr Gln Phe Asp Lys Asp Ser
                325                 330                 335
Asn Gly Gln Tyr Ile Val Asn Glu Asp Lys Phe Gln Ile Leu Tyr Asn
            340                 345                 350
Ser Ile Met Tyr Gly Phe Thr Glu Ile Glu Leu Gly Lys Lys Phe Asn
        355                 360                 365
Ile Lys Thr Arg Leu Ser Tyr Phe Ser Met Asn His Asp Pro Val Lys
    370                 375                 380
Ile Pro Asn Leu Leu Asp Asp Thr Ile Tyr Asn Asp Thr Glu Gly Phe
385                 390                 395                 400
Asn Ile Glu Ser Lys Asp Leu Lys Ser Glu Tyr Lys Gly Gln Asn Met
                405                 410                 415
Arg Val Asn Thr Asn Ala Phe Arg Asn Val Asp Gly Ser Gly Leu Val
            420                 425                 430
Ser Lys Leu Ile Gly Leu Cys Lys Lys Ile Ile Pro Pro Thr Asn Ile
        435                 440                 445
Arg Glu Asn Leu Tyr Asn Arg Thr Ala Ser Leu Thr Asp Leu Gly Gly
    450                 455                 460
Glu Leu Cys Ile Lys Ile Lys Asn Glu Asp Leu Thr Phe Ile Ala Glu
465                 470                 475                 480
Lys Asn Ser Phe Ser Glu Glu Pro Phe Gln Asp Glu Ile Val Ser Tyr
                485                 490                 495
Asn Thr Lys Asn Lys Pro Leu Asn Phe Asn Tyr Ser Leu Asp Lys Ile
            500                 505                 510
Ile Val Asp Tyr Asn Leu Gln Ser Lys Ile Thr Leu Pro Asn Asp Arg
        515                 520                 525
Thr Thr Pro Val Thr Lys Gly Ile Pro Tyr Ala Pro Glu Tyr Lys Ser
    530                 535                 540
Asn Ala Ala Ser Thr Ile Glu Ile His Asn Ile Asp Asp Asn Thr Ile
545                 550                 555                 560
Tyr Gln Tyr Leu Tyr Ala Gln Lys Ser Pro Thr Thr Leu Gln Arg Ile
                565                 570                 575
Thr Met Thr Asn Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile
            580                 585                 590
Tyr Ser Tyr Phe Pro Ser Val Ile Ser Lys Val Asn Gln Gly Ala Gln
        595                 600                 605
Gly Ile Leu Phe Leu Gln Trp Val Arg Asp Ile Ile Asp Asp Phe Thr
    610                 615                 620
Asn Glu Ser Ser Gln Lys Thr Thr Ile Asp Lys Ile Ser Asp Val Ser
625                 630                 635                 640
Thr Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile Val Lys Gln Gly
                645                 650                 655
Tyr Glu Gly Asn Phe Ile Gly Ala Leu Glu Thr Thr Gly Val Val Leu
            660                 665                 670
Leu Leu Glu Tyr Ile Pro Glu Ile Thr Leu Pro Val Ile Ala Ala Leu
        675                 680                 685
Ser Ile Ala Glu Ser Ser Thr Gln Lys Glu Lys Ile Ile Lys Thr Ile
    690                 695                 700
Asp Asn Phe Leu Glu Lys Arg Tyr Glu Lys Trp Ile Glu Val Tyr Lys
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705 710 715 720
Leu Val Lys Ala Lys Trp Leu Gly Thr Val Asn Thr Gln Phe Gln Lys
725 730 735
Arg Ser Tyr Gln Met Tyr Arg Ser Leu Glu Tyr Gln Val Asp Ala Ile
740 745 750
Lys Lys Ile Ile Asp Tyr Glu Tyr Lys Ile Tyr Ser Gly Pro Asp Lys
755 760 765
Glu Gln Ile Ala Asp Glu Ile Asn Asn Leu Lys Asn Lys Leu Glu Glu
770 775 780
Lys Ala Asn Lys Ala Met Ile Asn Ile Asn Ile Phe Met Arg Glu Ser
785 790 795 800
Ser Arg Ser Phe Leu Val Asn Gln Met Ile Asn Glu Ala Lys Lys Gln
805 810 815
Leu Leu Glu Phe Asp Thr Gln Ser Lys Asn Ile Leu Met Gln Tyr Ile
820 825 830
Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys Lys Leu Glu
835 840 845
Ser Lys Ile Asn Lys Val Phe Ser Thr Pro Ile Pro Phe Ser Tyr Ser
850 855 860
Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val Ile
865 870 875 880
Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile
885 890 895
Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala
900 905 910
Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn
915 920 925
Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn
930 935 940
Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys
945 950 955 960
Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile
965 970 975
Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser
980 985 990
Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala
995 1000 1005
Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn
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Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu
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Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys
1075 1080 1085
Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu
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Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn
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Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser
1125 1130 1135
Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr
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Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val
1185 1190 1195 1200
Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn
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Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
1235 1240 1245
Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser

1250 1255 1260
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Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp
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35 40 45
Arg Asn Ile Ile Gly Lys Lys Pro Ser Asp Phe Tyr Pro Pro Ile Ser
50 55 60
Leu Asp Ser Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
65 70 75 80
Asp Ala Glu Lys Asp Arg Phe Leu Lys Thr Val Ile Lys Leu Phe Asn
85 90 95
Arg Ile Asn Ser Asn Pro Ala Gly Gln Val Leu Leu Glu Glu Ile Lys
100 105 110
Asn Gly Lys Pro Tyr Leu Gly Asn Asp His Thr Ala Val Asn Glu Phe
115 120 125
Cys Ala Asn Asn Arg Ser Thr Ser Val Glu Ile Lys Glu Ser Asn Gly
130 135 140
Thr Thr Asp Ser Met Leu Leu Asn Leu Val Ile Leu Gly Pro Gly Pro
145 150 155 160
Asn Ile Leu Glu Cys Ser Thr Phe Pro Val Arg Ile Phe Pro Asn Asn
165 170 175
Ile Ala Tyr Asp Pro Ser Glu Lys Gly Phe Gly Ser Ile Gln Leu Met
180 185 190
Ser Phe Ser Thr Glu Tyr Glu Tyr Ala Phe Asn Asp Asn Thr Asp Leu
195 200 205
Phe Ile Ala Asp Pro Ala Ile Ser Leu Ala His Glu Leu Ile His Val
210 215 220
Leu His Gly Leu Tyr Gly Ala Lys Gly Val Thr Asn Lys Lys Val Ile
225 230 235 240
Glu Val Asp Gln Gly Ala Leu Met Ala Ala Glu Lys Asp Ile Lys Ile
245 250 255
Glu Glu Phe Ile Thr Phe Gly Gly Gln Asp Leu Asn Ile Ile Thr Asn
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Ser Thr Asn Gln Lys Ile Tyr Val Ile Leu Leu Ser Asn Tyr Thr Ala
275 280 285
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290 295 300
Thr Thr Tyr Tyr Lys Asn Phe Phe Gln Trp Lys Tyr Gly Leu Asp Gln
305 310 315 320
Asp Ser Asn Gly Asn Tyr Thr Val Asn Ile Ser Lys Phe Asn Ala Ile
325 330 335
Tyr Lys Lys Leu Phe Ser Phe Thr Glu Cys Asp Leu Ala Gln Lys Phe
340 345 350
Gln Val Lys Asn Arg Ser Asn Tyr Leu Phe His Phe Lys Pro Phe Arg
355 360 365
Leu Leu Asp Leu Leu Asp Asp Asn Ile Tyr Ser Ile Ser Glu Gly Phe
370 375 380
Asn Ile Gly Ser Leu Arg Val Asn Asn Asn Gly Gln Asn Ile Asn Leu
385 390 395 400
Asn Ser Arg Ile Val Gly Pro Ile Pro Asp Asn Gly Leu Val Glu Arg

405 410 415
Phe Val Gly Leu Cys Lys Ser Ile Val Ser Lys Lys Gly Thr Lys Asn
420 425 430
Ser Leu Cys Ile Lys Val Asn Asn Arg Asp Leu Phe Phe Val Ala Ser
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Glu Ser Ser Tyr Asn Glu Asn Gly Ile Asn Ser Pro Lys Glu Ile Asp
450 455 460
Asp Thr Thr Ile Thr Asn Asn Asn Tyr Lys Lys Asn Leu Asp Glu Val
465 470 475 480
Ile Leu Asp Tyr Asn Ser Asp Ala Ile Pro Asn Leu Ser Ser Arg Leu
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Leu Asn Thr Thr Ala Gln Asn Asp Ser Tyr Val Pro Lys Tyr Asp Ser
500 505 510
Asn Gly Thr Ser Glu Ile Lys Glu Tyr Thr Val Asp Lys Leu Asn Val
515 520 525
Phe Phe Tyr Leu Tyr Ala Gln Lys Ala Pro Glu Gly Glu Ser Ala Ile
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Ser Leu Thr Ser Ser Val Asn Thr Ala Leu Leu Asp Ala Ser Lys Val
545 550 555 560
Tyr Thr Phe Phe Ser Ser Asp Phe Ile Asn Thr Val Asn Lys Pro Val
565 570 575
Gln Ala Ala Leu Phe Ile Ser Trp Ile Gln Gln Val Ile Asn Asp Phe
580 585 590
Thr Thr Glu Ala Thr Gln Lys Ser Thr Ile Asp Lys Ile Ala Asp Ile
595 600 605
Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile Gly Asn Glu
610 615 620
Val Gln Lys Gly Asn Phe Lys Glu Ala Ile Glu Leu Leu Gly Ala Gly
625 630 635 640
Ile Leu Leu Glu Phe Val Pro Glu Leu Leu Ile Pro Thr Ile Leu Val
645 650 655
Phe Thr Ile Lys Ser Phe Ile Asn Ser Asp Asp Ser Lys Asn Lys Ile
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Ile Lys Ala Ile Asn Asn Ala Leu Arg Glu Arg Glu Leu Lys Trp Lys
675 680 685
Glu Val Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg Ile Asn Thr
690 695 700
Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn Gln
705 710 715 720
Val Asp Gly Ile Lys Lys Ile Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr
725 730 735
Leu Asp Glu Lys Asn Arg Leu Arg Ala Glu Tyr Asn Ile Tyr Ser Ile
740 745 750
Lys Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Gln Asn Ile Asp
755 760 765
Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile Asn
770 775 780
Glu Ala Lys Ile Asn Lys Leu Ser Glu Tyr Asp Lys Arg Val Asn Gln
785 790 795 800
Tyr Leu Leu Asn Tyr Ile Leu Glu Asn Ser Ser Thr Leu Gly Thr Ser
805 810 815
Ser Val Pro Glu Leu Asn Asn Leu Val Ser Asn Thr Leu Asn Asn Ser
820 825 830
Ile Pro Phe Glu Leu Ser Glu Tyr Thr Asn Asp Lys Ile Leu Ile His
835 840 845
Ile Leu Ile Arg Phe Tyr Lys Arg Ile Ile Asp Ser Ser Ile Leu Asn
850 855 860
Met Lys Tyr Glu Asn Asn Arg Phe Ile Asp Ser Ser Gly Tyr Gly Ser
865 870 875 880
Asn Ile Ser Ile Asn Gly Asp Ile Tyr Ile Tyr Ser Thr Asn Arg Asn
885 890 895
Gln Phe Gly Ile Tyr Ser Ser Arg Leu Ser Glu Val Asn Ile Thr Gln
900 905 910
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915 920 925
Phe Trp Val Arg Ile Pro Lys Tyr Asn Asn Leu Lys Asn Leu Asn Asn
930 935 940
Glu Tyr Thr Ile Ile Asn Cys Met Arg Asn Asn Asn Ser Gly Trp Lys

945 950 955 960
Ile Ser Leu Asn Tyr Asn Asn Ile Ile Trp Thr Leu Gln Asp Thr Thr
965 970 975
Gly Asn Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Asp Ile
980 985 990
Ser Asp Tyr Ile Asn Lys Trp Thr Phe Val Thr Ile Thr Asn Asn Arg
995 1000 1005
Leu Gly His Ser Lys Leu Tyr Ile Asn Gly Asn Leu Thr Asp Gln Lys
1010 1015 1020
Ser Ile Leu Asn Leu Gly Asn Ile His Val Asp Asp Asn Ile Leu Phe
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Lys Ile Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe
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Lys Ile Phe Asn Met Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr
1060 1065 1070
His Ser Glu Pro Asp Ser Thr Ile Leu Lys Asp Phe Trp Gly Asn Tyr
1075 1080 1085
Leu Leu Tyr Asn Lys Lys Tyr Tyr Leu Leu Asn Leu Leu Lys Pro Asn
1090 1095 1100
Met Ser Val Thr Lys Asn Ser Asp Ile Leu Asn Ile Asn Arg Gln Arg
1105 1110 1115 1120
Gly Ile Tyr Ser Lys Thr Asn Ile Phe Ser Asn Ala Arg Leu Tyr Thr
1125 1130 1135
Gly Val Glu Val Ile Ile Arg Lys Val Gly Ser Thr Asp Thr Ser Asn
1140 1145 1150
Thr Asp Asn Phe Val Arg Lys Asn Asp Thr Val Tyr Ile Asn Val Val
1155 1160 1165
Asp Gly Asn Ser Glu Tyr Gln Leu Tyr Ala Asp Val Ser Thr Ser Ala
1170 1175 1180
Val Glu Lys Thr Ile Lys Leu Arg Arg Ile Ser Asn Ser Asn Tyr Asn
1185 1190 1195 1200
Ser Asn Gln Met Ile Ile Met Asp Ser Ile Gly Asp Asn Cys Thr Met
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Asn Phe Lys Thr Asn Asn Gly Asn Asp Ile Gly Leu Leu Gly Phe His
1220 1225 1230
Leu Asn Asn Leu Val Ala Ser Ser Trp Tyr Tyr Lys Asn Ile Arg Asn
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Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
35 40 45
Gly Thr Ile Pro Gln Asp Phe Leu Pro Pro Thr Ser Leu Lys Asn Gly
50 55 60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Gln Glu Lys
65 70 75 80
Asp Lys Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asp
85 90 95
Asn Leu Ser Gly Arg Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100 105 110
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Gly Asp Phe Ile Ile Asn Asp
115 120 125
Ala Ser Ala Val Pro Ile Gln Phe Ser Asn Gly Ser Gln Ser Ile Leu
130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr

145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190
Arg Phe Lys Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
195 200 205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210 215 220
Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
225 230 235 240
Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
245 250 255
Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
260 265 270
Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
275 280 285
Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
290 295 300
Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305 310 315 320
Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
325 330 335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
340 345 350
Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
355 360 365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
370 375 380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr
385 390 395 400
Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val
405 410 415
Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly
420 425 430
Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile
435 440 445
Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr
450 455 460
Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala
465 470 475 480
Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
485 490 495
Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His
500 505 510
Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
515 520 525
Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala
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Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile
545 550 555 560
Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Gly Trp Ile
565 570 575
Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr
580 585 590
Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu
595 600 605
Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala
610 615 620
Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu
625 630 635 640
Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
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Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
660 665 670
Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
675 680 685
Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met

690 695 700

Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Leu Lys Ala Ile Ile Glu
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Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn
725 730 735
Lys Tyr Asp Ile Glu Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
740 745 750
Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser
755 760 765
Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu
770 775 780
Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asp Tyr Ile Ile Lys His
785 790 795 800
Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Ile
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Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp
820 825 830
Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys
835 840 845
Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp
850 855 860
Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys
865 870 875 880
Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser
885 890 895
Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr
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Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn
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Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg
930 935 940
Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile
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Trp Thr Leu Gln Asp Asn Ser Gly Ile Asn Gln Lys Leu Ala Phe Asn
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Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe
980 985 990
Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
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Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu
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Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser
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Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser
1125 1130 1135
Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe
1140 1145 1150
Val Ala Ser Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr
1155 1160 1165
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Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp Asn Thr
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Gln Glu Lys
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35 40 45
Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
50 55 60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
65 70 75 80
Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
85 90 95
Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100 105 110
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115 120 125
Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu
130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190
Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
195 200 205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210 215 220
Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
225 230 235 240
Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
245 250 255
Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
260 265 270
Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
275 280 285
Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
290 295 300
Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305 310 315 320
Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
325 330 335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
340 345 350
Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
355 360 365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
370 375 380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr
385 390 395 400
Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val
405 410 415
Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly
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Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile
435 440 445
Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr

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Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
                485                 490                 495
Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His
            500                 505                 510
Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
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Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala
    530                 535                 540
Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile
545                 550                 555                 560
Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile
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Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr
            580                 585                 590
Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu
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Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala
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Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Val Pro Glu Leu
625                 630                 635                 640
Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
                645                 650                 655
Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
            660                 665                 670
Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
        675                 680                 685
Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met
    690                 695                 700
Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Leu Lys Thr Ile Ile Glu
705                 710                 715                 720
Phe Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Lys Glu Leu Lys Asn
                725                 730                 735
Asn Tyr Asp Ile Glu Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
            740                 745                 750
Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser
        755                 760                 765
Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu
    770                 775                 780
Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asp Tyr Ile Ile Gln His
785                 790                 795                 800
Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Ile
                805                 810                 815
Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp
            820                 825                 830
Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys
        835                 840                 845
Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp
    850                 855                 860
Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Glu Ile Phe Ile
865                 870                 875                 880
Tyr Pro Thr Asn Lys Asn Gln Phe Thr Ile Phe Asn Ser Lys Pro Ser
                885                 890                 895
Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr
            900                 905                 910
Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn
        915                 920                 925
Lys Ile Val Asn Ile Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg
    930                 935                 940
Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile
945                 950                 955                 960
Trp Thr Leu Gln Asp Asn Ala Arg Ile Asn Gln Lys Leu Val Phe Lys
                965                 970                 975
Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe
            980                 985                 990
Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
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995 1000 1005
Gly His Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His
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Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg
1025 1030 1035 1040
Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu
1045 1050 1055
Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu
1060 1065 1070
Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Gly Tyr Tyr Leu
1075 1080 1085
Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser
1090 1095 1100
Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg
1105 1110 1115 1120
Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asp Ser Ser
1125 1130 1135
Thr Asn Asp Arg Phe Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Tyr
1140 1145 1150
Ile Ser Asn Ser Ser Ser Tyr Ser Leu Tyr Ala Asp Thr Asn Thr Thr
1155 1160 1165
Asp Lys Glu Lys Thr Ile Lys Ser Ser Ser Ser Gly Asn Arg Phe Asn
1170 1175 1180
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
1185 1190 1195 1200
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
1205 1210 1215
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
1220 1225 1230
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
1235 1240 1245
Gln Glu Lys
1250

<210> 26
<211> 5
<212> PRT
<213> Homo sapiens

<400> 26
Tyr Gly Gly Phe Leu
1 5

<210> 27
<211> 5
<212> PRT
<213> Homo sapiens

<400> 27
Tyr Gly Gly Phe Met
1 5

<210> 28
<211> 8
<212> PRT
<213> Homo sapiens

<400> 28
Tyr Gly Gly Phe Met Arg Gly Leu
1 5

<210> 29
<211> 7
<212> PRT

<213> Homo sapiens

<400> 29
Tyr Gly Gly Phe Met Arg Phe
1 5

<210> 30
<211> 22
<212> PRT
<213> Homo sapiens

<400> 30
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Met Asp
1 5 10 15
Tyr Gln Lys Arg Tyr Gly
20

<210> 31
<211> 22
<212> PRT
<213> Necturus maculosus

<400> 31
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Leu Asp
1 5 10 15
Tyr Gln Lys Arg Tyr Gly
20

<210> 32
<211> 22
<212> PRT
<213> Bombina orientalis

<400> 32
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Gln Asp
1 5 10 15
Tyr Gln Lys Arg Tyr Gly
20

<210> 33
<211> 22
<212> PRT
<213> Xenopus laevis

<400> 33
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Glu Asp
1 5 10 15
Tyr Gln Lys Arg Tyr Gly
20

<210> 34
<211> 22
<212> PRT
<213> Neoceratodus forsteri

<400> 34
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Lys Leu Asp
1 5 10 15
Asn Gln Lys Arg Tyr Gly
20

<210> 35

<211> 21
<212> PRT
<213> Danio rerio

<400> 35
Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Asp Trp Trp Gln Glu
 1   5   10   15
Ser Lys Arg Tyr Gly
            20

<210> 36
<211> 4
<212> PRT
<213> Homo sapiens

<400> 36
Tyr Pro Trp Phe
 1

<210> 37
<211> 4
<212> PRT
<213> Homo sapiens

<400> 37
Tyr Pro Phe Phe
 1

<210> 38
<211> 16
<212> PRT
<213> Homo sapiens

<400> 38
Tyr Gly Gly Phe Met Thr Ser Glu Lys Ser Gln Thr Pro Leu Val Thr
 1   5   10   15

<210> 39
<211> 10
<212> PRT
<213> Homo sapiens

<400> 39
Tyr Gly Gly Phe Leu Arg Lys Tyr Pro Lys
 1   5   10

<210> 40
<211> 31
<212> PRT
<213> Homo sapiens

<400> 40
Tyr Gly Gly Phe Met Thr Ser Glu Lys Ser Gln Thr Pro Leu Val Thr
 1   5   10   15
Leu Phe Lys Asn Ala Ile Ile Lys Asn Ala Tyr Lys Lys Gly Glu
            20   25   30

<210> 41
<211> 31
<212> PRT
<213> Homo sapiens

<400> 41
Tyr Gly Gly Phe Met Ser Ser Glu Lys Ser Gln Thr Pro Leu Val Thr
 1   5   10   15
Leu Phe Lys Asn Ala Ile Ile Lys Asn Ala His Lys Lys Gly Gln
            20   25   30

<210> 42
<211> 9
<212> PRT
<213> Homo sapiens

<400> 42
Tyr Gly Gly Phe Leu Arg Lys Tyr Pro
 1   5

<210> 43
<211> 16
<212> PRT
<213> Homo sapiens

<400> 43
Tyr Gly Gly Phe Met Thr Ser Glu Lys Ser Gln Thr Pro Leu Val Thr
 1   5   10   15

<210> 44
<211> 16
<212> PRT
<213> Homo sapiens

<400> 44
Tyr Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys Leu Lys Trp Asp Asn
 1   5   10   15

<210> 45
<211> 13
<212> PRT
<213> Homo sapiens

<400> 45
Tyr Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys Leu Lys
 1   5   10

<210> 46
<211> 16
<212> PRT
<213> Homo sapiens

<400> 46
Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys Leu Lys Trp Asp Asn Gln
 1   5   10   15

<210> 47
<211> 12
<212> PRT
<213> Homo sapiens

<400> 47
Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys Leu Lys
 1   5   10

<210> 48

<211> 17
<212> PRT
<213> Xenopus laevis

<400> 48
Tyr Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys Leu Arg Trp Asp Asn
 1   5   10   15
Gln

<210> 49
<211> 17
<212> PRT
<213> Xenopus laevis

<400> 49
Tyr Gly Gly Phe Leu Arg Arg Ile Arg Pro Arg Leu Arg Trp Asp Asn
 1   5   10   15
Gln

<210> 50
<211> 17
<212> PRT
<213> Protopterus annectens

<400> 50
Tyr Gly Gly Phe Met Arg Arg Ile Arg Pro Lys Ile Arg Trp Asp Asn
 1   5   10   15
Gln

<210> 51
<211> 17
<212> PRT
<213> Danio rerio

<400> 51
Tyr Gly Gly Phe Met Arg Arg Ile Arg Pro Lys Leu Arg Trp Asp Asn
 1   5   10   15
Gln

<210> 52
<211> 17
<212> PRT
<213> Anguilla rostrata

<400> 52
Tyr Gly Gly Phe Met Arg Arg Ile Arg Pro Lys Leu Lys Trp Asp Ser
 1   5   10   15
Gln

<210> 53
<211> 29
<212> PRT
<213> Homo sapiens

<400> 53
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
 1   5   10   15
Glu Asp Pro Asn Ala Tyr Ser Gly Glu Leu Phe Asp Ala

20 25

<210> 54
<211> 28
<212> PRT
<213> Rattus norvegicus

<400> 54
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Asn Pro Asn Thr Tyr Ser Glu Asp Leu Asp Val
20 25

<210> 55
<211> 28
<212> PRT
<213> Mus musculus

<400> 55
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Ser Pro Asn Thr Tyr Ser Glu Asp Leu Asp Val
20 25

<210> 56
<211> 29
<212> PRT
<213> Cavia porcellus

<400> 56
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Asp Pro Asn Ala Tyr Ser Glu Glu Phe Phe Asp Val
20 25

<210> 57
<211> 29
<212> PRT
<213> Sus scrofa

<400> 57
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Asp Pro Asn Ala Tyr Tyr Glu Glu Leu Phe Asp Val
20 25

<210> 58
<211> 29
<212> PRT
<213> Canis familiaris

<400> 58
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Asp Pro Asn Ala Tyr Ser Gly Glu Leu Leu Asp Gly
20 25

<210> 59
<211> 29
<212> PRT
<213> Bos taurus

<400> 59
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr Arg Ser Gln
1 5 10 15
Glu Asp Pro Ser Ala Tyr Tyr Glu Glu Leu Phe Asp Val
20 25

<210> 60
<211> 29
<212> PRT
<213> Bufo marinus

<400> 60
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Thr Thr Arg Ser Glu
1 5 10 15
Glu Asp Pro Ser Thr Phe Ser Gly Glu Leu Ser Asn Leu
20 25

<210> 61
<211> 29
<212> PRT
<213> Bombina orientalis

<400> 61
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Thr Thr Arg Ser Glu
1 5 10 15
Glu Glu Pro Gly Ser Phe Ser Gly Glu Ile Ser Asn Leu
20 25

<210> 62
<211> 29
<212> PRT
<213> Xenopus laevis

<400> 62
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Asn Ala Arg Ser Glu
1 5 10 15
Glu Asp Pro Thr Met Phe Ser Asp Glu Leu Ser Tyr Leu
20 25

<210> 63
<211> 29
<212> PRT
<213> Xenopus laevis

<400> 63
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Asn Ala Arg Ser Glu
1 5 10 15
Glu Asp Pro Thr Met Phe Ser Gly Glu Leu Ser Tyr Leu
20 25

<210> 64
<211> 29
<212> PRT
<213> Polypterus senegalus

<400> 64
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Ser Val Arg Ser Asp
1 5 10 15
Glu Glu Pro Ser Ser Tyr Ser Asp Glu Val Leu Glu Leu
20 25

<210> 65

<211> 27
<212> PRT
<213> Danio rerio

<400> 65
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Ser Val Arg Ser Asp
 1   5   10   15
Glu Glu Pro Ser Ser Tyr Glu Asp Tyr Ala Leu
            20   25

<210> 66
<211> 27
<212> PRT
<213> Anguilla rostrata

<400> 66
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Ser Val Arg Ser Asp
 1   5   10   15
Glu Glu Pro Gly Ser Tyr Asp Val Ile Gly Leu
            20   25

<210> 67
<211> 29
<212> PRT
<213> Neoceratodus forsteri

<400> 67
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Thr Val Arg Ser Asp
 1   5   10   15
Glu Asp Pro Ser Pro Tyr Leu Asp Glu Phe Ser Asp Leu
            20   25

<210> 68
<211> 27
<212> PRT
<213> Oncorhynchus masou

<400> 68
Tyr Gly Gly Phe Leu Arg Arg His Tyr Lys Leu Ser Val Arg Ser Asp
 1   5   10   15
Glu Glu Pro Ser Ser Tyr Asp Asp Phe Gly Leu
            20   25

<210> 69
<211> 13
<212> PRT
<213> Homo sapiens

<400> 69
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Val Thr
 1   5   10

<210> 70
<211> 13
<212> PRT
<213> Bufo marinus

<400> 70
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Thr Thr
 1   5   10

<210> 71

<211> 13
<212> PRT
<213> Xenopus laevis

<400> 71
Tyr Gly Gly Phe Leu Arg Arg Gln Phe Lys Val Asn Ala
 1   5   10

<210> 72
<211> 13
<212> PRT
<213> Polypterus senegalus

<400> 72
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Ser Val
 1   5   10

<210> 73
<211> 13
<212> PRT
<213> Neoceratodus forsteri

<400> 73
Tyr Gly Gly Phe Leu Arg Arg His Phe Lys Ile Thr Val
 1   5   10

<210> 74
<211> 13
<212> PRT
<213> Oncorhynchus masou

<400> 74
Tyr Gly Gly Phe Leu Arg Arg His Tyr Lys Leu Ser Val
 1   5   10

<210> 75
<211> 17
<212> PRT
<213> Homo sapiens

<400> 75
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala Arg Lys Arg Lys Asn
 1   5   10   15
Gln

<210> 76
<211> 17
<212> PRT
<213> Homo sapiens

<400> 76
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala Arg Lys Leu Ala Asn
 1   5   10   15
Gln

<210> 77
<211> 17
<212> PRT
<213> Homo sapiens

<400> 77
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala Arg Lys Tyr Ala Asn
 1   5   10   15
Gln

<210> 78
<211> 11
<212> PRT
<213> Homo sapiens

<400> 78
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala
 1   5   10

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

<400> 79
Phe Gly Gly Phe Thr Gly Ala Arg Lys Tyr Ala
 1   5   10

<210> 80
<211> 11
<212> PRT
<213> Homo sapiens

<400> 80
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Tyr
 1   5   10

<210> 81
<211> 13
<212> PRT
<213> Homo sapiens

<400> 81
Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala Arg Lys
 1   5   10

<210> 82
<211> 30
<212> PRT
<213> Homo sapiens

<400> 82
Met Pro Arg Val Arg Ser Leu Phe Gln Glu Gln Glu Glu Pro Glu Pro
 1   5   10   15
Gly Met Glu Glu Ala Gly Glu Met Glu Gln Lys Gln Leu Gln
            20   25   30

<210> 83
<211> 17
<212> PRT
<213> Homo sapiens

<400> 83
Phe Ser Glu Phe Met Arg Gln Tyr Leu Val Leu Ser Met Gln Ser Ser
 1   5   10   15
Gln

<210> 84
<211> 8
<212> PRT
<213> Homo sapiens

<400> 84
Thr Leu His Gln Asn Gly Asn Val
1 5

<210> 85
<211> 10
<212> PRT
<213> Homo sapiens

<400> 85
Leu Val Val Tyr Pro Trp Thr Gln Arg Phe
1 5 10

<210> 86
<211> 9
<212> PRT
<213> Homo sapiens

<400> 86
Val Val Tyr Pro Trp Thr Gln Arg Phe
1 5

<210> 87
<211> 8
<212> PRT
<213> Homo sapiens

<400> 87
Val Tyr Pro Trp Thr Gln Arg Phe
1 5

<210> 88
<211> 7
<212> PRT
<213> Homo sapiens

<400> 88
Tyr Pro Trp Thr Gln Arg Phe
1 5

<210> 89
<211> 9
<212> PRT
<213> Homo sapiens

<400> 89
Leu Val Val Tyr Pro Trp Thr Gln Arg
1 5

<210> 90
<211> 8
<212> PRT
<213> Homo sapiens

<400> 90
Leu Val Val Tyr Pro Trp Thr Gln
 1   5

<210> 91
<211> 7
<212> PRT
<213> Homo sapiens

<400> 91
Val Val Tyr Pro Trp Thr Gln
 1   5

<210> 92
<211> 7
<212> PRT
<213> Homo sapiens

<400> 92
Leu Val Val Tyr Pro Trp Thr
 1   5

<210> 93
<211> 6
<212> PRT
<213> Homo sapiens

<400> 93
Leu Val Val Tyr Pro Trp
 1   5

<210> 94
<211> 30
<212> PRT
<213> Homo sapiens

<400> 94
Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Pro His Ala Val
 1   5   10   15
Gly Asn His Arg Ser Phe Ser Asp Lys Asn Gly Leu Thr Ser
            20   25   30

<210> 95
<211> 59
<212> PRT
<213> Homo sapiens

<400> 95
Glu Leu Arg Pro Glu Asp Asp Met Lys Pro Gly Ser Phe Asp Arg Ser
 1   5   10   15
Ile Pro Glu Asn Asn Ile Met Arg Thr Ile Ile Glu Phe Leu Ser Phe
            20   25   30
Leu His Leu Lys Glu Ala Gly Ala Leu Asp Arg Leu Leu Asp Leu Pro
        35   40   45
Ala Ala Ala Ser Ser Glu Asp Ile Glu Arg Ser
    50   55

<210> 96
<211> 11
<212> PRT
<213> Homo sapiens

<400> 96
Arg Pro Lys Pro Gln Gln Phe Phe Gly Leu Met
 1   5   10

<210> 97
<211> 12
<212> PRT
<213> Homo sapiens

<400> 97
Arg Pro Lys Pro Gln Gln Phe Phe Gly Leu Met Gly
 1   5   10

<210> 98
<211> 13
<212> PRT
<213> Homo sapiens

<400> 98
Arg Pro Lys Pro Gln Gln Phe Phe Gly Leu Met Gly Lys
 1   5   10

<210> 99
<211> 14
<212> PRT
<213> Homo sapiens

<400> 99
Arg Pro Lys Pro Gln Gln Phe Phe Gly Leu Met Gly Lys Arg
 1   5   10

<210> 100
<211> 36
<212> PRT
<213> Homo sapiens

<400> 100
Asp Ala Asp Ser Ser Ile Glu Lys Gln Val Ala Leu Leu Lys Ala Leu
 1   5   10   15
Tyr Gly His Gly Gln Ile Ser His Lys Arg His Lys Thr Asp Ser Phe
            20   25   30
Val Gly Leu Met
        35

<210> 101
<211> 19
<212> PRT
<213> Homo sapiens

<400> 101
Gly His Gly Gln Ile Ser His Lys Arg His Lys Thr Asp Ser Phe Val
 1   5   10   15
Gly Leu Met

<210> 102
<211> 10
<212> PRT
<213> Homo sapiens

<400> 102
His Lys Thr Asp Ser Phe Val Gly Leu Met

1 5 10

<210> 103
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 103
Asp Met His Asp Phe Phe Val Gly Leu Met
1 5 10

<210> 104
<211> 10
<212> PRT
<213> Homo sapiens

<400> 104
Ser Arg Thr Arg Gln Phe Tyr Gly Leu Met
1 5 10

<210> 105
<211> 10
<212> PRT
<213> Homo sapiens

<400> 105
Gly Lys Ala Ser Gln Phe Phe Gly Leu Met
1 5 10

<210> 106
<211> 14
<212> PRT
<213> Homo sapiens

<400> 106
Lys Lys Ala Tyr Gln Leu Glu His Thr Phe Gln Gly Leu Leu
1 5 10

<210> 107
<211> 14
<212> PRT
<213> Homo sapiens

<400> 107
Val Gly Ala Tyr Gln Leu Glu His Thr Phe Gln Gly Leu Leu
1 5 10

<210> 108
<211> 36
<212> PRT
<213> Homo sapiens

<400> 108
Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15
Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30
Arg Gln Arg Tyr
35

<210> 109

<211> 36
<212> PRT
<213> Homo sapiens

<400> 109
Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
 1   5   10   15
Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
            20   25   30
Arg Gln Arg Tyr
        35

<210> 110
<211> 33
<212> PRT
<213> Homo sapiens

<400> 110
Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln Met Ala Gln
 1   5   10   15
Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr Arg Pro Arg
            20   25   30
Tyr

<210> 111
<211> 36
<212> PRT
<213> Homo sapiens

<400> 111
Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
 1   5   10   15
Met Ala Gln Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr
            20   25   30
Arg Pro Arg Tyr
        35

<210> 112
<211> 20
<212> PRT
<213> Homo sapiens

<400> 112
His Lys Glu Asp Thr Leu Ala Phe Ser Glu Trp Gly Ser Pro His Ala
 1   5   10   15
Ala Val Pro Arg
            20

<210> 113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Thrombin cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is S, T, an amidic amino acid like N
      and Q, a positive amino acid like H, K, and R, an
      aromatic hydrophobic amino acid like F, W, and Y,
      an aliphatic hydrophobic amino acid like, G, P, A,
      V, L, I, and M

<221> VARIANT
<222> 2, 6, 7, 8
<223> Position 1, 6, 7, and 8, are independently any amino acid

<221> VARIANT
<222> 3
<223> Position 3 is F, S, T, an amidic amino acid like N or Q, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 5
<223> Position 5 is S, T, a positive amino acid like H, K, and R, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 113
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 114
Leu Val Pro Arg Gly Ser
1 5

<210> 115
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 115
Leu Val Pro Lys Gly Ser
1 5

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 116
Phe Ile Pro Arg Thr Phe
1 5

<210> 117
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 117
Val Leu Pro Arg Ser Phe
1 5

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 118
Ile Val Pro Arg Ser Phe
1 5

<210> 119
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 119
Ile Val Pro Arg Gly Tyr
1 5

<210> 120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 120
Val Val Pro Arg Gly Val
1 5

<210> 121
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 121
Val Leu Pro Arg Leu Ile
1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 122
Val Met Pro Arg Ser Leu
1 5

<210> 123
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thrombin cleavage site

<400> 123
Met Phe Pro Arg Ser Leu
1 5

<210> 124
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Coagulation Factor VIIa cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is an acidic amino acid like D and E, an amidic amino acid like N and Q, a basic amino acid like K and R, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 2 is Q, S, T, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is Q, S, T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 5, 6, 7 8
<223> Position 5, 6, 7, and 8 are independently any amino acid

<400> 124
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 125
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 125
Lys Leu Thr Arg Ala Glu Thr Val
1 5

<210> 126
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 126
Asp Phe Thr Arg Val Val Gly Gly
1 5

<210> 127
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 127
Leu Ser Pro Arg Thr Phe His Pro
1 5

<210> 128
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 128
Leu Ile Gln Arg Asn Leu Ser Pro
1 5

<210> 129
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 129
Met Ala Thr Arg Lys Met His Asp
1 5

<210> 130
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 130
Leu Gly Ile Arg Ser Phe Arg Asn
1 5

<210> 131
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 131
Pro Gln Gly Arg Ile Val Gly Gly
1 5

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 132
Asn Leu Thr Arg Ile Val Gly Gly
1 5

<210> 133
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor VIIa cleavage site

<400> 133
Gln Val Val Arg Ile Val Gly Gly
1 5

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consenus sequence for Coagulation Factor IXa cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is an acidic amino acid like D and E, an amidic amino acid like N and Q, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 2 is an acidic amino acid like D and E, an amidic amino acid like N and Q, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT

<222> 3
<223> Position 3 is, S, T, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 5, 6, 7, 8
<223> Positions 5, 6, 7, and 8 are independently any amino acid

<400> 134
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 135
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor IXa cleavage site

<400> 135
Pro Gln Gly Arg Ile Val Gly Gly
1 5

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor IXa cleavage site

<400> 136
Pro Gln Leu Arg Met Lys Asn Asn
1 5

<210> 137
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor IXa cleavage site

<400> 137
Asn Leu Thr Arg Ile Val Gly Gly
1 5

<210> 138
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor IXa cleavage site

<400> 138
Gln Val Val Arg Ile Val Gly Gly

1 5

<210> 139
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Coagulation Factor Xa cleavage site

<221> VARIANT
<222> 1, 6, 7, 8
<223> Positions 1, 6, 7, and 8 are independantly any amino acid

<221> VARIANT
<222> 2
<223> Position 2 is G, A, S, an acidic amino acid like D and E, an amidic amino acid like Q and N, or an aromatic hydrophobic amino acid like F, W and Y

<221> VARIANT
<222> 3
<223> Position 3 is an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 5
<223> Position 5 is an amidic amino acid like N and Q, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 139
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 140
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 140
Ile Asp Gly Arg
1

<210> 141
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 141
Ile Glu Gly Arg

1

<210> 142
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 142
Ile Asp Gly Arg Ser Val Gly Gly
1 5

<210> 143
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 143
Ile Asp Gly Arg Thr Val Gly Gly
1 5

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 144
Ile Asp Gly Arg Ile Val Gly Gly
1 5

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 145
Ile Glu Gly Arg Ser Val Gly Gly
1 5

<210> 146
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 146
Ile Glu Gly Arg Thr Val Gly Gly
1 5

<210> 147
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 147
Ile Glu Gly Arg Ile Val Gly Gly
 1   5

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 148
Pro Gln Gly Arg Ile Val Gly Gly
 1   5

<210> 149
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 149
Ile Glu Gly Arg Thr Ser Glu Asp
 1   5

<210> 150
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 150
Ile Glu Gly Arg Ile Val Glu Gly
 1   5

<210> 151
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 151
Ile Asp Gly Arg Ile Val Glu Gly
 1   5

<210> 152
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 152
Phe Asn Pro Arg Thr Phe Gly Ser
 1   5

<210> 153
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 153
Phe Asp Glu Arg Thr Phe Gly Leu
 1   5

<210> 154
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 154
Ile Asp Glu Arg Ile Val Gly Gly
 1   5

<210> 155
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor Xa cleavage site

<400> 155
Phe Asn Glu Lys Thr Phe Gly Leu
 1   5

<210> 156
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Coagulation Factor XIa
      cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is an acidic amino acid like D or E, a
      basic amino acid like K and R, or an aliphatic
      hydrophobic amino acid like, G, P, A, V, L, I, and
      M

<221> VARIANT
<222> 2
<223> Position 2 is an acidic amino acid like D or E, an

amidic amino acid like Q and N, a basic amino acid like K and R, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is H, an uncharged amino acid like C, S, and T, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 5, 8
<223> Positions 5 and 6 are independantly H, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> (6)...(6)
<223> Position 6 is an acidic amino acid like D and E, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> (7)...(7)
<223> Position 7 is an amidic amino acid like Q and N, an uncharged amino acid like C, S, and T, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 156
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 157
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 157
Ala Phe Trp Lys Thr Asp Ala Ser
1 5

<210> 158
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 158
Lys Leu Thr Arg Ala Glu Thr Val
1 5

<210> 159
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 159
Lys Leu Thr Arg Ala Glu Thr Ile
1 5

<210> 160
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 160
Asp Phe Thr Arg Val Val Gly Gly
1 5

<210> 161
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 161
Glu Phe Ser Arg Val Val Gly Gly
1 5

<210> 162
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 162
Lys Leu Thr Arg Ala Glu Thr Val
1 5

<210> 163
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 163
Asp Phe Thr Arg Val Val Gly Gly
1 5

<210> 164
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 164
Ile Lys Pro Arg Ile Val Gly Gly
 1   5

<210> 165
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 165
Asp Leu His Arg His Ile Phe Trp
 1   5

<210> 166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIa cleavage site

<400> 166
Lys Gln Leu Arg Val Val Asn Gly
 1   5

<210> 167
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Coagulation Factor XIIa cleavage site

<221> VARIANT
<222> 1, 6
<223> Positions 1 and 6 are independantly an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 2 is an acidic amino acid like D and E, a basic amino acid like K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is a basic amino acid like K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4

<223> Position 4 is K or R

<221> VARIANT
<222> 5, 7, 8
<223> Positions 5, 7 and 8 are independantly an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 167
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIIa cleavage site

<400> 168
Pro Gln Gly Arg Ile Val Gly Gly
1 5

<210> 169
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIIa cleavage site

<400> 169
Ile Lys Pro Arg Ile Val Gly Gly
1 5

<210> 170
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIIa cleavage site

<400> 170
Ser Met Thr Arg Val Val Gly Gly
1 5

<210> 171
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Coagulation Factor XIIa cleavage site

<400> 171
Thr Ser Thr Arg Ile Val Gly Gly
1 5

<210> 172
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Coagulation Factor XIIa cleavage site

<400> 172
Pro Met Lys Arg Leu Thr Leu Gly
1 5

<210> 173
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Kallikrein 1 cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is an acidic amino acid like D and E, an amidic amino acid like Q and N, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2, 3, 6, 7, 8
<223> Positions 2, 3, 6, 7 and 8 are independently any amino acid

<221> VARIANT
<222> 4
<223> Position 4 is a positive amino acid like H, K, and R, a large non-polar amino acid like F, I, L, M and V, or an aromatic hydrophobic amino acid like F, W and Y

<221> VARIANT
<222> 5
<223> Position 5 is S, K, or R

<400> 173
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 174
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 174
Ser Met Thr Arg Val Val Gly Gly
1 5

<210> 175
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 175
Ser Pro Phe Arg Ser Ser Asp Ile
1 5

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 176
Ser Leu Met Lys Arg Pro Pro Gly
1 5

<210> 177
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 177
Tyr Asp Trp Arg Thr Pro Tyr Leu
1 5

<210> 178
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 178
Ser Pro Phe Arg Ser Val Gln Val
1 5

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 179
Ser Pro Phe Arg Thr Pro Tyr Leu
1 5

<210> 180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 180
Thr Phe His Lys Ala Glu Tyr Arg
1 5

<210> 181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 181
Pro Arg Phe Lys Ile Ile Gly Gly
1 5

<210> 182
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 182
Ile Ser Leu Met Lys Arg Pro Pro
1 5

<210> 183
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 183
Leu Glu Ala Arg Ser Ala Tyr His
1 5

<210> 184
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 184
Glu Ala Lys Arg Ser Tyr His Ser
1 5

<210> 185
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 185
Pro Asn Arg Trp Ser Thr Gly Ala
1 5

<210> 186

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 186
Glu Ala Phe Tyr Ser Gln Phe Gly
1 5

<210> 187
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 187
Asn Ala Ala Arg Ser Thr Gly Ala
1 5

<210> 188
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 188
Ser Ser Glu Trp Ser Met Pro Tyr
1 5

<210> 189
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 189
Gly Thr Leu Phe Arg Ser Gly Asn
1 5

<210> 190
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 190
Ala Arg Leu Tyr Ser Arg Gly Ala
1 5

<210> 191
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 191
Glu Ala Ser Arg Ser Ala Thr Leu
1 5

<210> 192
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 192
Glu Ala Ser Tyr Arg Arg Lys Gln
1 5

<210> 193
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 193
Thr Thr Phe Tyr Arg Arg Gly Ala
1 5

<210> 194
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 194
Ala Ala Trp Tyr Arg Thr Ser Arg
1 5

<210> 195
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 195
Ser Phe His Tyr Arg Met Val Gly
1 5

<210> 196
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 196
Ala Ser Ser Tyr Arg Thr Ser Arg
1 5

<210> 197
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 197
Thr Arg Phe Tyr Ser Arg Gly Arg
1 5

<210> 198
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Kallikrein 1 cleavage site

<400> 198
Ile Lys Phe Phe Ser Ala Gln Thr
1 5

<210> 199
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Protein C cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is a basic amino acid like K and R, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 2 is an acidic amino acid like D and E, an amidic amino acid like Q and N, a basic amino acid like K and R, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3, 5
<223> Positions 3 and 5 is an amidic amino acid like Q and N, a basic amino acid like K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 6
<223> Position 6 is an amidic amino acid like Q and N, a

basic amino acid like K and R, an aromatic hydrophobic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> (7)...(7)
<223> Position 7 is an amidic amino acid like Q and N, a positive amino acid like H, K, and R, an uncharged amino acid like C, S, and T, or an aromatic hydrophobic amino acid like F, W and Y

<221> VARIANT
<222> (8)...(8)
<223> Position 8 is an acidic amino acid like D and E, an amidic amino acid like Q and N, a basic amino acid like K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 199
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 200
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 200
Lys Lys Thr Arg Asn Leu Lys Lys
1 5

<210> 201
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 201
Leu Asp Arg Arg Gly Leu Gln Arg
1 5

<210> 202
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 202
Met Ala Thr Arg Lys Met His Asp
1 5

<210> 203
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 203
Arg Leu Lys Lys Ser Gln Phe Leu
1 5

<210> 204
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 204
Pro Gln Leu Arg Met Lys Asn Asn
1 5

<210> 205
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 205
Val Asp Gln Arg Gly Asn Gln Ile
1 5

<210> 206
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 206
Ile Glu Pro Arg Ser Pro Ser Gln
1 5

<210> 207
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 207
Lys Lys Thr Arg Ser Pro Lys Thr
1 5

<210> 208
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 208
Leu Asp Gln Arg Gly Val Gln Arg
1 5

<210> 209
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein C cleavage site

<400> 209
Pro Asp Pro Arg Ser Lys Asn Asn
1 5

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

<220>
<223> Consensus sequence for Plasminogen cleavage site

<221> VARIANT
<222> 1, 5, 6
<223> Positions 1, 5, and 6 are independantly a positive amino acid like H, K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 3 is an amidic amino acid like N and Q, a positive amino acid like H, K and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is an amidic amino acid like N and Q, an uncharged amino acid like C, S, and T, an aromatic amino acid like F, W and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 7
<223> Position 7 is any amino acid

<221> VARIANT
<222> (8)...(8)
<223> Position 8 is H, F, Y, R, an uncharged amino acid like C, S, and T, an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 210
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

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

<220>
<223> Plasminogen cleavage site

<400> 211
Gly Glu Ala Arg Gly Ser Val Ile
1 5

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

<220>
<223> Plasminogen cleavage site

<400> 212
Gly His Ala Arg Leu Val His Val
1 5

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

<220>
<223> Plasminogen cleavage site

<400> 213
Ala Glu Phe Arg His Asp Ser Gly
1 5

<210> 214
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Plasminogen cleavage site

<400> 214
His His Gln Lys Leu Val Phe Phe
1 5

<210> 215
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Plasminogen cleavage site

<400> 215
Gly Ser Asn Lys Gly Ala Leu Leu
1 5

<210> 216
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
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Arg Ala Gln Arg Ser Ala Gly Ala
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Ala Phe Trp Lys Thr Asp Ala Ser
 1   5

<210> 218
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Met Ser Met Arg Val Arg Arg His
 1   5

<210> 219
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Arg Gly Val Arg Arg Thr Ala Ser
 1   5

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<220>
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Arg Ala Ala Arg Ser Gln Cys Thr
 1   5

<210> 221
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Pro Gln Ser Arg Ser Val Pro Pro
 1   5

<210> 222
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Pro Tyr Leu Lys Val Phe Asn Pro
 1   5

<210> 223
<211> 8
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<220>
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<210> 224
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<210> 225
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<210> 226
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1 5

<210> 227
<211> 8
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<210> 228
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<220>
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<210> 229
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<210> 231
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<220>
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1 5

<210> 232
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<220>
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Pro Lys Ala Lys Ser His Ala Pro
1 5

<210> 233
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1 5

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Leu Phe Glu Lys Lys Val Tyr Leu
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<400> 235
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1 5

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Pro Arg Phe Lys Ile Ile Gly Gly
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<210> 238
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<400> 238
Pro Arg Cys Arg His Arg Pro His
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<210> 239
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<220>
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Lys Gly Tyr Arg Ser Gln Arg Gly
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<210> 240
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<220>
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Asp Val Ala Gln Phe Val Leu Thr
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<210> 241
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<220>
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<221> VARIANT
<222> 1, 3, 4, 6, 7, 8
<223> Positions 1, 3, 4, 6, 7, 8 are independantly any
      amino acid

<221> VARIANT
<222> 2
<223> Position 2 is P, A, V, L, or I

<221> VARIANT
<222> 5
<223> Position 5 is V, L, I, F, or Q

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 1   5

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<211> 8
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<220>
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Gln Pro Val Ser Val Lys Val Gly
 1   5

<210> 243
<211> 8
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<220>
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<400> 243
Arg Gly Val Gly Ile Lys Ser Thr
 1   5

<210> 244
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<400> 244
Phe Val Asp Cys Leu Ile Glu Gln
 1   5

<210> 245
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<220>
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<400> 245
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 1   5

<210> 246
<211> 8
<212> PRT
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<220>
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Tyr His Ala Asp Ile Tyr Asp Lys
 1   5

<210> 247
<211> 8
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<220>
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<400> 247
Arg Ala Cys Arg Leu Ala Lys Ala
 1   5

<210> 248
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<212> PRT
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<220>
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<400> 248
Gln Gly Ala Tyr Gln Glu Ala Phe
 1   5

<210> 249
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<220>
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 1   5

<210> 250
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<220>
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 1   5

<210> 251
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<220>
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<400> 251
His Ile Ser Ser Leu Ile Lys Leu

1 5

<210> 252
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<220>
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Asp Pro Asn Asn Leu Leu Asn Asp
1 5

<210> 253
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<220>
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1 5

<210> 254
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<220>
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<400> 254
Lys Pro Lys Thr Ile Thr Gly Pro
1 5

<210> 255
<211> 8
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<220>
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Val Val His Pro Leu Val Leu Leu
1 5

<210> 256
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<220>
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1 5

<210> 257
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<220>
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<400> 257
Ala Val Ala Leu Leu Ile Gly Pro
1 5

<210> 258
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<220>
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<400> 258
Gln Pro Leu Gln Leu Leu Asp Ala
1 5

<210> 259
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Tyr Ile Gln Gly Ile Asn Leu Val
1 5

<210> 260
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<210> 261
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1 5

<210> 262
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<400> 262
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1 5

<210> 264
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<400> 264
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<400> 265
Ala Val Ser Trp Leu Leu Thr Ala
1 5

<210> 266
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<400> 266
Ser Leu Arg Arg Leu Thr Ala Ala
1 5

<210> 267
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<400> 267
Ser Leu Ser Arg Leu Thr Ala Leu
1 5

<210> 268
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<400> 268
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1 5

<210> 269
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<400> 269
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1 5

<210> 270
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<220>
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<400> 270
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1 5

<210> 271
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<220>
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<400> 271
Ser Pro Ala Tyr Tyr Thr Ala Leu
1 5

<210> 272
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<400> 272

Met His Lys Ala Leu Thr Ala Ala
1 5

<210> 273
<211> 8
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<220>
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<400> 273
Leu Arg Leu Ala Ile Thr Ala Leu
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<210> 274
<211> 8
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<213> Artificial Sequence

<220>
<223> Consensus sequence for MMP-9 cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is F, an acidic amino acid like D and E, an amidic amino acid like N and Q, a positive amino acid like H, K, and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2
<223> Position 2 is F, Y, S, T, an acidic amino acid like D and E, an amidic amino acid like N and Q, a positive amino acid like H, K, and R, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3, 8
<223> Positions 3 and 8 are independantly F, Y, an acidic amino acid like D and E, an amidic amino acid like N and Q, a positive amino acid like H, K, and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4, 6, 7
<223> Positions 4, 6 and 7 are independantly any amino acid

<221> VARIANT
<222> 5
<223> Position 5 is S, T, an acidic amino acid like D and E, an amidic amino acid like N and Q, a positive amino acid like H, K, and R, an aromatic hydrophobic amino acid like F, W, and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 274
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1 5

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<400> 276
Met Asp Ile Ala Ile His His Pro
1 5

<210> 277
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Ser Pro Ser Arg Leu Phe Asp Gln
1 5

<210> 278
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<400> 278
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1 5

<210> 279
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<400> 279
Phe Ser Val Asn Leu Asp Val Lys
1 5

<210> 280
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Arg Leu Phe Asp Gln Phe Phe Gly
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<210> 281
<211> 8
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Phe Phe Gly Glu His Leu Leu Glu
 1   5

<210> 282
<211> 8
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Gly Leu Ser Glu Met Arg Leu Glu
 1   5

<210> 283
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Ser Pro Glu Glu Leu Lys Val Lys
 1   5

<210> 284
<211> 8
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<400> 284
Asp Val Ile Glu Val His Gly Lys
 1   5

<210> 285
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<220>
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<400> 285
Glu Val His Gly Lys His Glu Glu
 1   5

<210> 286
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Asp Glu His Gly Phe Ile Ser Arg
 1   5

<210> 287
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<210> 288
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<210> 289
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 1   5

<210> 290
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Leu Ser Pro Phe Tyr Leu Arg Pro
1 5

<210> 291
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<400> 291
Pro Pro Ser Phe Leu Arg Ala Pro
1 5

<210> 292
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Asn Pro Leu Glu Asn Ser Gly Phe
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<210> 293
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<220>
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<400> 293
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1 5

<210> 294
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<220>
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<400> 294
Pro Pro Leu Lys Leu Met His Ser
1 5

<210> 295
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<400> 295
Gly Pro Glu Gly Leu Arg Val Gly
1 5

<210> 296
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<400> 296
Phe Met Lys Gly Leu Ser Lys Ala
1 5

<210> 297
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<212> PRT
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<220>
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<400> 297
Val Val Thr Gly Val Thr Ala Val
1 5

<210> 298
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<220>
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<400> 298
Ala Ile Ile Gly Leu Met Val Gly
1 5

<210> 299
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<220>
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<400> 299
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1 5

<210> 300
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<400> 300
Val Pro Tyr Gly Leu Gly Ser Pro
1 5

<210> 301

<211> 8
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<220>
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<400> 301
Gly Ala Ala Gly Val Lys Gly Asp
 1   5

<210> 302
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<220>
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Gly Pro Thr Gly Lys Gln Gly Asp
 1   5

<210> 303
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Gly Pro Ser Gly Asp Gln Gly Ala
 1   5

<210> 304
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<220>
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Gly Pro Ser Gly Phe Pro Phe Pro
 1   5

<210> 305
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Gly Ala Pro Gly Phe Pro Gly Pro
 1   5

<210> 306
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Gly Ala Pro Gly Asn Arg Gly Phe
1 5

<210> 307
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<400> 307
Gly Leu Arg Gly Glu Arg Gly Glu
1 5

<210> 308
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Gly Pro Pro Gly Ser Gln Gly Asn
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<210> 309
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<210> 310
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<400> 310
Gly Pro Pro Gly Lys Asp Gly Thr
1 5

<210> 311
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1 5

<210> 312
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<400> 312
Gly Ser Pro Gly Tyr Gln Gly Pro
1 5

<210> 313
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<220>
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<400> 313
Gly Pro Val Ser Ala Val Leu Thr
1 5

<210> 314
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<400> 314
Gly Pro Leu Gly Met Leu Ser Gln
1 5

<210> 315
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<220>
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<400> 315
Gly Pro Leu Gly Met Trp Ala Gln
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<210> 316
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<400> 316
Gly Pro Gln Gly Ile Phe Gly Gln

1 5

<210> 317
<211> 8
<212> PRT
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<220>
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<400> 317
Leu Pro Arg Ser Ala Lys Glu Leu
1 5

<210> 318
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<220>
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<400> 318
Asn Ser Phe Gly Leu Arg Phe Gly
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<210> 319
<211> 8
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<220>
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Arg Ala Ile His Ile Asn Ala Glu
1 5

<210> 320
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<220>
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<221> VARIANT
<222> 2, 5, 6, 7, 8
<223> Positions 2, 5, 6, 7, and 8 are independantly any amino acid

<221> VARIANT
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<223> Position 3 is R, K, A, or P

<221> VARIANT
<222> (0)...(0)

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1 5

<210> 321
<211> 8
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<400> 321
Arg Pro Arg Arg Ala Lys Arg Phe
1 5

<210> 322
<211> 8
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<220>
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<400> 322
Arg Lys Lys Arg Gly Leu Tyr Ala
1 5

<210> 323
<211> 8
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<400> 323
Arg Glu Arg Arg Arg Lys Lys Arg
1 5

<210> 324
<211> 8
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<220>
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<400> 324
Arg Lys Lys Arg Gly Leu Tyr Ala
1 5

<210> 325
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<400> 325
Arg Lys Lys Arg Thr Thr Ser Ala
1 5

<210> 326
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<400> 326
Arg His Lys Arg Glu Thr Leu Lys
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<210> 327
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<400> 327
Arg Leu Lys Arg Asp Val Val Thr
 1   5

<210> 328
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<400> 328
Arg Met Lys Arg Glu Asp Leu Asn
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<210> 329
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<400> 329
Arg Ala Lys Arg Phe Ala Ser Leu
 1   5

<210> 330
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<400> 330
Arg Lys Lys Arg Phe Val Ser Ser
 1   5

<210> 331
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<400> 331
Arg Thr Lys Arg Phe Leu Ser Tyr
 1   5

<210> 332
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<223> Furin cleavage site

<400> 332
Arg Arg Ala Arg Ser Val Asp Gly
 1   5

<210> 333
<211> 8
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<220>
<223> Furin cleavage site

<400> 333
Val Phe Arg Arg Asp Ala His Lys
 1   5

<210> 334
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 334
Val Phe Arg Arg Glu Ala His Lys
 1   5

<210> 335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 335
Arg Val Ala Arg Asp Ile Thr Met
 1   5

<210> 336
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Furin cleavage site

<400> 336
Arg Ile Ser Arg Ser Leu Pro Gln
 1   5

<210> 337
<211> 8
<212> PRT
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<220>
<223> Furin cleavage site

<400> 337
Arg Ser Arg Arg Ala Ala Thr Ser
 1   5

<210> 338
<211> 8
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<220>
<223> Furin cleavage site

<400> 338
Arg Ala Lys Arg Ser Pro Lys His
 1   5

<210> 339
<211> 8
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<220>
<223> Furin cleavage site

<400> 339
Phe Trp His Arg Gly Val Thr Lys
 1   5

<210> 340
<211> 8
<212> PRT
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<220>
<223> Furin cleavage site

<400> 340
Ala Lys Arg Arg Thr Lys Arg Asp
 1   5

<210> 341
<211> 8
<212> PRT
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<220>
<223> Furin cleavage site

<400> 341

Ala Lys Arg Arg Ala Lys Arg Asp
1 5

<210> 342
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 342
Ala Lys Gln Arg Ala Lys Arg Asp
1 5

<210> 343
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 343
Arg Asp Val Arg Gly Phe Ala Ser
1 5

<210> 344
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 344
Arg Lys Arg Arg Ser Val Asn Pro
1 5

<210> 345
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin cleavage site

<400> 345
Arg Gln Lys Arg Phe Val Leu Ser
1 5

<210> 346
<211> 8
<212> PRT
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<220>
<223> Furin cleavage site

<400> 346
Arg Ser Lys Arg Ser Leu Ser Cys
1 5

<210> 347
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for u-PA cleavage site

<221> VARIANT
<222> 1, 5, 8
<223> Positions 1, 5, and 8 are independantly any amino acid

<221> VARIANT
<222> 2, 7
<223> Positions 2 and 7 are independantly an uncharged amino acid like C, S, and T, an aromatic amino acid like F, W, and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is an amidic amino acid like N and Q, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<221> VARIANT
<222> 6
<223> Position 6 is a basic amino acid like K and R, an aromatic amino acid like F, W, and Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 347
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 348
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 348
Gly Ser Gly Lys Ser Ala Thr Leu
1 5

<210> 349
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 349
Gln Arg Gly Arg Ser Ala Thr Leu
1 5

<210> 350
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 350
Arg Gly Ser Val Ile Leu Thr Val
1 5

<210> 351
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 351
Pro Ser Ser Arg Arg Arg Val Asn
1 5

<210> 352
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 352
Cys Pro Gly Arg Val Val Gly Gly
1 5

<210> 353
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 353
Pro Gly Ala Arg Gly Arg Ala Phe
1 5

<210> 354
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 354
Ser Ser Ser Arg Gly Pro Thr His
1 5

<210> 355

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 355
Val Ser Asn Lys Tyr Phe Ser Asn
1 5

<210> 356
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 356
Asn Ser Gly Arg Ala Val Thr Tyr
1 5

<210> 357
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 357
Thr Tyr Ser Arg Ser Arg Tyr Leu
1 5

<210> 358
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 358
Asn Ser Gly Arg Ala Val Thr Tyr
1 5

<210> 359
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 359
Pro Ser Gly Arg Gly Arg Thr Leu
1 5

<210> 360
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 360
Ala Gly Ser Arg Ala Val Tyr Tyr
 1   5

<210> 361
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 361
Thr Tyr Gly Arg Ser Arg Thr Asn
 1   5

<210> 362
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 362
Asn Ser Ser Arg Gly Val Tyr Leu
 1   5

<210> 363
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 363
Pro Ser Ser Arg Ser Val Tyr Asn
 1   5

<210> 364
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 364
Ala Ser Gly Arg Gly Arg Thr Tyr
 1   5

<210> 365
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 365
Thr Ser Ser Arg Ala Val Tyr Leu
1 5

<210> 366
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 366
Asn Ser Gly Arg Ser Arg Thr Leu
1 5

<210> 367
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 367
Val Ser Gly Arg Ile Arg Thr Gly
1 5

<210> 368
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> u-PA cleavage site

<400> 368
Ser Ser Gly Arg Ile Arg Thr Val
1 5

<210> 369
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for t-PA cleavage site

<221> VARIANT
<222> 1, 2, 3, 5, 6, 7, 8
<223> Positions 1, 2, 3, 5, 6, 7, and 8 are
independantly any amino acid

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<400> 369
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 370

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> t-PA cleavage site

<400> 370
Asn Ala Leu Arg Tyr Ala Pro Asp
1 5

<210> 371
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> t-PA cleavage site

<400> 371
Cys Pro Gly Arg Val Val Gly Gly
1 5

<210> 372
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> t-PA cleavage site

<400> 372
Pro Gln Phe Arg Ile Lys Gly Gly
1 5

<210> 373
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> t-PA cleavage site

<400> 373
Ala Leu Ser Arg Met Ala Val Leu
1 5

<210> 374
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Tryptase-epsilon cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is K or R

<221> VARIANT
<222> 2, 3, 4, 5
<223> Positions 2, 3, 4, and 5 are independantly an aliphatic hydrophobic amino acid like, G, P, A, V,

L, I, and M

<221> VARIANT
<222> 6
<223> Position 6 is D or E

<400> 374
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 375
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 375
Arg Val Val Gly Gly Glu
1 5

<210> 376
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 376
Arg Ile Val Gly Gly Glu
1 5

<210> 377
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 377
Arg Ile Ile Gly Gly Glu
1 5

<210> 378
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 378
Arg Val Val Gly Gly Asp
1 5

<210> 379
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 379
Arg Ile Val Gly Gly Asp
 1   5

<210> 380
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 380
Arg Ile Ile Gly Gly Asp
 1   5

<210> 381
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 381
Lys Val Val Gly Gly Glu
 1   5

<210> 382
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 382
Lys Ile Val Gly Gly Glu
 1   5

<210> 383
<211> 6
<212> PRT
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<220>
<223> Tryptase-epsilon cleavage site

<400> 383
Lys Ile Ile Gly Gly Glu
 1   5

<210> 384
<211> 6
<212> PRT
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<220>
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<400> 384
Lys Val Val Gly Gly Asp
1 5

<210> 385
<211> 6
<212> PRT
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<220>
<223> Tryptase-epsilon cleavage site

<400> 385
Lys Ile Val Gly Gly Asp
1 5

<210> 386
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tryptase-epsilon cleavage site

<400> 386
Lys Ile Ile Gly Gly Asp
1 5

<210> 387
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for mMCP-7 cleavage site

<221> VARIANT
<222> 1, 5, 6, 7, 8
<223> Positions 1, 5, 6, 7, and 8 are independently any amino acid

<221> VARIANT
<222> 2
<223> Potition 2 is an amidic amino acid like N or Q, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3
<223> Position 3 is an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is K or R

<400> 387
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 388
<211> 8
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<220>
<223> mMCP-7 cleavage site

<400> 388
Leu Ser Ser Arg Gln Ser Pro Gly
1 5

<210> 389
<211> 8
<212> PRT
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<220>
<223> mMCP-7 cleavage site

<400> 389
Leu Gln Ala Arg Gly Ala Ser Leu
1 5

<210> 390
<211> 8
<212> PRT
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<220>
<223> mMCP-7 cleavage site

<400> 390
Leu Gly Pro Lys Ala Ile Thr Met
1 5

<210> 391
<211> 8
<212> PRT
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<220>
<223> mMCP-7 cleavage site

<400> 391
Leu Gly Pro Arg Ser Ala Val Tyr
1 5

<210> 392
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for ECE-1 cleavage site

<221> VARIANT
<222> 1, 2, 3, 4, 6, 7, 8
<223> Positions 1, 2, 3, 4, 6, 7, and 8 are independantly any amino acid

<221> VARIANT
<222> 5
<223> Position 5 is F, L, I, V, or Y

<400> 392
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 393
<211> 8
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<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 393
His Gln Lys Leu Val Phe Phe Ala
1 5

<210> 394
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 394
His His Gln Lys Leu Val Phe Phe
1 5

<210> 395
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 395
Lys Leu Val Phe Phe Ala Glu Asp
1 5

<210> 396
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 396
Asp Arg Val Tyr Ile His Pro Phe
1 5

<210> 397
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 397
Tyr Ile His Pro Phe His Leu Val
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<210> 398

<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 398
Tyr Gly Leu Gly Ser Pro Arg Ser
1 5

<210> 399
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 399
Thr Pro Glu His Val Val Pro Tyr
1 5

<210> 400
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 400
Asp Ile Ile Trp Val Asn Thr Pro
1 5

<210> 401
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 401
Asp Ile Ile Trp Ile Asn Thr Pro
1 5

<210> 402
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 402
Cys His Leu Asp Ile Ile Trp Val
1 5

<210> 403
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 403
His Leu Asp Ile Ile Trp Val Asn
 1   5

<210> 404
<211> 8
<212> PRT
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<220>
<223> ECE-1 cleavage site

<400> 404
Cys Val Tyr Phe Cys His Leu Asp
 1   5

<210> 405
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 405
Ser Cys Ser Ser Leu Met Asp Lys
 1   5

<210> 406
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 406
Glu Cys Val Tyr Phe Cys His Leu
 1   5

<210> 407
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 407
Arg Ser Lys Arg Cys Ser Cys Ser
 1   5

<210> 408
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 408
Arg Ser Lys Arg Ala Leu Glu Asn
 1   5

<210> 409
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 409
Gly Phe Ser Pro Phe Arg Ser Ser
 1   5

<210> 410
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 410
Pro Arg Arg Pro Tyr Ile Leu Pro
 1   5

<210> 411
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 411
Lys Pro Gln Gln Phe Phe Gly Leu
 1   5

<210> 412
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ECE-1 cleavage site

<400> 412
Pro Gln Gln Phe Phe Gly Leu Met
 1   5

<210> 413
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for KBGP cleavage site

<221> VARIANT
<222> 1

<223> Position 1 is an acidic amino acid like D and E

<221> VARIANT
<222> 2, 5
<223> Positions 2 and 5 are independantly T or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 3, 8
<223> Positions 3 and 8 are independantly an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 4
<223> Position 4 is an aromatic amino acid like F, W

<221> VARIANT
<222> 6
<223> Position 6 is an amidic amino acid like N and Q

<221> VARIANT
<222> (7)...(7)
<223> Position 7 is an uncharged amino acid like C, S, and T, or a C-beta branched amino acid like I, V, or T

<400> 413
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 414
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> KBGP cleavage site

<400> 414
Asp Ile Ile Trp Val Asn Thr Pro
1 5

<210> 415
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> KBGP cleavage site

<400> 415
Asp Ile Ile Trp Ile Asn Thr Pro
1 5

<210> 416
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Cathepsin L cleavage site

<221> VARIANT

<222> 1
<223> Position 1 is W, an acidic amino acid like D and E, an amidic amino acid like N and Q, a positive amino acid like H, K, and R, an uncharged amino acid like C, S, and T, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 2, 4, 5, 6, 7, 8
<223> Positions 2, 4, 5, 6, 7, 8 are independantly any amino acid

<221> VARIANT
<222> 3
<223> Position 3 is L, V, F or Y

<400> 416
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 417
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 417
Met Phe Leu Glu Ala Ile Pro Met
1 5

<210> 418
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 418
Lys Val Phe Gln Glu Pro Leu Phe
1 5

<210> 419
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 419
Ala Thr Leu Thr Phe Asp His Ser
1 5

<210> 420
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 420
Pro Leu Phe Tyr Glu Ala Pro Arg
1 5

<210> 421
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 421
Thr Gly Leu Arg Asp Pro Phe Asn
1 5

<210> 422
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 422
Lys Ile Leu His Leu Pro Thr Ser
1 5

<210> 423
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 423
Ala His Leu Lys Asn Ser Gln Glu
1 5

<210> 424
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 424
Ala Pro Leu Thr Ala Glu Ile Gln
1 5

<210> 425
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 425
Glu Ala Leu Phe Ala Glu Arg Lys
1 5

<210> 426
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 426
Glu Pro Leu Ala Ala Glu Arg Lys
1 5

<210> 427
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 427
Gly Thr Phe Thr Ser Asp Tyr Ser
1 5

<210> 428
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 428
Lys Tyr Leu Asp Ser Arg Arg Ala
1 5

<210> 429
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 429
Gln Asp Phe Val Gln Trp Leu Met
1 5

<210> 430
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 430
Lys Gln Leu Ala Thr Lys Ala Ala
1 5

<210> 431

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 431
Ser Thr Phe Glu Glu Arg Ser Tyr
 1   5

<210> 432
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 432
Leu Arg Leu Glu Trp Pro Tyr Gln
 1   5

<210> 433
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 433
Arg Gly Phe Phe Tyr Thr Pro Lys
 1   5

<210> 434
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 434
Gly Phe Phe Tyr Thr Pro Lys Ala
 1   5

<210> 435
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 435
His Phe Phe Lys Asn Ile Val Thr
 1   5

<210> 436
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 436
Arg Gly Leu Ser Leu Ser Arg Phe
1 5

<210> 437
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 437
Gln Trp Leu Gly Ala Pro Val Pro
1 5

<210> 438
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 438
Asn Met Leu Lys Arg Gly Leu Pro
1 5

<210> 439
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 439
Leu Ser Leu Ala His Thr His Gln
1 5

<210> 440
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 440
Thr Pro Phe Ala Ala Thr Ser Ser
1 5

<210> 441
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 441
Lys Leu Leu Ala Val Ser Gly Pro
1 5

<210> 442
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 442
Gln Leu Phe Arg Arg Ala Val Leu
1 5

<210> 443
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cathepsin L cleavage site

<400> 443
Pro Arg Phe Lys Ile Ile Gly Gly
1 5

<210> 444
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for PAR1 cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is a small non-polar amino acid like A, C G, S, and T

<221> VARIANT
<222> 2, 3
<223> Positions 2 and 3 are independantly a large non-polar amino acid like F, I, L, M, V, or an aromatic amino acid like F, H, W, or Y

<221> VARIANT
<222> 4
<223> Position 4 is an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 5
<223> Position 5 is K or R

<221> VARIANT
<222> 6
<223> Position 6 is an amidic amino acid like N and Q, or an aromatic hydrophobic amino acid like F, W, or Y

<400> 444
Xaa Xaa Xaa Xaa Xaa Xaa

1 5

<210> 445
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 445
Ser Phe Leu Leu Arg Asn
1 5

<210> 446
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 446
Ser Phe Phe Leu Arg Asn
1 5

<210> 447
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 447
Ser Phe Phe Leu Lys Asn
1 5

<210> 448
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 448
Thr Phe Leu Leu Arg Asn
1 5

<210> 449
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 449
Gly Phe Pro Gly Lys Phe
1 5

<210> 450
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 450
Gly Tyr Pro Ala Lys Phe
1 5

<210> 451
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 451
Gly Tyr Pro Leu Lys Phe
1 5

<210> 452
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR1 cleavage site

<400> 452
Gly Tyr Pro Ile Lys Phe
1 5

<210> 453
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for PAR2 cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is a small non-polar amino acid like A,
C G, S, and T

<221> VARIANT
<222> 2, 3, 6
<223> Positions 2, 3, and 6 are independantly a large
non-polar amino acid like F, I, L, M, V

<221> VARIANT
<222> 4
<223> Position 4 is an aliphatic hydrophobic amino acid
like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 5
<223> Position 5 is K or R

<400> 453
Xaa Xaa Xaa Xaa Xaa Xaa

1 5

<210> 454
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR2 cleavage site

<400> 454
Ser Leu Ile Gly Lys Val
1 5

<210> 455
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR2 cleavage site

<400> 455
Ser Leu Ile Gly Arg Leu
1 5

<210> 456
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for PAR3 cleavage site

<221> VARIANT
<222> 1, 4
<223> Positions 1 and 4 are independantly a small non-polar amino acid like A, C G, S, and T

<221> VARIANT
<222> 2
<223> Position 2 is a large non-polar amino acid like F, I, L, M, V

<221> VARIANT
<222> 3
<223> Position 3 is an amidic amino acid like N and Q, or a basic amino acid like K and R

<221> VARIANT
<222> 5
<223> Position 5 is a small non-polar amino acid like A, C G, S, and T, or a small polar amino acid like D, N, or P

<221> VARIANT
<222> 6
<223> Position 6 is an acidic amino acid like D and E, or a small polar amino acid like D, N, or P

<400> 456
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 457
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR3 cleavage site

<400> 457
Thr Phe Arg Gly Ala Pro
1 5

<210> 458
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR3 cleavage site

<400> 458
Ser Phe Asn Gly Gly Pro
1 5

<210> 459
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR3 cleavage site

<400> 459
Ser Phe Asn Gly Asn Glu
1 5

<210> 460
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for PAR4 cleavage site

<221> VARIANT
<222> 1
<223> Position 1 is a small non-polar amino acid like A, C G, S, and T

<221> VARIANT
<222> 2
<223> Position 2 is a large non-polar amino acid like F, I, L, M, V, or an aromatic amino acid like F, H, W, or Y

<221> VARIANT
<222> 3, 4
<223> Positions 3 and 4 are independantly an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<221> VARIANT
<222> 5
<223> Position 5 is K or R

<221> VARIANT
<222> 6
<223> Position 6 is a basic amino acid like K and R, an aromatic hydrophobic amino acid like F, W, or Y, or an aliphatic hydrophobic amino acid like, G, P, A, V, L, I, and M

<400> 460
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 461
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 461
Gly Tyr Pro Gly Gln Val
1 5

<210> 462
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 462
Ala Tyr Pro Gly Lys Phe
1 5

<210> 463
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 463
Thr Tyr Pro Gly Lys Phe
1 5

<210> 464
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 464
Gly Tyr Pro Gly Lys Tyr
1 5

<210> 465
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 465
Gly Tyr Pro Gly Lys Trp
1 5

<210> 466
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 466
Gly Tyr Pro Gly Lys Lys
1 5

<210> 467
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 467
Gly Tyr Pro Gly Lys Phe
1 5

<210> 468
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 468
Gly Tyr Pro Gly Arg Phe
1 5

<210> 469
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 469
Gly Tyr Pro Gly Phe Lys
1 5

<210> 470
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 470
Gly Tyr Pro Ala Lys Phe
1 5

<210> 471
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 471
Gly Phe Pro Gly Lys Phe
1 5

<210> 472
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PAR4 cleavage site

<400> 472
Gly Phe Pro Gly Lys Pro
1 5

<210> 473
<211> 6
<212> PRT
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<220>
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<400> 473
Ser Tyr Pro Gly Lys Phe
1 5

<210> 474
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 474
Ser Tyr Pro Ala Lys Phe
1 5

<210> 475
<211> 6
<212> PRT
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<220>
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<400> 475
Ser Tyr Pro Gly Arg Phe

1 5

<210> 476
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 476
Ser Tyr Ala Gly Lys Phe
1 5

<210> 477
<211> 6
<212> PRT
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<220>
<223> PAR4 cleavage site

<400> 477
Ser Phe Pro Gly Gln Pro
1 5

<210> 478
<211> 6
<212> PRT
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<220>
<223> PAR4 cleavage site

<400> 478
Ser Phe Pro Gly Gln Ala
1 5

<210> 479
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> ADAMTS13 cleavage site

<400> 479
Asn Leu Val Tyr Met Val Thr Gly
1 5

<210> 480
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Bovine enterokinase protease cleavage site

<400> 480
Asp Asp Asp Asp Lys
1 5

<210> 481
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for TEV protease cleavage site

<221> VARIANT
<222> 2, 3, 5
<223> Positions 2, 3, and 5 are independantly any amino
amino acid

<400> 481
Glu Xaa Xaa Tyr Xaa Gln Gly
1 5

<210> 482
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for TEV protease cleavage site

<221> VARIANT
<222> 2, 3, 5
<223> Positions 2, 3, and 5 are independantly any amino
acid

<400> 482
Glu Xaa Xaa Tyr Xaa Gln Ser
1 5

<210> 483
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 483
Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 484
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 484
Glu Asn Leu Tyr Phe Gln Ser
1 5

<210> 485
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> TEV protease cleavage site

<400> 485
Glu Asn Ile Tyr Thr Gln Gly
 1   5

<210> 486
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 486
Glu Asn Ile Tyr Thr Gln Ser
 1   5

<210> 487
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 487
Glu Asn Ile Tyr Leu Gln Gly
 1   5

<210> 488
<211> 7
<212> PRT
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<220>
<223> TEV protease cleavage site

<400> 488
Glu Asn Ile Tyr Leu Gln Ser
 1   5

<210> 489
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 489
Glu Asn Val Tyr Phe Gln Gly
 1   5

<210> 490
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 490

Glu Asn Val Tyr Ser Gln Ser
1 5

<210> 491
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 491
Glu Asn Val Tyr Ser Gln Gly
1 5

<210> 492
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease cleavage site

<400> 492
Glu Asn Val Tyr Ser Gln Ser
1 5

<210> 493
<211> 7
<212> PRT
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<220>
<223> Consensus sequence for TVMV protease cleavage site

<221> VARIANT
<222> 1, 2
<223> Positions 1 and 2 are independantly any amino acid

<400> 493
Xaa Xaa Val Arg Phe Gln Gly
1 5

<210> 494
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for TVMV protease cleavage site

<221> VARIANT
<222> 1, 2
<223> Positions 1 and 2 are independantly any amino acid

<400> 494
Xaa Xaa Val Arg Phe Gln Ser
1 5

<210> 495
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TVMV protease cleavage site

<400> 495
Glu Thr Val Arg Phe Gln Gly
1 5

<210> 496
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TVMV protease cleavage site

<400> 496
Glu Thr Val Arg Phe Gln Ser
1 5

<210> 497
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TVMV protease cleavage site

<400> 497
Asn Asn Val Arg Phe Gln Gly
1 5

<210> 498
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TVMV protease cleavage site

<400> 498
Asn Asn Val Arg Phe Gln Ser
1 5

<210> 499
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for HR3C protease cleavage site

<221> VARIANT
<222> 1
<223> Position 1 can be amino acid, with D or E
preferred

<221> VARIANT
<222> 2
<223> Position 2 is S, T, and an aliphatic hydrophobic
amino acid like G, P, A, V, L, I, and M

<400> 499
Xaa Xaa Leu Phe Gln Gly Pro

1 5

<210> 500
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 500
Glu Ala Leu Phe Gln Gly Pro
1 5

<210> 501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 501
Glu Val Leu Phe Gln Gly Pro
1 5

<210> 502
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 502
Glu Leu Leu Phe Gln Gly Pro
1 5

<210> 503
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 503
Asp Ala Leu Phe Gln Gly Pro
1 5

<210> 504
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 504
Asp Val Leu Phe Gln Gly Pro
1 5

<210> 505
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HR3C protease cleavage site

<400> 505
Asp Leu Leu Phe Gln Gly Pro
1 5

<210> 506
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Subtilisin protease cleavage site

<221> VARIANT
<222> 1, 2, 3, 4
<223> Positions 1, 2, 3, and 4 are independantly any amino acid

<400> 506
Xaa Xaa Xaa Xaa His Tyr
1 5

<210> 507
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Subtilisin protease cleavage site

<221> VARIANT
<222> 1, 2, 3, 4
<223> Positions 1, 2, 3, and 4 are independantly any amino acid

<400> 507
Xaa Xaa Xaa Xaa Tyr His
1 5

<210> 508
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Subtilisin protease cleavage site

<400> 508
His Tyr
1

<210> 509
<211> 2
<212> PRT
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<220>
<223> Subtilisin protease cleavage site

<400> 509
Tyr His
 1

<210> 510
<211> 6
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<220>
<223> Subtilisin protease cleavage site

<400> 510
Pro Gly Ala Ala His Tyr
 1   5

<210> 511
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Hydroxylamine cleavage site

<400> 511
Asn Gly Asn Gly Asn Gly
 1   5

<210> 512
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Hydroxylamine cleavage site

<400> 512
Asn Gly
 1

<210> 513
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for SUMO/ULP-1 protease
      cleavage site

<221> VARIANT
<222> 3, 4, 5
<223> Positions 3, 4, and 5 are independantly any amino
      acid

<400> 513
Gly Gly Xaa Xaa Xaa
 1   5

<210> 514

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> SUMO/ULP-1 protease cleavage site

<400> 514
Met Ala Asp Ser Glu Val Asn Gln Glu Ala Lys Pro Glu Val Lys Pro
 1   5   10   15
Glu Val Lys Pro Glu Thr His Ile Asn Leu Lys Val Ser Asp Gly Ser
            20   25   30
Ser Glu Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg Arg Leu
        35   40   45
Met Glu Ala Phe Ala Lys Arg Gln Gly Lys Glu Met Asp Ser Leu Arg
    50   55   60
Phe Leu Tyr Asp Gly Ile Arg Ile Gln Ala Asp Gln Thr Pro Glu Asp
65   70   75   80
Leu Asp Met Glu Asp Asn Asp Ile Ile Glu Ala His Arg Glu Gln Ile
                85   90   95
Gly Gly

<210> 515
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for Caspase 3 protease cleavage
      site

<221> VARIANT
<222> 2
<223> Position 2 can be any amino acid with E preferred

<221> VARIANT
<222> 3
<223> Position 3 is any amino acid

<221> VARIANT
<222> 5
<223> Position 5 can be any amino acid with G or S
      preferred

<400> 515
Asp Xaa Xaa Asp Xaa
 1   5

<210> 516
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 516
Asp Glu Val Asp Gly
 1   5

<210> 517
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 517
Asp Glu Val Asp Ser
 1   5

<210> 518
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 518
Asp Glu Pro Asp Gly
 1   5

<210> 519
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 519
Asp Glu Pro Asp Ser
 1   5

<210> 520
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 520
Asp Glu Leu Asp Gly
 1   5

<210> 521
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 521
Asp Glu Leu Asp Ser
 1   5

<210> 522
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible G-spacer

<400> 522
Gly Gly Gly Gly
 1

<210> 523
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible G-spacer

<400> 523
Gly Gly Gly Gly Ser
 1   5

<210> 524
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible A-spacer

<400> 524
Ala Ala Ala Ala
 1

<210> 525
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible A-spacer

<400> 525
Ala Ala Ala Ala Val
 1   5

<210> 526
<211> 3939
<212> DNA
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<220>
<223> DNA encoding a BoNT/A with a HIS tag

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ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240
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aaacgtaacg aaaaatggga tgaggtgtat aagtatattg ttaccaactg gctcgctaaa 2160
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tacattaacg tggtggtgaa gaataaagaa tatcgtctgg cgaccaatgc tagtcaggcg 3600
ggcgtggaga aaattctgtc tgcacttgaa atcccggatg tgggtaattt atcccaggtg 3660
gttgtgatga aaagtaaaaa tgaccaaggg atcaccaata aatgcaaaat gaatctgcaa 3720
gataacaacg gcaacgacat tggttttatc ggcttccacc aattcaataa tatcgcgaaa 3780
ctggtggcct caaattggta caaccgtcag attgagcgca gctcccgcac tttaggctgt 3840
agctgggagt tcattccggt agatgacggt tggggagaac gcccattgaa agtcgacaag 3900
cttgcggccg cactcgagca ccaccaccac caccactga                         3939
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<210> 527
<211> 1312
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A with a HIS tag

<400> 527

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Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
 1               5                  10                  15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
```

```
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465                 470                 475                 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545                 550                 555                 560
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
                565                 570                 575
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
            580                 585                 590
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Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
755 760 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
770 775 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785 790 795 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
805 810 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
820 825 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
850 855 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865 870 875 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
885 890 895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
900 905 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
915 920 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
965 970 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
980 985 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
995 1000 1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
1010 1015 1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025 1030 1035 1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
1045 1050 1055
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
1060 1065 1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
1075 1080 1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
1090 1095 1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105 1110 1115 1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
1125 1130 1135

```
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
                1285                1290                1295
Lys Val Asp Lys Leu Ala Ala Ala Leu Glu His His His His His His
            1300                1305                1310
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<210> 528
<211> 3921
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a BoNT/A-TEV with a HIS tag

<400> 528

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aaaatttggg tgatcccgga gcgcgatacg ttcacgaacc cggaagaagg agatttaaac 180
ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240
gacaatgaaa aggacaacta cctgaaaggt gttaccaaac tgttcgagcg catttattcg 300
acagatctcg gtcgcatgtt gctgacttct attgtgcgcg gcattccgtt ttggggtggt 360
agcaccatcg atacagaact caaagtgatt gacaccaact gcatcaatgt gattcagcct 420
gatgggagct accggtccga agagcttaac ctcgtaatca ttggcccgag cgcggatatt 480
atccaattcg aatgtaaatc ttttgggcat gaagtcctga atctgacgcg gaatggctat 540
ggatcgacgc agtatattcg tttttctcca gatttcacat ttggatttga agaaagcctc 600
gaagttgata cgaaccctct tttaggcgcg ggaaaattcg cgacggaccc agcggtgacc 660
ttggcacatg aacttattca tgccgggcat cgcttgtatg gaatcgccat taacccgaac 720
cgtgttttca aggtgaatac gaacgcgtat tacgagatgt cgggcttaga agtgtccttt 780
gaagaactgc gcacgtttgg cggtcatgat gcaaaattta ttgatagtct gcaagaaaac 840
gaatttcggc tgtactatta caataaattc aaagacattg catcaacctt aaacaaggcg 900
aaaagcattg tgggtaccac ggctagctta caatatatga aaaacgtttt caaagaaaaa 960
tacctcctta gcgaagacac ttccggcaaa ttctctgtcg ataaactgaa atttgataaa 1020
ctgtataaaa tgctcaccga gatctacaca gaggataact ttgtcaaatt cttcaaggtc 1080
ttgaatcgga aaacctatct gaacttcgat aaagccgtct ttaagatcaa catcgtaccg 1140
aaagttaact acaccatcta tgatggcttt aatctgcgca atacgaatct ggcggcgaac 1200
tttaacggcc agaacaccga aatcaacaac atgaacttta ctaaactgaa aaattttacc 1260
ggcttgtttg aattctataa gctcctgtgt gtccgcggta ttatcaccag caaaggcggt 1320
ggttctggcg gtggtgaaaa cctgtacttc cagggcggtg gctccggtgg tggtgcgctc 1380
aatgatttat gcatcaaggt gaacaactgg gacttgtttt tctctccatc tgaagataat 1440
tttactaacg acttgaacaa aggagaggaa attacttccg ataccaacat cgaagcagcg 1500
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gagcctgaga acatttccat tgagaatctc agctctgaca tcatcggcca gctggaactg 1620
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accattatca ttccctatat tggccctgca ctgaacattg gtaacatgct gtataaagat 1980
gattttgtgg gcgccctgat cttttcaggc gctgttatcc tgctggaatt tatcccggaa 2040
atcgccattc cagtactcgg taccttttgcg ctggtgtcct atatcgcaaa caaagttttg 2100
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actgtccaga cgatcgacaa cgcgctcagt aaacgtaacg aaaaatggga tgaggtgtat 2160
aagtatattg ttaccaactg gctcgctaaa gtaaacaccc agattgacct gattcgcaag 2220
aagatgaaag aagcgctgga aaaccaagca gaagcgacca aagctattat caactatcaa 2280
tataaccagt acacagagga agaaaagaat aacatcaact tcaacatcga cgacttatct 2340
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aactcctccc tctatcgcgg tactaaattt attatcaaga aatatgcctc tggcaacaag 3540
gacaatatcg tacgcaataa cgatcgcgtc tacattaacg tggtggtgaa gaataaagaa 3600
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ggcttccacc aattcaataa tatcgcgaaa ctggtggcct caaattggta caaccgtcag 3840
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tggggagaac gcccattgta a 3921

<210> 529
<211> 1306
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A-TEV with a HIS tag

<400> 529
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 1   5   10   15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
            20   25   30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35   40   45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50   55   60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65   70   75   80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85   90   95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100   105   110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115   120   125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130   135   140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145   150   155   160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165   170   175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180   185   190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195   200   205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu

210 215 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430
Gly Ile Ile Thr Ser Lys Gly Gly Gly Ser Gly Gly Gly Glu Asn Leu
435 440 445
Tyr Phe Gln Gly Gly Gly Ser Gly Gly Gly Ala Leu Asn Asp Leu Cys
450 455 460
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
465 470 475 480
Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn
485 490 495
Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr
500 505 510
Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu
515 520 525
Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile
530 535 540
Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met
545 550 555 560
Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile
565 570 575
Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val
580 585 590
Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr
595 600 605
Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe
610 615 620
Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile
625 630 635 640
Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met
645 650 655
Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val
660 665 670
Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr
675 680 685
Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr
690 695 700
Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr
705 710 715 720
Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp
725 730 735
Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala
740 745 750
Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu

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        755                 760                 765
Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn
    770                 775                 780
Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln
785                 790                 795                 800
Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys
                805                 810                 815
Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr
            820                 825                 830
Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys
        835                 840                 845
Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser
    850                 855                 860
Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile
865                 870                 875                 880
Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn
                885                 890                 895
His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser
            900                 905                 910
Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn
        915                 920                 925
Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr
    930                 935                 940
Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro
945                 950                 955                 960
Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn
                965                 970                 975
Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu
            980                 985                 990
Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val
        995                 1000                1005
Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp
    1010                1015                1020
Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr
1025                1030                1035                1040
Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn
                1045                1050                1055
Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp
            1060                1065                1070
Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu
        1075                1080                1085
Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
    1090                1095                1100
Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro
1105                1110                1115                1120
Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn
                1125                1130                1135
Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser
            1140                1145                1150
Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
        1155                1160                1165
Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val
    1170                1175                1180
Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu
1185                1190                1195                1200
Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu
                1205                1210                1215
Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val
            1220                1225                1230
Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn
        1235                1240                1245
Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln
    1250                1255                1260
Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln
1265                1270                1275                1280
Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro
                1285                1290                1295
Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
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<210> 530
<211> 3945
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a BoNT/A comprising Thrombin (N880)
and Thrombin (D890)

<400> 530
atgccgttcg taaacaaaca gttcaactat aaagacccag tcaacggcgt ggacattgcc 60
tatatcaaaa tcccgaatgc gggtcaaatg cagcccgtga aagcatttaa aatccataac 120
aaaatttggg tgatcccgga gcgcgatacg ttcacgaacc cggaagaagg agatttaaac 180
ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240
gacaatgaaa aggacaacta cctgaaaggt gttaccaaac tgttcgagcg catttattcg 300
acagatctcg gtcgcatgtt gctgacttct attgtgcgcg gcattccgtt ttggggtggt 360
agcaccatcg atacagaact caaagtgatt gacaccaact gcatcaatgt gattcagcct 420
gatgggagct accggtccga agagcttaac ctcgtaatca ttggcccgag cgcggatatt 480
atccaattcg aatgtaaatc ttttgggcat gaagtcctga atctgacgcg gaatggctat 540
ggatcgacgc agtatattcg tttttctcca gatttcacat ttggatttga agaaagcctc 600
gaagttgata cgaaccctct ttaggcgcg ggaaaattcg cgacggaccc agcggtgacc 660
ttggcacatg aacttattca tgccgggcat cgcttgtatg gaatcgccat taacccgaac 720
cgtgttttca aggtgaatac gaacgcgtat tacgagatgt cgggcttaga agtgtccttt 780
gaagaactgc gcacgtttgg cggtcatgat gcaaaattta ttgatagtct gcaagaaaac 840
gaatttcggc tgtactatta caataaattc aaagacattg catcaacctt aaacaaggcg 900
aaaagcattg tgggtaccac ggctagctta caatatatga aaaacgtttt caaagaaaaa 960
tacctcctta gcgaagacac ttccggcaaa ttctctgtcg ataaactgaa atttgataaa 1020
ctgtataaaa tgctcaccga gatctacaca gaggataact ttgtcaaatt cttcaaggtc 1080
ttgaatcgga aaacctatct gaacttcgat aaagccgtct ttaagatcaa catcgtaccg 1140
aaagttaact acaccatcta tgatggcttt aatctgcgca atacgaatct ggcggcgaac 1200
tttaacggcc agaacaccga aatcaacaac atgaacttta ctaaactgaa aaattttacc 1260
ggcttgtttg aattctataa gctcctgtgt gtccgcggta ttatcaccag caaaggcggt 1320
ggttctggcg gtggtgaaaa cctgtacttc cagggcggtg gctccggtgg tggtgcgctc 1380
aatgatttat gcatcaaggt gaacaactgg gacttgtttt tctctccatc tgaagataat 1440
tttactaacg acttgaacaa aggagaggaa attacttccg ataccaacat cgaagcagcg 1500
gaagagaata ttagtctaga tcttattcaa caatattacc tgacctttaa ttttgataac 1560
gagcctgaga acatttccat tgagaatctc agctctgaca tcatcggcca gctggaactg 1620
atgccgaata tcgaacgctt tcctaatgga aagaaatatg aattggacaa atacaccatg 1680
ttccactatc tccgcgcgca ggagtttgag cacggcaagt ctcgtattgc tctgaccaat 1740
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gattttgtgg gcgccctgat cttttcaggc gctgttatcc tgctggaatt tatcccggaa 2040
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aagatgaaag aagcgctgga aaaccaagca gaagcgacca aagctattat caactatcaa 2280
tataaccagt acacagagga agaaaagaat aacatcaact tcaacatcga cgacttatct 2340
tcaaagctga atgaatctat taacaaagcg atgattaata ttaacaagtt cttgaaccaa 2400
tgtagtgtca gctatctgat gaactcgatg atcccttacg gtgtgaaacg tctggaagac 2460
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attggccaag tggatcgctt aaaagataaa gtcaacaaca cgctgagtac agacatccct 2580
tttcagctgt ctaaatatgt ggacaatcag cgcctgctgt ccacgtttac ggaatacatc 2640
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aagattgaag ttatcttaaa aaatgcgatt gtatataatt caatgtacga aaatttctct 2880
acgagctttt ggattcgtat tccgaaatat ttcaacagta tctctttaaa caacgagtat 2940
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atcatctgga ctctgcagga cactcaagaa attaaacaac gcgtggtgtt taaatactca 3060
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cggctgaaca acagcaaaat ttacattaac ggtcgcctga tcgatcagaa accaatcagt 3180
aatctcggta acattcacgc atcgaataat atcatgttca aactggatgg ttgtcgcgac 3240
acgcaccgtt acatttggat caaatacttc aatttattcg acaaagaact caacgaaaag 3300

gagattaagg atctttatga caatcagtct aattcgggta ttctgaaaga cttttggggt 3360
gattaccttc agtacgataa accgtattat atgttaaact tatatgatcc gaataaatac 3420
gttgacgtca acaacgttgg cattcgcggc tatatgtatc tgaaagggcc gcgtggcagc 3480
gtgatgacca ctaacattta cttaaactcc tccctctatc gcggtactaa atttattatc 3540
aagaaatatg cctctggcaa caaggacaat atcgtacgca ataacgatcg cgtctacatt 3600
aacgtggtgg tgaagaataa agaatatcgt ctggcgacca atgctagtca ggcgggcgtg 3660
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atgaaaagta aaaatgacca agggatcacc aataaatgca aaatgaatct gcaagataac 3780
aacggcaacg acattggttt tatcggcttc caccaattca ataatatcgc gaagcttgtg 3840
gcctcaaatt ggtacaaccg tcagattgag cgcagctccc gcactttagg ctgtagctgg 3900
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<210> 531
<211> 1314
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A comprising Thrombin (N880) and Thrombin (D890)

<400> 531

Met	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly
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Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Ala	Gly	Gln	Met	Gln	Pro
		20					25					30			
Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	Glu	Arg
	35					40					45				
Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	Pro	Pro	Glu
50					55					60					
Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	Tyr	Leu	Ser	Thr
65				70					75					80	
Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	Thr	Lys	Leu	Phe	Glu
			85					90					95		
Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	Leu	Leu	Thr	Ser	Ile	Val
		100					105					110			
Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	Thr	Ile	Asp	Thr	Glu	Leu	Lys
	115					120					125				
Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr
130					135					140					
Arg	Ser	Glu	Glu	Leu	Asn	Leu	Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile
145				150					155					160	
Ile	Gln	Phe	Glu	Cys	Lys	Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr
			165					170					175		
Arg	Asn	Gly	Tyr	Gly	Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe
		180					185					190			
Thr	Phe	Gly	Phe	Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu
	195					200					205				
Gly	Ala	Gly	Lys	Phe	Ala	Thr	Asp	Pro	Ala	Val	Thr	Leu	Ala	His	Glu
210					215					220					
Leu	Ile	His	Ala	Gly	His	Arg	Leu	Tyr	Gly	Ile	Ala	Ile	Asn	Pro	Asn
225				230					235					240	
Arg	Val	Phe	Lys	Val	Asn	Thr	Asn	Ala	Tyr	Tyr	Glu	Met	Ser	Gly	Leu
			245					250					255		
Glu	Val	Ser	Phe	Glu	Glu	Leu	Arg	Thr	Phe	Gly	Gly	His	Asp	Ala	Lys
		260					265					270			
Phe	Ile	Asp	Ser	Leu	Gln	Glu	Asn	Glu	Phe	Arg	Leu	Tyr	Tyr	Tyr	Asn
	275					280					285				
Lys	Phe	Lys	Asp	Ile	Ala	Ser	Thr	Leu	Asn	Lys	Ala	Lys	Ser	Ile	Val
290					295					300					
Gly	Thr	Thr	Ala	Ser	Leu	Gln	Tyr	Met	Lys	Asn	Val	Phe	Lys	Glu	Lys
305				310					315					320	
Tyr	Leu	Leu	Ser	Glu	Asp	Thr	Ser	Gly	Lys	Phe	Ser	Val	Asp	Lys	Leu
			325					330					335		
Lys	Phe	Asp	Lys	Leu	Tyr	Lys	Met	Leu	Thr	Glu	Ile	Tyr	Thr	Glu	Asp
		340					345					350			
Asn	Phe	Val	Lys	Phe	Phe	Lys	Val	Leu	Asn	Arg	Lys	Thr	Tyr	Leu	Asn
	355					360					365				

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Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Gly Gly Gly Ser Gly Gly Gly Glu Asn Leu
        435                 440                 445
Tyr Phe Gln Gly Gly Gly Ser Gly Gly Gly Ala Leu Asn Asp Leu Cys
    450                 455                 460
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
465                 470                 475                 480
Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn
                485                 490                 495
Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr
            500                 505                 510
Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu
        515                 520                 525
Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile
    530                 535                 540
Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met
545                 550                 555                 560
Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile
                565                 570                 575
Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val
            580                 585                 590
Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr
        595                 600                 605
Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe
    610                 615                 620
Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile
625                 630                 635                 640
Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met
                645                 650                 655
Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val
            660                 665                 670
Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr
        675                 680                 685
Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr
    690                 695                 700
Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr
705                 710                 715                 720
Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp
                725                 730                 735
Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala
            740                 745                 750
Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu
        755                 760                 765
Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn
    770                 775                 780
Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln
785                 790                 795                 800
Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys
                805                 810                 815
Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr
            820                 825                 830
Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys
        835                 840                 845
Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser
    850                 855                 860
Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile
865                 870                 875                 880
Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Val Pro Arg Gly Ser
                885                 890                 895
Tyr Glu Ser Asn His Leu Ile Asp Leu Val Pro Arg Gly Ser Arg Tyr
            900                 905                 910
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Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
        915                 920                 925
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
    930                 935                 940
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
945                 950                 955                 960
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
                965                 970                 975
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
            980                 985                 990
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
        995                 1000                1005
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
    1010                1015                1020
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
1025                1030                1035                1040
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
                1045                1050                1055
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
            1060                1065                1070
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
        1075                1080                1085
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
    1090                1095                1100
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
1105                1110                1115                1120
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
                1125                1130                1135
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
            1140                1145                1150
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
        1155                1160                1165
Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
    1170                1175                1180
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
1185                1190                1195                1200
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
                1205                1210                1215
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
            1220                1225                1230
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
        1235                1240                1245
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
    1250                1255                1260
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
1265                1270                1275                1280
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
                1285                1290                1295
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
            1300                1305                1310
Pro Leu
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<210> 532
<211> 3945
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a BoNT/A comprising FXa (N872) and
Thrombin (E884)

<400> 532
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aaaatttggg tgatcccgga gcgcgatacg ttcacgaacc cggaagaagg agatttaaac 180
ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240

gacaatgaaa aggacaacta cctgaaaggt gttaccaaac tgttcgagcg catttattcg 300
acagatctcg gtcgcatgtt gctgacttct attgtgcgcg gcattccgtt ttggggtggt 360
agcaccatcg atacagaact caaagtgatt gacaccaact gcatcaatgt gattcagcct 420
gatgggagct accggtccga agagcttaac ctcgtaatca ttggcccgag cgcggatatt 480
atccaattcg aatgtaaatc ttttgggcat gaagtcctga atctgacgcg gaatggctat 540
ggatcgacgc agtatattcg tttttctcca gatttcacat ttggatttga agaaagcctc 600
gaagttgata cgaaccctct ttaggcgcg ggaaaattcg cgacggaccc agcggtgacc 660
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cgtgttttca aggtgaatac gaacgcgtat tacgagatgt cgggcttaga agtgtccttt 780
gaagaactgc gcacgtttgg cggtcatgat gcaaaattta ttgatagtct gcaagaaaac 840
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ttgaatcgga aaacctatct gaacttcgat aaagccgtct ttaagatcaa catcgtaccg 1140
aaagttaact acaccatcta tgatggcttt aatctgcgca atacgaatct ggcggcgaac 1200
tttaacggcc agaacaccga aatcaacaac atgaacttta ctaaactgaa aaattttacc 1260
ggcttgtttg aattctataa gctcctgtgt gtccgcggta ttatcaccag caaaggcggt 1320
ggttctggcg gtggtgaaaa cctgtacttc cagggcggtg gctccggtgg tggtgcgctc 1380
aatgatttat gcatcaaggt gaacaactgg gacttgtttt tctctccatc tgaagataat 1440
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gaagagaata ttagtctaga tcttattcaa caatattacc tgacctttaa ttttgataac 1560
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accattatca ttccctatat tggccctgca ctgaacattg gtaacatgct gtataaagat 1980
gattttgtgg gcgccctgat cttttcaggc gctgttatcc tgctggaatt tatcccggaa 2040
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aagtatattg ttaccaactg gctcgctaaa gtaaacaccc agattgacct gattcgcaag 2220
aagatgaaag aagcgctgga aaaccaagca gaagcgacca aagctattat caactatcaa 2280
tataaccagt acacagagga agaaaagaat aacatcaact tcaacatcga cgacttatct 2340
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tgtagtgtca gctatctgat gaactcgatg atcccttacg gtgtgaaacg tctggaagac 2460
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attggccaag tggatcgctt aaaagataaa gtcaacaaca cgctgagtac agacatccct 2580
tttcagctgt ctaaatatgt ggacaatcag cgcctgctgt ccacgtttac ggaatacatc 2640
aaaaacattg agggccgtat caacactagt attctgaact tgcgttacga gttggtgcca 2700
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atcatctgga ctctgcagga cactcaagaa attaaacaac gcgtggtgtt taaatactca 3060
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gattaccttc agtacgataa accgtattat atgttaaact tatatgatcc gaataaatac 3420
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gtgatgacca ctaacattta cttaaactcc tccctctatc gcggtactaa atttattatc 3540
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aacgtggtgg tgaagaataa agaatatcgt ctggcgacca atgctagtca ggcgggcgtg 3660
gagaaaattc tgtctgcact tgaaatcccg gatgtgggta atttatccca ggtggttgtg 3720
atgaaaagta aaaatgacca agggatcacc aataaatgca aaatgaatct gcaagataac 3780
aacggcaacg acattggttt tatcggcttc caccaattca ataatatcgc gaagcttgtg 3840
gcctcaaatt ggtacaaccg tcagattgag cgcagctccc gcactttagg ctgtagctgg 3900
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<210> 533
<211> 1314
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A comprising FXa (N872) and Thrombin (E884)

<400> 533

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Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Gly Gly Gly Ser Gly Gly Gly Glu Asn Leu
        435                 440                 445
Tyr Phe Gln Gly Gly Gly Ser Gly Gly Gly Ala Leu Asn Asp Leu Cys
    450                 455                 460
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
465                 470                 475                 480
Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn
                485                 490                 495
Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr
            500                 505                 510
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Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu
515 520 525
Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile
530 535 540
Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met
545 550 555 560
Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile
565 570 575
Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val
580 585 590
Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr
595 600 605
Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe
610 615 620
Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile
625 630 635 640
Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met
645 650 655
Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val
660 665 670
Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr
675 680 685
Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr
690 695 700
Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr
705 710 715 720
Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp
725 730 735
Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala
740 745 750
Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu
755 760 765
Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn
770 775 780
Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln
785 790 795 800
Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys
805 810 815
Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr
820 825 830
Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys
835 840 845
Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser
850 855 860
Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile
865 870 875 880
Lys Asn Ile Glu Gly Arg Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr
885 890 895
Glu Leu Val Pro Arg Gly Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
900 905 910
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
915 920 925
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
930 935 940
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
945 950 955 960
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
965 970 975
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
980 985 990
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
995 1000 1005
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
1010 1015 1020
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
1025 1030 1035 1040
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
1045 1050 1055

Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
1060 1065 1070
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
1075 1080 1085
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
1090 1095 1100
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
1105 1110 1115 1120
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
1125 1130 1135
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
1140 1145 1150
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
1155 1160 1165
Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
1170 1175 1180
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
1185 1190 1195 1200
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
1205 1210 1215
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
1220 1225 1230
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
1235 1240 1245
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
1250 1255 1260
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
1265 1270 1275 1280
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1285 1290 1295
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
1300 1305 1310
Pro Leu

<210> 534
<211> 3921
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a BoNT/A comprising MMP-9 (I870)

<400> 534
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tatatcaaaa tcccgaatgc gggtcaaatg cagcccgtga aagcatttaa aatccataac 120
aaaatttggg tgatcccgga gcgcgatacg ttcacgaacc cggaagaagg agatttaaac 180
ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240
gacaatgaaa aggacaacta cctgaaaggt gttaccaaac tgttcgagcg catttattcg 300
acagatctcg gtcgcatgtt gctgacttct attgtgcgcg gcattccgtt ttggggtggt 360
agcaccatcg atacagaact caaagtgatt gacaccaact gcatcaatgt gattcagcct 420
gatgggagct accggtccga agagcttaac ctcgtaatca ttggcccgag cgcggatatt 480
atccaattcg aatgtaaatc ttttgggcat gaagtcctga atctgacgcg gaatggctat 540
ggatcgacgc agtatattcg tttttctcca gatttcacat ttggatttga agaaagcctc 600
gaagttgata cgaaccctct tttaggcgcg ggaaaattcg cgacggaccc agcggtgacc 660
ttggcacatg aacttattca tgccgggcat cgcttgtatg gaatcgccat taacccgaac 720
cgtgttttca aggtgaatac gaacgcgtat tacgagatgt cgggcttaga agtgtccttt 780
gaagaactgc gcacgtttgg cggtcatgat gcaaaattta ttgatagtct gcaagaaaac 840
gaatttcggc tgtactatta caataaattc aaagacattg catcaacctt aaacaaggcg 900
aaaagcattg tgggtaccac ggctagctta caatatatga aaaacgtttt caaagaaaaa 960
tacctcctta gcgaagacac ttccggcaaa ttctctgtcg ataaactgaa atttgataaa 1020
ctgtataaaa tgctcaccga gatctacaca gaggataact ttgtcaaatt cttcaaggtc 1080
ttgaatcgga aaacctatct gaacttcgat aaagccgtct ttaagatcaa catcgtaccg 1140
aaagttaact acaccatcta tgatggcttt aatctgcgca atacgaatct ggcggcgaac 1200
tttaacggcc agaacaccga aatcaacaac atgaacttta ctaaactgaa aaattttacc 1260
ggcttgtttg aattctataa gctcctgtgt gtccgcggta ttatcaccag caaaggcggt 1320
ggttctggcg gtggtgaaaa cctgtacttc cagggcggtg gctccggtgg tggtgcgctc 1380

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tttactaacg acttgaacaa aggagaggaa attacttccg ataccaacat cgaagcagcg 1500
gaagagaata ttagtctaga tcttattcaa caatattacc tgacctttaa ttttgataac 1560
gagcctgaga acatttccat tgagaatctc agctctgaca tcatcggcca gctggaactg 1620
atgccgaata tcgaacgctt tcctaatgga aagaaatatg aattggacaa atacaccatg 1680
ttccactatc tccgcgcgca ggagtttgag cacggcaagt ctcgtattgc tctgaccaat 1740
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gttaaaaaag tgaacaaggc gaccgaagcg gcgatgtttt tgggatgggt ggaacaactg 1860
gtatatgact ttacggatga aacttctgaa gtctcgacca ccgacaaaat tgccgatatt 1920
accattatca ttccctatat tggccctgca ctgaacattg gtaacatgct gtataaagat 1980
gattttgtgg gcgccctgat cttttcaggc gctgttatcc tgctggaatt tatcccggaa 2040
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actgtccaga cgatcgacaa cgcgctcagt aaacgtaacg aaaaatggga tgaggtgtat 2160
aagtatattg ttaccaactg gctcgctaaa gtaaacaccc agattgacct gattcgcaag 2220
aagatgaaag aagcgctgga aaaccaagca gaagcgacca aagctattat caactatcaa 2280
tataaccagt acacagagga agaaaagaat aacatcaact tcaacatcga cgacttatct 2340
tcaaagctga atgaatctat taacaaagcg atgattaata ttaacaagtt cttgaaccaa 2400
tgtagtgtca gctatctgat gaactcgatg atcccttacg gtgtgaaacg tctggaagac 2460
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caagaaatta aacaacgcgt ggtgtttaaa tactcacaga tgattaacat ctcggattat 3060
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aataatatca tgttcaaact ggatggttgt cgcgacacgc accgttacat ttggatcaaa 3240
tacttcaatt tattcgacaa agaactcaac gaaaaggaga ttaaggatct ttatgacaat 3300
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gacaatatcg tacgcaataa cgatcgcgtc tacattaacg tggtggtgaa gaataaagaa 3600
tatcgtctgg cgaccaatgc tagtcaggcg ggcgtggaga aaattctgtc tgcacttgaa 3660
atcccggatg tgggtaattt atcccaggtg gttgtgatga aaagtaaaaa tgaccaaggg 3720
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ggcttccacc aattcaataa tatcgcgaag cttgtggcct caaattggta caaccgtcag 3840
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tggggagaac gcccattgta a                                           3921
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<210> 535
<211> 1306
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A comprising MMP-9 (I870)

<400> 535

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            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
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        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Gly Gly Gly Ser Gly Gly Gly Glu Asn Leu
        435                 440                 445
Tyr Phe Gln Gly Gly Gly Ser Gly Gly Gly Ala Leu Asn Asp Leu Cys
    450                 455                 460
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
465                 470                 475                 480
Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn
                485                 490                 495
Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr
            500                 505                 510
Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu
        515                 520                 525
Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile
    530                 535                 540
Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met
545                 550                 555                 560
Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile
                565                 570                 575
Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val
            580                 585                 590
Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr
        595                 600                 605
Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe
    610                 615                 620
Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile
625                 630                 635                 640
Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met
                645                 650                 655
Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val
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660 665 670
Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr
675 680 685
Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr
690 695 700
Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr
705 710 715 720
Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp
725 730 735
Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala
740 745 750
Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu
755 760 765
Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn
770 775 780
Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln
785 790 795 800
Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys
805 810 815
Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr
820 825 830
Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys
835 840 845
Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser
850 855 860
Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile
865 870 875 880
Gly Pro Leu Gly Leu Trp Ala Gln Leu Asn Leu Arg Tyr Glu Ser Asn
885 890 895
His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser
900 905 910
Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn
915 920 925
Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr
930 935 940
Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro
945 950 955 960
Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn
965 970 975
Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu
980 985 990
Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val
995 1000 1005
Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp
1010 1015 1020
Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr
1025 1030 1035 1040
Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn
1045 1050 1055
Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp
1060 1065 1070
Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu
1075 1080 1085
Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
1090 1095 1100
Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro
1105 1110 1115 1120
Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn
1125 1130 1135
Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser
1140 1145 1150
Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
1155 1160 1165
Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val
1170 1175 1180
Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu
1185 1190 1195 1200
Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu

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                1205                1210                1215
Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val
            1220                1225                1230
Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn
        1235                1240                1245
Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln
    1250                1255                1260
Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln
1265                1270                1275                1280
Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro
                1285                1290                1295
Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
            1300                1305
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<210> 536
<211> 3916
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding a BoNT/A comprising Fxa (N872)

<400> 536

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aaaatttggg tgatcccgga gcgcgatacg ttcacgaacc cggaagaagg agatttaaac 180
ccaccgcctg aggctaaaca ggtcccggtg tcttactatg atagcacata cctgagtacc 240
gacaatgaaa aggacaacta cctgaaaggt gttaccaaac tgttcgagcg catttattcg 300
acagatctcg gtcgcatgtt gctgacttct attgtgcgcg gcattccgtt ttggggtggt 360
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gatgggagct accggtccga agagcttaac ctcgtaatca ttggcccgag cgcggatatt 480
atccaattcg aatgtaaatc ttttgggcat gaagtcctga atctgacgcg gaatggctat 540
ggatcgacgc agtatattcg tttttctcca gatttcacat ttggatttga agaaagcctc 600
gaagttgata cgaaccctct tttaggcgcg ggaaaattcg cgacggaccc agcggtgacc 660
ttggcacatg aacttattca tgccgggcat cgcttgtatg gaatcgccat taacccgaac 720
cgtgttttca aggtgaatac gaacgcgtat tacgagatgt cgggcttaga agtgtccttt 780
gaagaactgc gcacgtttgg cggtcatgat gcaaaattta ttgatagtct gcaagaaaac 840
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tttcaacagt atctctttaa acaacgagta tactatcatc aattgtatgg agaataacag 2940
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<210> 537
<211> 1309
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A comprising Fxa (N872)

<400> 537

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            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
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Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Gly Gly Gly Ser Gly Gly Gly Glu Asn Leu
        435                 440                 445
Tyr Phe Gln Gly Gly Gly Ser Gly Gly Gly Ala Leu Asn Asp Leu Cys
    450                 455                 460
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
465                 470                 475                 480
Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn
                485                 490                 495
Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr
            500                 505                 510
Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu
        515                 520                 525
Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile
    530                 535                 540
Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met
545                 550                 555                 560
Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile
                565                 570                 575
Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val
            580                 585                 590
Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr
        595                 600                 605
Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe
    610                 615                 620
Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile
625                 630                 635                 640
Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met
                645                 650                 655
Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val
            660                 665                 670
Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr
        675                 680                 685
Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr
    690                 695                 700
Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr
705                 710                 715                 720
Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp
                725                 730                 735
Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala
            740                 745                 750
Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu
        755                 760                 765
Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn
    770                 775                 780
Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln
785                 790                 795                 800
Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys
                805                 810                 815
Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr
            820                 825                 830
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Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys
        835                 840                 845
Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser
    850                 855                 860
Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile
865                 870                 875                 880
Lys Asn Ile Glu Gly Arg Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr
                885                 890                 895
Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn
            900                 905                 910
Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln
        915                 920                 925
Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala
    930                 935                 940
Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile
945                 950                 955                 960
Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr
                965                 970                 975
Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn
            980                 985                 990
Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln
        995                 1000                1005
Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile
    1010                1015                1020
Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser
1025                1030                1035                1040
Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn
                1045                1050                1055
Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly
            1060                1065                1070
Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe
        1075                1080                1085
Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln
    1090                1095                1100
Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr
1105                1110                1115                1120
Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val
                1125                1130                1135
Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro
            1140                1145                1150
Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr
        1155                1160                1165
Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp
    1170                1175                1180
Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys
1185                1190                1195                1200
Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
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Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln
            1220                1225                1230
Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys
        1235                1240                1245
Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly
    1250                1255                1260
Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr
1265                1270                1275                1280
Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu
                1285                1290                1295
Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
            1300                1305
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