SEQUENCE LISTING

<110> IPSEN BIOPHARM LIMITED

<120> CLOSTRIDIAL NEUROTOXINS COMPRISING AN EXOGENOUS ACTIVATION LOOP

<130> P59901WO

<150> GB1815817.0
<151> 2018-09-28

<160> 81

<170> PatentIn version 3.5

<210> 1
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> C1 Activation Loop Consensus Sequence

<220>
<221> SITE
<222> (2)..(2)
<223> Xaa is 1-10 residues of any amino acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is Asp or Glu

<220>
<221> SITE
<222> (7)..(7)
<223> Xaa is 4-15 residues of any amino acid

<400> 1

Cys Xaa Ile Xaa Gly Arg Xaa Cys
1 5

<210> 2
<211> 17
<212> PRT
<213> Clostridium botulinum

<400> 2

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp
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Cys

<210> 3
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> C1 Activation Loop Variant

<400> 3

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Cys

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<211> 3891
<212> DNA
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<223> BoNT/X with a C1 Activation Loop

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tttcaggtga ttaaaaacat ttggattgtg ccggaacgct acaactttac caataatacc 180

aacgatctga acattccgag cgaaccgatt atggaagcag atgccattta taacccgaac 240

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gatattgcaa ataatgcaac ctatggtctg tatagcaccc cgattagtaa tggtgaaggt 540

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gaactgaacc agaacgaagt ggtgaaactg tataactact acttcaacag caactacatt 3240

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<212> PRT
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<220>
<223> BoNT/X with a C1 Activation Loop

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Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
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Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser
225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys His Lys Ala Ile Asp Gly Arg Ser Leu
420 425 430

Tyr Asn Lys Thr Leu Asp Cys Ile Glu Val Glu Asn Lys Asp Leu Phe
435 440 445

Leu Ile Ser Asn Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu
450 455 460

Lys Ile Lys Pro Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro
465 470 475 480

Gln Asp Ile Thr Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile
485 490 495

Pro Ser Ile Ser Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr
500 505 510

Glu Pro Ile Arg Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp
515 520 525

Lys Leu Thr Thr Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser
530 535 540

Ile Asp Ser Ser Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu
545 550 555 560

Ala Leu Ser Asn Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser
565 570 575

Asn Thr Ile Asn Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe
580 585 590

Tyr Gln Trp Leu Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly
595 600 605

Lys Ile Asp Val Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro
610 615 620

Tyr Ile Gly Pro Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp

625 630 635 640

Phe Val Gly Ala Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr
645 650 655

Val Pro Glu Phe Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly
660 665 670

Gly Glu Leu Ala Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu
675 680 685

Asp Lys Arg Asp Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala
690 695 700

Gln Trp Trp Gly Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His
705 710 715 720

Thr Tyr Lys Ala Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met
725 730 735

Glu Phe Gln Leu Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys
740 745 750

Ile Lys Asn Ala Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val
755 760 765

Glu Gln Ala Met Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn
770 775 780

Ser Tyr Leu Thr Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys
785 790 795 800

Asn Phe Asp Leu Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu
805 810 815

Lys Glu Asp Ile Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys
820 825 830

Val Ser Ile Arg Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile
835 840 845

Pro Phe Ser Glu Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile
850 855 860

Glu Asp Tyr Glu Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys
865 870 875 880

Asp Leu Ser Gly Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu
885 890 895

Leu Ala Asp Gly Arg Glu Asn Lys Ala Ile Lys Ile Lys Gly Ser Glu
900 905 910

Asn Ser Thr Ile Lys Ile Ala Met Asn Lys Tyr Leu Arg Phe Ser Ala
915 920 925

Thr Asp Asn Phe Ser Ile Ser Phe Trp Ile Lys His Pro Lys Pro Thr
930 935 940

Asn Leu Leu Asn Asn Gly Ile Glu Tyr Thr Leu Val Glu Asn Phe Asn
945 950 955 960

Gln Arg Gly Trp Lys Ile Ser Ile Gln Asp Ser Lys Leu Ile Trp Tyr
965 970 975

Leu Arg Asp His Asn Asn Ser Ile Lys Ile Val Thr Pro Asp Tyr Ile
980 985 990

Ala Phe Asn Gly Trp Asn Leu Ile Thr Ile Thr Asn Asn Arg Ser Lys
995 1000 1005

Gly Ser Ile Val Tyr Val Asn Gly Ser Lys Ile Glu Glu Lys Asp
1010 1015 1020

Ile Ser Ser Ile Trp Asn Thr Glu Val Asp Asp Pro Ile Ile Phe
1025 1030 1035

Arg Leu Lys Asn Asn Arg Asp Thr Gln Ala Phe Thr Leu Leu Asp
1040 1045 1050

Gln Phe Ser Ile Tyr Arg Lys Glu Leu Asn Gln Asn Glu Val Val
1055 1060 1065

Lys Leu Tyr Asn Tyr Tyr Phe Asn Ser Asn Tyr Ile Arg Asp Ile
1070 1075 1080

Trp Gly Asn Pro Leu Gln Tyr Asn Lys Lys Tyr Tyr Leu Gln Thr
1085 1090 1095

Gln Asp Lys Pro Gly Lys Gly Leu Ile Arg Glu Tyr Trp Ser Ser
1100 1105 1110

Phe Gly Tyr Asp Tyr Val Ile Leu Ser Asp Ser Lys Thr Ile Thr
1115 1120 1125

Phe Pro Asn Asn Ile Arg Tyr Gly Ala Leu Tyr Asn Gly Ser Lys
1130 1135 1140

Val Leu Ile Lys Asn Ser Lys Lys Leu Asp Gly Leu Val Arg Asn
1145 1150 1155

Lys Asp Phe Ile Gln Leu Glu Ile Asp Gly Tyr Asn Met Gly Ile
1160 1165 1170

Ser Ala Asp Arg Phe Asn Glu Asp Thr Asn Tyr Ile Gly Thr Thr
1175 1180 1185

Tyr Gly Thr Thr His Asp Leu Thr Thr Asp Phe Glu Ile Ile Gln
1190 1195 1200

Arg Gln Glu Lys Tyr Arg Asn Tyr Cys Gln Leu Lys Thr Pro Tyr
1205 1210 1215

Asn Ile Phe His Lys Ser Gly Leu Met Ser Thr Glu Thr Ser Lys
1220 1225 1230

Pro Thr Phe His Asp Tyr Arg Asp Trp Val Tyr Ser Ser Ala Trp
1235 1240 1245

Tyr Phe Gln Asn Tyr Glu Asn Leu Asn Leu Arg Lys His Thr Lys
1250 1255 1260

Thr Asn Trp Tyr Phe Ile Pro Lys Asp Glu Gly Trp Asp Glu Asp
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Leu Glu Val Leu Phe Gln Gly Pro His His His His His His His
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His His His
1295

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<212> DNA
<213> Artificial Sequence

<220>
<223> BoNT/XA [LHNX-HCA] with a C1 Activation Loop

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tttcaggtga ttaaaaacat ttggattgtg ccggaacgct acaactttac caataatacc 180

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aacattgcca aactggttgc gagcaattgg tataatcgtc agattgaacg tagcagtcgt 3900

accctgggtt gtagctggga atttattccg gttgatgatg gttggggtga acgtccgctg 3960

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<211> 1330
<212> PRT
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<223> BoNT/XA [LHNX-HCA] with a C1 Activation Loop

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35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser
225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys His Lys Ala Ile Asp Gly Arg Ser Leu
420 425 430

Tyr Asn Lys Thr Leu Asp Cys Ile Glu Val Glu Asn Lys Asp Leu Phe
435 440 445

Leu Ile Ser Asn Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu
450 455 460

Lys Ile Lys Pro Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro
465 470 475 480

Gln Asp Ile Thr Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile
485 490 495

Pro Ser Ile Ser Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr
500 505 510

Glu Pro Ile Arg Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp
515 520 525

Lys Leu Thr Thr Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser
530 535 540

Ile Asp Ser Ser Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu
545 550 555 560

Ala Leu Ser Asn Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser
565 570 575

Asn Thr Ile Asn Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe
580 585 590

Tyr Gln Trp Leu Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly
595 600 605

Lys Ile Asp Val Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro
610 615 620

Tyr Ile Gly Pro Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp
625 630 635 640

Phe Val Gly Ala Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr
645 650 655

Val Pro Glu Phe Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly
660 665 670

Gly Glu Leu Ala Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu
675 680 685

Asp Lys Arg Asp Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala
690 695 700

Gln Trp Trp Gly Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His
705 710 715 720

Thr Tyr Lys Ala Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met
725 730 735

Glu Phe Gln Leu Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys
740 745 750

Ile Lys Asn Ala Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val
755 760 765

Glu Gln Ala Met Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn
770 775 780

Ser Tyr Leu Thr Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys
785 790 795 800

Asn Phe Asp Leu Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu
805 810 815

Lys Glu Asp Ile Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys
820 825 830

Val Ser Ile Arg Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile
835 840 845

Pro Phe Ser Glu Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile
850 855 860

Glu Asp Tyr Glu Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys
865 870 875 880

Asp Leu Ser Gly Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu

885 890 895

Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
900 905 910

Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
915 920 925

Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
930 935 940

Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
945 950 955 960

Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
965 970 975

Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
980 985 990

Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
995 1000 1005

Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe
1010 1015 1020

Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp
1025 1030 1035

Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile
1040 1045 1050

Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu
1055 1060 1065

Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly
1070 1075 1080

Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu
1085 1090 1095

Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
1100 1105 1110

Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
1115 1120 1125

Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro
1130 1135 1140

Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
1145 1150 1155

Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
1160 1165 1170

Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys
1175 1180 1185

Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
1190 1195 1200

Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
1205 1210 1215

Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu
1220 1225 1230

Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
1235 1240 1245

Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu
1250 1255 1260

Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln
1265 1270 1275

Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg
1280 1285 1290

Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe
1295 1300 1305

Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu His His His
1310 1315 1320

His His His His His His His
1325 1330

<210> 8
<211> 4017
<212> DNA
<213> Artificial Sequence

<220>
<223> BoNT/XB [LHNX-HCB] with a C1 Activation Loop

<400> 8
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accatgcgtc cgcctcgtca tagcgataaa atcaataaag gtaaaggtcc gttcaaagcc 120

tttcaggtga ttaaaaacat ttggattgtg ccggaacgct acaactttac caataatacc 180

aacgatctga acattccgag cgaaccgatt atggaagcag atgccattta taacccgaac 240

tatctgaata ccccgagcga aaaagatgaa tttctgcagg gtgttatcaa agtgctggaa 300

cgcattaaaa gcaaaccgga aggtgaaaaa ctgctggaac tgattagcag cagcattccg 360

ctgccgctgg ttagcaatgg tgcactgacc ctgagcgata atgaaaccat tgcatatcaa 420

gagaacaaca acattgtgag caatctgcag gcaaacctgg ttatttatgg tccgggtcct 480

gatattgcaa ataatgcaac ctatggtctg tatagcaccc cgattagtaa tggtgaaggt 540

acactgagcg aagttagctt tagcccgttt tatctgaaac cgtttgatga aagctatggc 600

aattatcgta gcctggtgaa tatcgtgaac aaattcgtga aacgtgaatt tgcacctgat 660

ccggcaagca ccctgatgca tgaactggtt catgttaccc ataatctgta tggtattagc 720

aaccgcaact tctactataa ctttgacacc ggcaaaattg aaaccagccg tcagcagaat 780

agcctgattt ttgaagaact gctgaccttt ggtggcattg atagcaaagc aattagcagc 840

ctgatcatca agaaaattat cgaaaccgcc aagaacaact ataccacgct gattagcgaa 900

cgcctgaata ccgttaccgt tgaaaatgat ctgctgaaat atatcaaaaa caaaatcccg 960

gttcagggtc gtctgggtaa ctttaaactg gataccgcag aattcgagaa aaagctgaat 1020

accattctgt ttgtgctgaa cgaaagcaat ctggcacagc gttttagcat tctggttcgt 1080

aaacattacc tgaaagaacg tccgattgat ccgatttatg tgaacattct ggatgacaat 1140

agctacagca ccctggaagg ttttaacatt agcagtcagg gtagcaatga ttttcagggc 1200

cagctgctgg aaagcagcta ttttgaaaaa attgaatcca atgcgctgcg tgcctttatc 1260

aaaatttgtc ataaagccat tgatggtcgc agcctgtata acaaaaccct ggattgtatt 1320

gaagtggaaa acaaagacct gttcctgatt agcaataaag atagcctgaa cgatatcaac 1380

ctgagcgaag aaaaaatcaa accggaaacc accgtgttct tcaaagataa actgcctccg 1440

caggatatta ccctgagcaa ttatgatttt accgaagcca atagcattcc gagcattagc 1500

cagcagaaca ttctggaacg taatgaagaa ctgtatgaac cgattcgcaa tagcctgttt 1560

gaaatcaaaa ccatctatgt ggataagctg accacctttc attttctgga agcccagaat 1620

attgatgaga gcattgatag cagcaaaatt cgtgttgaac tgaccgatag cgttgatgaa 1680

gcactgagca atccgaataa agtttatagc ccgttcaaga acatgagcaa caccattaat 1740

agcattgaaa ccggtattac cagcacctac atcttttatc agtggctgcg tagcatcgtg 1800

aaagatttta gtgatgaaac cggcaaaatc gacgtgattg ataaaagcag cgataccctg 1860

gccattgttc cgtatattgg tccgctgctg aatattggta atgatattcg tcatggcgat 1920

tttgtgggtg caattgaact ggcaggcatt accgcactgc tggaatatgt tccggaattt 1980

accattccga ttctggttgg tctggaagtt attggtggcg aactggcacg tgaacaggtt 2040

gaagcaattg ttaataatgc cctggataaa cgcgatcaga aatgggcaga agtttacaat 2100

attaccaaag cacagtggtg gggcaccatt catttacaga ttaatacccg tctggcccat 2160

acctataaag ccctgagccg tcaggcaaat gccattaaaa tgaatatgga atttcagctg 2220

gccaactaca aaggcaacat tgatgataaa gccaagatca aaaacgccat cagcgaaacc 2280

gaaattctgc tgaacaaaag cgttgaacag gccatgaaaa acaccgagaa attcatgatt 2340

aaactgagca acagctacct gaccaaagaa atgattccga aagttcagga caacctgaaa 2400

aactttgatc tggaaaccaa aaagaccctg gacaagttca tcaaagagaa agaagatatc 2460

ctgggcacca atctgagcag cagcctgcgt cgtaaagtta gcattcgtct gaataaaaac 2520

attgccttcg acatcaacga tatcccgttt agcgaatttg atgatctgat caaccagtac 2580

aaaaacgaga tcgaagatta tgaagtgctg aatctgggtg cagaagatgg caaaatcaaa 2640

gatctgagcg gtacaaccag cgatattaac attggtagcg atatcgaaat cctgaacaac 2700

attattctga acctgcgcta taaagataac aacctgattg atctgagtgg ctatggtgca 2760

aaagttgaag tttatgatgg tgtggaactg aacgacaaaa accagttcaa actgaccagc 2820

agcgcaaatt caaaaattcg cgttacccag aaccagaaca tcatttttaa cagcgtgttt 2880

ctggatttca gcgtgagctt ttggattcgt attccgaaat ataagaacga cggcatccag 2940

aactatatcc acaatgaata taccatcatc aactgcatga agaataacag cggttggaaa 3000

attagcatcc gtggcaatcg tattatttgg accctgatcg atattaatgg caaaaccaag 3060

agcgtgtttt tcgagtataa catccgtgaa gatatcagcg aatacatcaa ccgttggttt 3120

tttgtgacca ttaccaacaa tctgaacaac gccaaaatct acattaacgg caaactggaa 3180

agcaacaccg atatcaaaga tattcgtgaa gtgattgcca acggcgagat tatctttaaa 3240

ctggatggtg atattgatcg cacccagttt atttggatga aatacttcag catcttcaac 3300

accgaactga gccagagcaa tattgaagaa cgctataaaa tccagagcta cagcgagtat 3360

ctgaaagact tttggggtaa tccgctgatg tacaacaaag aatactacat gtttaatgcc 3420

ggtaacaaaa acagctatat caaactgaaa aaggatagtc cggtgggtga aattctgacc 3480

cgtagcaaat ataaccagaa tagcaagtat atcaactatc gcgatctgta catcggcgag 3540

aaatttatca ttcgtcgtaa aagcaactcc cagagcatta acgatgatat tgtgcgcaaa 3600

gaggattaca tctacctgga ttttttcaac ctgaatcaag agtggcgtgt gtacacctat 3660

aagtacttca aaaaagaaga aatgaaactg tttctggcac cgatctatga tagcgacgaa 3720

ttttacaata ccattcagat taaagaatat gatgaacagc cgacctatag ctgtcagctg 3780

ctgtttaaaa aggatgaaga aagcacggat gaaattggcc tgattggtat ccatcgtttt 3840

tatgaaagcg gcatcgtgtt cgaagagtac aaagattatt tctgcatcag caaatggtat 3900

cttaaagagg tgaaacgcaa accgtataat ctgaaactgg gttgcaattg gcagttcatc 3960

ccgaaagatg aaggttggac cgaacatcat caccaccatc accatcatca tcactga 4017

<210> 9
<211> 1338
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/XB [LHNX-HCB] with a C1 Activation Loop

<400> 9

Met Lys Leu Glu Ile Asn Lys Phe Asn Tyr Asn Asp Pro Ile Asp Gly
1 5 10 15

Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
20 25 30

Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser

225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys His Lys Ala Ile Asp Gly Arg Ser Leu
420 425 430

Tyr Asn Lys Thr Leu Asp Cys Ile Glu Val Glu Asn Lys Asp Leu Phe
435 440 445

Leu Ile Ser Asn Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu
450 455 460

Lys Ile Lys Pro Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro
465 470 475 480

Gln Asp Ile Thr Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile
485 490 495

Pro Ser Ile Ser Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr
500 505 510

Glu Pro Ile Arg Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp
515 520 525

Lys Leu Thr Thr Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser
530 535 540

Ile Asp Ser Ser Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu
545 550 555 560

Ala Leu Ser Asn Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser
565 570 575

Asn Thr Ile Asn Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe
580 585 590

Tyr Gln Trp Leu Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly
595 600 605

Lys Ile Asp Val Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro
610 615 620

Tyr Ile Gly Pro Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp
625 630 635 640

Phe Val Gly Ala Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr
645 650 655

Val Pro Glu Phe Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly
660 665 670

Gly Glu Leu Ala Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu
675 680 685

Asp Lys Arg Asp Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala
690 695 700

Gln Trp Trp Gly Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His
705 710 715 720

Thr Tyr Lys Ala Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met
725 730 735

Glu Phe Gln Leu Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys
740 745 750

Ile Lys Asn Ala Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val
755 760 765

Glu Gln Ala Met Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn
770 775 780

Ser Tyr Leu Thr Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys
785 790 795 800

Asn Phe Asp Leu Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu
805 810 815

Lys Glu Asp Ile Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys
820 825 830

Val Ser Ile Arg Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile
835 840 845

Pro Phe Ser Glu Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile
850 855 860

Glu Asp Tyr Glu Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys
865 870 875 880

Asp Leu Ser Gly Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu
885 890 895

Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu
900 905 910

Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val
915 920 925

Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser
930 935 940

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

Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn
965 970 975

Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys
980 985 990

Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile
995 1000 1005

Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr Lys Ser Val Phe
1010 1015 1020

Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr Ile Asn Arg
1025 1030 1035

Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala Lys Ile
1040 1045 1050

Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp Ile
1055 1060 1065

Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp Gly
1070 1075 1080

Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile
1085 1090 1095

Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys

1100 1105 1110

Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
1115 1120 1125

Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys
1130 1135 1140

Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
1145 1150 1155

Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr
1160 1165 1170

Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser
1175 1180 1185

Asn Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr
1190 1195 1200

Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr
1205 1210 1215

Thr Tyr Lys Tyr Phe Lys Lys Glu Glu Met Lys Leu Phe Leu Ala
1220 1225 1230

Pro Ile Tyr Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys
1235 1240 1245

Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys
1250 1255 1260

Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His
1265 1270 1275

Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr
1280 1285 1290

Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro
1295 1300 1305

Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp
1310 1315 1320

Glu Gly Trp Thr Glu His His His His His His His His His
1325 1330 1335

<210> 10
<211> 3762
<212> DNA
<213> Artificial Sequence

<220>
<223> BoNT/E with a C1 Activation Loop

<400> 10
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atcaaaccgg gtggttgcca ggagttctac aaatctttca acatcatgaa aaacatctgg 120

atcatcccgg aacgtaacgt tatcggtacc accccgcagg acttccaccc gccgacctct 180

ctgaaaaacg gtgactcttc ttactacgac ccgaactacc tccagtctga cgaagaaaaa 240

gaccgtttcc tgaaaatcgt taccaaaatc ttcaaccgta tcaacaacaa cctgtctggt 300

ggtatcctgc tggaagaact gtctaaagct aacccgtacc tgggtaacga caacaccccg 360

gacaaccagt tccacatcgg tgacgcttct gctgttgaaa tcaaattctc taacggttct 420

caggacatcc tgctgccgaa cgttatcatc atgggtgctg aaccggacct gttcgaaacc 480

aactcttcta acatctctct gcgtaacaac tacatgccgt ctaaccacgg tttcggttct 540

atcgctatcg ttaccttctc tccggaatac tctttccgtt tcaacgacaa cagcatgaac 600

gagttcatcc aggacccggc tctgaccctg atgcaccaac tgatctattc tctgcacggt 660

ctgtacggtg ctaaaggtat caccaccaaa tacaccatca cccagaaaca gaacccgctg 720

atcaccaaca tccgtggtac caacatcgaa gagttcctga ccttcggtgg taccgacctg 780

aacatcatca cctctgctca gtctaacgac atctacacca acctgctggc tgactacaaa 840

aaaatcgctt ctaaactgtc taaagttcag gtttctaacc cgctgctgaa cccgtacaaa 900

gacgttttcg aagctaaata cggtctggac aaagacgctt ctggtatcta ctctgttaac 960

atcaacaaat tcaacgacat cttcaaaaaa ctgtactctt tcaccgagtt cgacctggcg 1020

accaaattcc aggttaaatg ccgtcagacc tacatcggtc agtacaaata cttcaaactg 1080

tctaacctgc tgaacgactc tatctacaac atctctgaag gttacaacat caacaacctg 1140

aaagttaact tccgtggtca gaacgctaac ctgaacccgc gtatcatcac cccgatcacc 1200

ggtcgtggtc tggttaaaaa aatcatccgt ttctgccaca aagcgattga tggccgctct 1260

ctctataaca aaacgctgga ttgcatcgaa atcaacaacg gtgaactgtt cttcgttgct 1320

tctgaaaact cttacaacga cgacaacatc aacaccccga aagaaatcga cgacaccgtt 1380

acctctaaca acaactacga aaacgacctg gaccaggtta tcctgaactt caactctgaa 1440

tctgctccgg gtctgtctga cgaaaaactg aacctgacca tccagaacga cgcttacatc 1500

ccgaaatacg actctaacgg tacctctgac atcgaacagc acgacgttaa cgaactgaac 1560

gttttcttct acctggacgc tcagaaagtt ccggaaggtg aaaacaacgt taacctgacc 1620

tcttctatcg acaccgctct gctggaacag ccgaaaatct acaccttctt ctcttctgag 1680

ttcatcaaca acgttaacaa accggttcag gctgctctgt tcgtttcttg gattcagcag 1740

gttctggttg acttcaccac cgaagctaac cagaaatcta ccgttgacaa aatcgctgac 1800

atctctatcg ttgttccgta catcggtctg gctctgaaca tcggtaacga agctcagaaa 1860

ggtaacttca aagacgctct ggaactgctg ggtgctggta tcctgctgga gttcgaaccg 1920

gaactgctga tcccgaccat cctggttttc accatcaaat ctttcctggg ttcttctgac 1980

aacaaaaaca aagttatcaa agctatcaac aacgctctga aagaacgtga cgaaaaatgg 2040

aaagaagttt actctttcat cgtttctaac tggatgacca aaatcaacac ccagttcaac 2100

aaacgtaaag aacagatgta ccaggctctc cagaaccagg ttaacgctat caaaaccatc 2160

atcgaatcta aatacaactc ttacaccctg gaagaaaaaa acgaactgac caacaaatac 2220

gacatcaaac agatcgaaaa cgaactgaac cagaaagttt ctatcgctat gaacaacatc 2280

gaccgtttcc tgaccgaatc ttctatctct tacctgatga aactcatcaa cgaagttaaa 2340

atcaacaaac tgcgtgaata cgacgaaaac gttaaaacct acctgctgaa ctacatcatc 2400

cagcacggtt ctatcctggg tgaatctcag caggaactga actctatggt taccgacacc 2460

ctgaacaact ctatcccgtt caaactgtct tcttacaccg acgacaaaat cctgatctct 2520

tacttcaaca aattctttaa acgcattaag agttcatcgg ttctgaatat gcggtacaaa 2580

aatgataaat atgtcgatac ttctggatat gatagcaata tcaacattaa cggcgacgtg 2640

tataaatatc cgacaaataa aaaccagttt gggatatata acgacaagct gtcggaggtc 2700

aatatttctc aaaacgacta tatcatttac gataataaat ataaaaactt tagcattagt 2760

ttttgggttc gtatacctaa ttatgacaat aaaattgtaa atgtgaataa cgagtatacc 2820

attataaact gtatgcgcga caataacagt ggttggaagg tatcgctgaa ccataatgag 2880

attatctgga ccctgcagga taatgcaggt ataaaccaga aactggcttt taactatgga 2940

aacgcaaatg ggatctcaga ttacattaat aaatggattt ttgttaccat tacgaacgat 3000

cgcttaggcg actcaaaact ttatattaat ggcaatctga tagatcagaa atcaatctta 3060

aatttgggca atattcatgt ctctgataac atcttgttca agatcgttaa ttgcagttac 3120

actcgttata ttggcattcg ttactttaat atcttcgata aagaactgga cgagacggaa 3180

atccagactc tgtattcaaa cgagcccaat actaatatat tgaaagattt ttggggtaac 3240

tatcttttat atgataaaga atactatctc ctgaatgtat tgaagccaaa caatttcata 3300

gatagacgca aggatagcac attaagtatc aacaatatca gatctactat actgttagca 3360

aatcgcctct actccggtat taaagtgaag attcagcggg ttaataactc cagtaccaat 3420

gataatctgg tccgtaagaa cgatcaggta tacatcaatt tcgtcgcgag caaaactcat 3480

ctcttcccgc tttacgccga tacagctacg acaaacaagg aaaaaaccat aaaaatttcc 3540

agctccggaa acagattcaa tcaagtagtt gtaatgaact ctgtgggtaa taattgtacg 3600

atgaacttta agaataacaa tgggaacaat attggacttt tgggcttcaa agccgacaca 3660

gtggtggcgt ccacctggta ttacacgcac atgcgggacc atacgaattc gaacggttgc 3720

ttctggaact ttatctcgga agaacacggg tggcaagaaa aa 3762

<210> 11
<211> 1254
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/E with a C1 Activation Loop

<400> 11

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 Gln Leu Ile Tyr 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 His Lys Ala Ile
405 410 415

Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp Cys Ile Glu Ile Asn
420 425 430

Asn Gly Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp
435 440 445

Asn Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn
450 455 460

Asn Tyr Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu
465 470 475 480

Ser Ala Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn

485 490 495

Asp Ala Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu
500 505 510

Gln His Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln
515 520 525

Lys Val Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp
530 535 540

Thr Ala Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu
545 550 555 560

Phe Ile Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser
565 570 575

Trp Ile Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys
580 585 590

Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile
595 600 605

Gly Leu Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys
610 615 620

Asp Ala Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro
625 630 635 640

Glu Leu Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu
645 650 655

Gly Ser Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala
660 665 670

Leu Lys Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val
675 680 685

Ser Asn Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu
690 695 700

Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile
705 710 715 720

Ile Glu Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu
725 730 735

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

Val Ser Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser
755 760 765

Ile Ser Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu
770 775 780

Arg Glu Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile
785 790 795 800

Gln His Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met
805 810 815

Val Thr Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr
820 825 830

Thr Asp Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg
835 840 845

Ile Lys Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr
850 855 860

Val Asp Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val
865 870 875 880

Tyr Lys Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys
885 890 895

Leu Ser Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn
900 905 910

Lys Tyr Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr
915 920 925

Asp Asn Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys
930 935 940

Met Arg Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu
945 950 955 960

Ile Ile Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala
965 970 975

Phe Asn Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp
980 985 990

Ile Phe Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr
995 1000 1005

Ile Asn Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly
1010 1015 1020

Asn Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys
1025 1030 1035

Ser Tyr Thr Arg Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp
1040 1045 1050

Lys Glu Leu Asp Glu Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu
1055 1060 1065

Pro Asn Thr Asn Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu
1070 1075 1080

Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val Leu Lys Pro Asn Asn
1085 1090 1095

Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser Ile Asn Asn Ile
1100 1105 1110

Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser Gly Ile Lys
1115 1120 1125

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

Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser Lys
1145 1150 1155

Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
1160 1165 1170

Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln
1175 1180 1185

Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
1190 1195 1200

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
1220 1225 1230

His Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu
1235 1240 1245

His Gly Trp Gln Glu Lys
1250

<210> 12
<211> 3867
<212> DNA
<213> Artificial Sequence

<220>
<223> BoNT/A1C1 with a C1 Activation Loop

<400> 12
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tacatcaaga ttccgaacgc cggtcaaatg cagccggtta aggcttttaa gatccacaac 120

aagatttggg ttatcccgga gcgtgacacc ttcacgaacc cggaagaagg cgatctgaac 180

ccgccaccgg aagcgaagca agtccctgtc agctactacg attcgacgta cctgagcacg 240

gataacgaaa aagataacta cctgaaaggt gtgaccaagc tgttcgaacg tatctacagc 300

acggatctgg gtcgcatgct gctgactagc attgttcgcg gtatcccgtt ctggggtggt 360

agcacgattg acaccgaact gaaggttatc gacactaact gcattaacgt tattcaaccg 420

gatggtagct atcgtagcga agagctgaat ctggtcatca ttggcccgag cgcagacatt 480

atccaattcg agtgcaagag ctttggtcac gaggttctga atctgacccg caatggctat 540

ggtagcaccc agtacattcg tttttcgccg gattttacct tcggctttga agagagcctg 600

gaggttgata ccaatccgtt gctgggtgcg ggcaaattcg ctaccgatcc ggctgtcacg 660

ctggcccatg aactgatcca cgcaggccac cgcctgtacg gcattgccat caacccaaac 720

cgtgtgttca aggttaatac gaatgcatac tacgagatga gcggcctgga agtcagcttc 780

gaagaactgc gcaccttcgg tggccatgac gctaaattca ttgacagctt gcaagagaat 840

gagttccgtc tgtactacta taacaaattc aaagacattg caagcacgtt gaacaaggcc 900

aaaagcatcg ttggtactac cgcgtcgttg cagtatatga agaatgtgtt taaagagaag 960

tacctgctgt ccgaggatac ctccggcaag tttagcgttg ataagctgaa gtttgacaaa 1020

ctgtacaaga tgctgaccga gatttacacc gaggacaact ttgtgaaatt cttcaaagtg 1080

ttgaatcgta aaacctatct gaattttgac aaagcggttt tcaagattaa catcgtgccg 1140

aaggtgaact acaccatcta tgacggtttt aacctgcgta acaccaacct ggcggcgaac 1200

tttaacggtc agaatacgga aatcaacaac atgaatttca cgaagttgaa gaacttcacg 1260

ggtctgttcg agttctataa gctgctgtgc cacaaagcga ttgatggccg ctctctctat 1320

aacaaaacgc tggattgcat taaggtaaac aattgggatc tgttcttttc gccatccgaa 1380

gataatttta ccaacgacct gaacaagggt gaagaaatca ccagcgatac gaatattgaa 1440

gcagcggaag agaatatcag cctggatctg atccagcagt actatctgac ctttaacttc 1500

gacaatgaac cggagaacat tagcattgag aatctgagca gcgacattat cggtcagctg 1560

gaactgatgc cgaatatcga acgtttcccg aacggcaaaa agtacgagct ggacaagtac 1620

actatgttcc attacctgcg tgcacaggag tttgaacacg gtaaaagccg tatcgcgctg 1680

accaacagcg ttaacgaggc cctgctgaac ccgagccgtg tctatacctt cttcagcagc 1740

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gatattacca tcattatccc gtatattggt ccggcactga acattggcaa catgctgtac 1920

aaagacgatt ttgtgggtgc cctgatcttc tccggtgccg tgattctgct ggagttcatt 1980

ccggagattg cgatcccggt gttgggtacc ttcgcgctgg tgtcctacat cgcgaataag 2040

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gtttacaaat acattgttac gaattggctg gcgaaagtca atacccagat cgacctgatc 2160

cgtaagaaaa tgaaagaggc gctggagaat caggcggagg ccaccaaagc aattatcaac 2220

taccaataca accagtacac ggaagaagag aagaataaca ttaacttcaa tatcgatgat 2280

ttgagcagca agctgaatga atctatcaac aaagcgatga tcaatatcaa caagtttttg 2340

aatcagtgta gcgtttcgta cctgatgaat agcatgattc cgtatggcgt caaacgtctg 2400

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acgctgattg gccaagttga ccgcttgaaa gacaaagtta acaataccct gagcaccgac 2520

atcccatttc aactgagcaa gtatgttgat aatcaacgtc tgttgagcac tttcaccgag 2580

tatatcaaaa acattaatga cagcaaaatt ctgagcctgc agaatcgtaa gaatacgctg 2640

gtagatacca gtggatataa tgcggaagtc tcagaagagg gtgatgtaca gctgaacccg 2700

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aatgaggatt cggaacagag cattaacttc tcctacgaca tcagcaacaa tgcaccaggg 3000

tataacaaat ggttcttcgt aacggtgacg aacaatatga tgggcaatat gaaaatctac 3060

attaacggga aacttatcga caccattaaa gtgaaagagc ttactgggat caattttagt 3120

aaaaccatta cctttgagat caacaaaatt ccggacacgg gtctgattac ctccgattcg 3180

gataatatca atatgtggat tcgcgacttt tatatcttcg ccaaagaact tgatggcaaa 3240

gatatcaaca ttttgtttaa ttccctgcag tataccaatg tcgttaagga ctattggggc 3300

aatgatctcc gctacaataa agaatactac atggttaaca tcgactatct caatcgctac 3360

atgtatgcta actcgcgtca aattgtgttt aacacacgtc gtaacaacaa cgattttaac 3420

gaaggttata aaatcattat caaacggatc cgcggcaata cgaacgatac tcgtgttcgt 3480

ggcggtgaca ttctgtattt cgacatgacg attaataata aagcgtacaa tctgttcatg 3540

aagaacgaaa ccatgtacgc cgataaccat tccactgaag atatctacgc aatcggactt 3600

cgcgaacaga ccaaagacat taacgacaac atcatctttc agattcaacc gatgaataat 3660

acctactact atgcctccca gatcttcaaa agtaatttca acggcgaaaa catttcaggc 3720

atttgctcaa tcggcactta tcggttccgg ttaggtggtg attggtatcg tcacaactac 3780

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tggggttttg tgccagtcag tgaataa 3867

<210> 13
<211> 1288
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/A1C1 with a C1 Activation Loop

<400> 13

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 His Lys
420 425 430

Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp Cys Ile Lys
435 440 445

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
450 455 460

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

Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu
485 490 495

Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu
500 505 510

Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
515 520 525

Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His
530 535 540

Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu
545 550 555 560

Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr
565 570 575

Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala
580 585 590

Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp
595 600 605

Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr Ile
610 615 620

Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met Leu Tyr
625 630 635 640

Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu
645 650 655

Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala
660 665 670

Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr Ile Asp
675 680 685

Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr Lys Tyr
690 695 700

Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp Leu Ile
705 710 715 720

Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys
725 730 735

Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn
740 745 750

Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser
755 760 765

Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser
770 775 780

Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu
785 790 795 800

Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr

805 810 815

Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys
820 825 830

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr
835 840 845

Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
850 855 860

Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu
865 870 875 880

Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val
885 890 895

Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly
900 905 910

Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr
915 920 925

Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn
930 935 940

Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys
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Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe
965 970 975

Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr
980 985 990

Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr
995 1000 1005

Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly
1010 1015 1020

Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn
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Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr
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Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg
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Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn
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Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn
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Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr
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Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn
1160 1165 1170

Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
1175 1180 1185

Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln
1190 1195 1200

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Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe
1220 1225 1230

Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg
1235 1240 1245

Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro
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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 Pro 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 Gly Thr Leu Asn Asn 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
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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

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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

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Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly
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Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val
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Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe
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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

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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

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820 825 830

Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile
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Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr
850 855 860

Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys
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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
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Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe
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1160 1165 1170

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Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
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Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr
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<400> 17

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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 Pro 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

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
1010 1015 1020

Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr
1025 1030 1035

Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile
1040 1045 1050

Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met
1055 1060 1065

Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys
1070 1075 1080

Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val Val
1085 1090 1095

Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
1100 1105 1110

Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser
1115 1120 1125

Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
1130 1135 1140

Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn
1145 1150 1155

Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr
1160 1165 1170

Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met
1175 1180 1185

Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu
1190 1195 1200

Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile
1205 1210 1215

Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
1220 1225 1230

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
1250 1255 1260

Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu
1265 1270 1275

Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
1280 1285 1290

<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Enterokinase and Factor Xa Cleavage Site

<400> 18

Ile Asp Gly Arg
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<210> 19
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Enterokinase and Factor Xa Cleavage Site Variant

<400> 19

Ile Glu Gly Arg
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<210> 20
<211> 45
<212> PRT
<213> Clostridium botulinum

<400> 20

Cys Pro Arg Asn Gly Leu Leu Tyr Asn Ala Ile Tyr Arg Asn Ser Lys
1 5 10 15

Asn Tyr Leu Asn Asn Ile Asp Leu Glu Asp Lys Lys Thr Thr Ser Lys
20 25 30

Thr Asn Val Ser Tyr Pro Cys Ser Leu Leu Asn Gly Cys
35 40 45

<210> 21
<211> 25
<212> PRT
<213> Clostridium botulinum

<400> 21

Cys Val Arg Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly
1 5 10 15

Tyr Asn Lys Ala Leu Asn Asp Leu Cys
20 25

<210> 22
<211> 10
<212> PRT
<213> Clostridium botulinum

<400> 22

Cys Lys Ser Val Arg Ala Pro Gly Ile Cys
1 5 10

<210> 23
<211> 14
<212> PRT
<213> Clostridium botulinum

<400> 23

Cys Leu Arg Leu Thr Lys Asn Ser Arg Asp Asp Ser Thr Cys
1 5 10

<210> 24
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 24

Cys Lys Asn Ile Val Ser Val Lys Gly Ile Arg Lys Ser Ile Cys
1 5 10 15

<210> 25
<211> 17
<212> PRT
<213> Clostridium botulinum

<400> 25

Cys Lys Ser Val Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu
1 5 10 15

Cys

<210> 26
<211> 17
<212> PRT
<213> Clostridium botulinum

<400> 26

Cys Lys Ser Ile Ile Pro Arg Lys Gly Thr Lys Gln Ser Pro Ser Leu
1 5 10 15

Cys

<210> 27
<211> 17
<212> PRT
<213> Clostridium botulinum

<400> 27

Cys Lys Ser Ile Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu

1 5 10 15

Cys

<210> 28
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 28

Cys Leu Asn Ser Ser Phe Lys Lys Asn Thr Lys Lys Pro Leu Cys
1 5 10 15

<210> 29
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 29

Cys Lys Ser Ile Val Ser Lys Lys Gly Thr Lys Asn Ser Leu Cys
1 5 10 15

<210> 30
<211> 29
<212> PRT
<213> Clostridium tetani

<400> 30

Cys Lys Lys Ile Ile Pro Pro Thr Asn Ile Arg Glu Asn Leu Tyr Asn
1 5 10 15

Arg Thr Ala Ser Leu Thr Asp Leu Gly Gly Glu Leu Cys
20 25

<210> 31
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 31

Cys Lys Pro Val Met Tyr Lys Asn Thr Gly Lys Ser Glu Gln Cys
1 5 10 15

<210> 32
<211> 3972
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-Type BoNT/X-10HT

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accatgcgtc cgcctcgtca tagcgataaa atcaataaag gtaaaggtcc gttcaaagcc 120

tttcaggtga ttaaaaacat ttggattgtg ccggaacgct acaactttac caataatacc 180

aacgatctga acattccgag cgaaccgatt atggaagcag atgccattta taacccgaac 240

tatctgaata ccccgagcga aaaagatgaa tttctgcagg gtgttatcaa agtgctggaa 300

cgcattaaaa gcaaaccgga aggtgaaaaa ctgctggaac tgattagcag cagcattccg 360

ctgccgctgg ttagcaatgg tgcactgacc ctgagcgata atgaaaccat tgcatatcaa 420

gagaacaaca acattgtgag caatctgcag gcaaacctgg ttatttatgg tccgggtcct 480

gatattgcaa ataatgcaac ctatggtctg tatagcaccc cgattagtaa tggtgaaggt 540

acactgagcg aagttagctt tagcccgttt tatctgaaac cgtttgatga aagctatggc 600

aattatcgta gcctggtgaa tatcgtgaac aaattcgtga aacgtgaatt tgcacctgat 660

ccggcaagca ccctgatgca tgaactggtt catgttaccc ataatctgta tggtattagc 720

aaccgcaact tctactataa ctttgacacc ggcaaaattg aaaccagccg tcagcagaat 780

agcctgattt ttgaagaact gctgaccttt ggtggcattg atagcaaagc aattagcagc 840

ctgatcatca agaaaattat cgaaaccgcc aagaacaact ataccacgct gattagcgaa 900

cgcctgaata ccgttaccgt tgaaaatgat ctgctgaaat atatcaaaaa caaaatcccg 960

gttcagggtc gtctgggtaa ctttaaactg gataccgcag aattcgagaa aaagctgaat 1020

accattctgt ttgtgctgaa cgaaagcaat ctggcacagc gttttagcat tctggttcgt 1080

aaacattacc tgaaagaacg tccgattgat ccgatttatg tgaacattct ggatgacaat 1140

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cagctgctgg aaagcagcta ttttgaaaaa attgaaagca atgccctgcg tgccttcatt 1260

aaaatctgtc cgcgtaatgg tctgctgtat aatgccattt atcgcaacag caaaaactac 1320

ctgaacaaca ttgatctgga agataaaaag accacgagca aaaccaatgt tagctatccg 1380

tgtagcctgc tgaatggttg tattgaagtt gaaaacaaag acctgttcct gattagcaac 1440

aaagatagcc tgaacgatat taacctgagc gaagaaaaaa tcaaaccgga aaccaccgtg 1500

ttcttcaaag ataaactgcc tccgcaggat attacgctga gcaattatga ttttaccgaa 1560

gccaatagca ttccgagcat tagccagcag aacattctgg aacgtaatga agaactgtat 1620

gaaccgattc gcaatagcct gtttgaaatc aaaaccatct atgtggataa gctgaccacc 1680

tttcattttc tggaagccca gaatattgat gagagcattg atagcagcaa aattcgtgtt 1740

gaactgaccg atagcgttga tgaagcactg agcaatccga ataaagttta tagcccgttc 1800

aagaacatga gcaacaccat taatagcatt gaaaccggta ttaccagcac ctacatcttt 1860

tatcagtggc tgcgtagcat cgtgaaagat tttagtgatg aaaccggcaa aatcgacgtg 1920

attgataaaa gcagcgatac cctggcaatt gttccgtata ttggtccgct gctgaatatt 1980

ggtaatgata ttcgtcatgg cgattttgtg ggtgcaattg aactggcagg cattaccgca 2040

ctgctggaat atgttccgga atttaccatt ccgattctgg ttggtctgga agttattggt 2100

ggcgaactgg cacgtgaaca ggttgaagca attgttaata atgccctgga taaacgcgat 2160

cagaaatggg cagaagttta caatattacc aaagcacagt ggtggggcac cattcattta 2220

cagattaata cccgtctggc ccatacctat aaagccctga gccgtcaggc aaatgccatt 2280

aaaatgaata tggaatttca gctggccaac tacaaaggca acatcgatga taaagccaaa 2340

atcaaaaacg ccatcagcga aaccgaaatc ctgctgaaca aaagcgttga acaggcaatg 2400

aaaaacaccg agaaattcat gatcaaactg agcaacagct atctgaccaa agaaatgatt 2460

ccgaaagtgc aggataacct gaaaaatttc gatctggaaa ccaagaaaac cctggacaaa 2520

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tttgatgatc tgatcaacca gtacaaaaac gagatcgaag attatgaagt gctgaatctg 2700

ggtgcagaag atgggaaaat caaagatctg agcggtacaa ccagcgatat caatattggt 2760

tcagatatcg aactggccga tggtcgtgaa aataaagcca ttaagattaa aggcagcgag 2820

aacagcacca tcaaaattgc aatgaacaaa tatctgcgtt ttagcgcgac cgataacttt 2880

agcattagct tttggatcaa acatccgaaa ccgaccaatc tgcttaataa cggtattgaa 2940

tataccctgg tcgagaactt taatcagcgt ggttggaaaa ttagcatcca ggatagcaaa 3000

ctgatttggt atctgcgcga tcacaataac agcatcaaaa tcgttacacc ggattatatt 3060

gcgtttaatg gctggaacct gattaccatt acaaacaatc gtagcaaagg cagcattgtg 3120

tatgtgaacg gtagcaaaat tgaagagaag gatattagca gcatctggaa taccgaagtg 3180

gatgatccga ttatctttcg cctgaaaaac aatcgcgata cccaggcgtt taccctgctg 3240

gatcagttta gcatttatcg gaaagaactg aaccagaacg aagtggtgaa actgtataac 3300

tactacttca acagcaacta cattcgcgat atttggggta atccgctgca gtacaacaaa 3360

aaatactatc tgcagaccca ggacaaacct ggtaaaggtc tgatccgcga atattggagc 3420

agctttggtt atgattatgt gattctgagc gatagcaaga cgattacctt tccgaataat 3480

atccgttatg gtgccctgta taacggcagc aaagttctga tcaaaaatag caaaaaactg 3540

gatggtctgg tgcgcaataa agatttcatt cagctggaaa tcgatggcta taatatgggt 3600

attagcgcag atcgctttaa cgaggatacc aactatattg gcaccaccta tggtacaacc 3660

catgatctga ccaccgattt tgaaattatt cagcgccaag agaaataccg caattattgt 3720

cagctgaaaa ccccgtataa catctttcat aaaagcggtc tgatgagcac cgaaaccagc 3780

aaaccgacct ttcatgatta tcgtgactgg gtttatagca gcgcatggta ttttcagaac 3840

tatgaaaatc tgaacctgcg caaacatacc aaaaccaact ggtattttat cccgaaagat 3900

gaaggttggg atgaagatct tgaagttctg tttcagggtc cgcatcatca ccaccatcac 3960

catcatcatc ac 3972

<210> 33
<211> 1306
<212> PRT
<213> Clostridium botulinum

<400> 33

Met Lys Leu Glu Ile Asn Lys Phe Asn Tyr Asn Asp Pro Ile Asp Gly
1 5 10 15

Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
20 25 30

Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser
225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu

275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys Pro Arg Asn Gly Leu Leu Tyr Asn Ala
420 425 430

Ile Tyr Arg Asn Ser Lys Asn Tyr Leu Asn Asn Ile Asp Leu Glu Asp
435 440 445

Lys Lys Thr Thr Ser Lys Thr Asn Val Ser Tyr Pro Cys Ser Leu Leu
450 455 460

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

Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu Lys Ile Lys Pro
485 490 495

Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro Gln Asp Ile Thr
500 505 510

Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile Pro Ser Ile Ser
515 520 525

Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr Glu Pro Ile Arg
530 535 540

Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp Lys Leu Thr Thr
545 550 555 560

Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser Ile Asp Ser Ser
565 570 575

Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu Ala Leu Ser Asn
580 585 590

Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser Asn Thr Ile Asn
595 600 605

Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe Tyr Gln Trp Leu
610 615 620

Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly Lys Ile Asp Val
625 630 635 640

Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro Tyr Ile Gly Pro
645 650 655

Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp Phe Val Gly Ala
660 665 670

Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr Val Pro Glu Phe
675 680 685

Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly Gly Glu Leu Ala
690 695 700

Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu Asp Lys Arg Asp
705 710 715 720

Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala Gln Trp Trp Gly
725 730 735

Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His Thr Tyr Lys Ala
740 745 750

Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met Glu Phe Gln Leu
755 760 765

Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys Ile Lys Asn Ala
770 775 780

Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val Glu Gln Ala Met
785 790 795 800

Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn Ser Tyr Leu Thr
805 810 815

Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys Asn Phe Asp Leu
820 825 830

Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu Lys Glu Asp Ile
835 840 845

Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys Val Ser Ile Arg
850 855 860

Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile Pro Phe Ser Glu
865 870 875 880

Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile Glu Asp Tyr Glu
885 890 895

Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys Asp Leu Ser Gly
900 905 910

Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu Leu Ala Asp Gly
915 920 925

Arg Glu Asn Lys Ala Ile Lys Ile Lys Gly Ser Glu Asn Ser Thr Ile
930 935 940

Lys Ile Ala Met Asn Lys Tyr Leu Arg Phe Ser Ala Thr Asp Asn Phe
945 950 955 960

Ser Ile Ser Phe Trp Ile Lys His Pro Lys Pro Thr Asn Leu Leu Asn
965 970 975

Asn Gly Ile Glu Tyr Thr Leu Val Glu Asn Phe Asn Gln Arg Gly Trp
980 985 990

Lys Ile Ser Ile Gln Asp Ser Lys Leu Ile Trp Tyr Leu Arg Asp His
995 1000 1005

Asn Asn Ser Ile Lys Ile Val Thr Pro Asp Tyr Ile Ala Phe Asn
1010 1015 1020

Gly Trp Asn Leu Ile Thr Ile Thr Asn Asn Arg Ser Lys Gly Ser
1025 1030 1035

Ile Val Tyr Val Asn Gly Ser Lys Ile Glu Glu Lys Asp Ile Ser
1040 1045 1050

Ser Ile Trp Asn Thr Glu Val Asp Asp Pro Ile Ile Phe Arg Leu
1055 1060 1065

Lys Asn Asn Arg Asp Thr Gln Ala Phe Thr Leu Leu Asp Gln Phe
1070 1075 1080

Ser Ile Tyr Arg Lys Glu Leu Asn Gln Asn Glu Val Val Lys Leu
1085 1090 1095

Tyr Asn Tyr Tyr Phe Asn Ser Asn Tyr Ile Arg Asp Ile Trp Gly
1100 1105 1110

Asn Pro Leu Gln Tyr Asn Lys Lys Tyr Tyr Leu Gln Thr Gln Asp
1115 1120 1125

Lys Pro Gly Lys Gly Leu Ile Arg Glu Tyr Trp Ser Ser Phe Gly
1130 1135 1140

Tyr Asp Tyr Val Ile Leu Ser Asp Ser Lys Thr Ile Thr Phe Pro

1145 1150 1155

Asn Asn Ile Arg Tyr Gly Ala Leu Tyr Asn Gly Ser Lys Val Leu
1160 1165 1170

Ile Lys Asn Ser Lys Lys Leu Asp Gly Leu Val Arg Asn Lys Asp
1175 1180 1185

Phe Ile Gln Leu Glu Ile Asp Gly Tyr Asn Met Gly Ile Ser Ala
1190 1195 1200

Asp Arg Phe Asn Glu Asp Thr Asn Tyr Ile Gly Thr Thr Tyr Gly
1205 1210 1215

Thr Thr His Asp Leu Thr Thr Asp Phe Glu Ile Ile Gln Arg Gln
1220 1225 1230

Glu Lys Tyr Arg Asn Tyr Cys Gln Leu Lys Thr Pro Tyr Asn Ile
1235 1240 1245

Phe His Lys Ser Gly Leu Met Ser Thr Glu Thr Ser Lys Pro Thr
1250 1255 1260

Phe His Asp Tyr Arg Asp Trp Val Tyr Ser Ser Ala Trp Tyr Phe
1265 1270 1275

Gln Asn Tyr Glu Asn Leu Asn Leu Arg Lys His Thr Lys Thr Asn
1280 1285 1290

Trp Tyr Phe Ile Pro Lys Asp Glu Gly Trp Asp Glu Asp
1295 1300 1305

<210> 34
<211> 1324
<212> PRT
<213> Artificial Sequence

<220>
<223> Wild-Type BoNT/X-10HT

<400> 34

Met Lys Leu Glu Ile Asn Lys Phe Asn Tyr Asn Asp Pro Ile Asp Gly
1 5 10 15

Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
20 25 30

Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser

225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys Pro Arg Asn Gly Leu Leu Tyr Asn Ala
420 425 430

Ile Tyr Arg Asn Ser Lys Asn Tyr Leu Asn Asn Ile Asp Leu Glu Asp
435 440 445

Lys Lys Thr Thr Ser Lys Thr Asn Val Ser Tyr Pro Cys Ser Leu Leu
450 455 460

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

Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu Lys Ile Lys Pro
485 490 495

Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro Gln Asp Ile Thr
500 505 510

Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile Pro Ser Ile Ser
515 520 525

Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr Glu Pro Ile Arg
530 535 540

Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp Lys Leu Thr Thr
545 550 555 560

Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser Ile Asp Ser Ser
565 570 575

Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu Ala Leu Ser Asn
580 585 590

Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser Asn Thr Ile Asn
595 600 605

Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe Tyr Gln Trp Leu
610 615 620

Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly Lys Ile Asp Val
625 630 635 640

Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro Tyr Ile Gly Pro
645 650 655

Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp Phe Val Gly Ala
660 665 670

Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr Val Pro Glu Phe
675 680 685

Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly Gly Glu Leu Ala
690 695 700

Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu Asp Lys Arg Asp
705 710 715 720

Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala Gln Trp Trp Gly
725 730 735

Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His Thr Tyr Lys Ala
740 745 750

Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met Glu Phe Gln Leu
755 760 765

Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys Ile Lys Asn Ala
770 775 780

Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val Glu Gln Ala Met
785 790 795 800

Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn Ser Tyr Leu Thr
805 810 815

Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys Asn Phe Asp Leu
820 825 830

Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu Lys Glu Asp Ile
835 840 845

Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys Val Ser Ile Arg
850 855 860

Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile Pro Phe Ser Glu
865 870 875 880

Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile Glu Asp Tyr Glu
885 890 895

Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys Asp Leu Ser Gly
900 905 910

Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu Leu Ala Asp Gly
915 920 925

Arg Glu Asn Lys Ala Ile Lys Ile Lys Gly Ser Glu Asn Ser Thr Ile
930 935 940

Lys Ile Ala Met Asn Lys Tyr Leu Arg Phe Ser Ala Thr Asp Asn Phe
945 950 955 960

Ser Ile Ser Phe Trp Ile Lys His Pro Lys Pro Thr Asn Leu Leu Asn
965 970 975

Asn Gly Ile Glu Tyr Thr Leu Val Glu Asn Phe Asn Gln Arg Gly Trp
980 985 990

Lys Ile Ser Ile Gln Asp Ser Lys Leu Ile Trp Tyr Leu Arg Asp His
995 1000 1005

Asn Asn Ser Ile Lys Ile Val Thr Pro Asp Tyr Ile Ala Phe Asn
1010 1015 1020

Gly Trp Asn Leu Ile Thr Ile Thr Asn Asn Arg Ser Lys Gly Ser
1025 1030 1035

Ile Val Tyr Val Asn Gly Ser Lys Ile Glu Glu Lys Asp Ile Ser
1040 1045 1050

Ser Ile Trp Asn Thr Glu Val Asp Asp Pro Ile Ile Phe Arg Leu
1055 1060 1065

Lys Asn Asn Arg Asp Thr Gln Ala Phe Thr Leu Leu Asp Gln Phe
1070 1075 1080

Ser Ile Tyr Arg Lys Glu Leu Asn Gln Asn Glu Val Val Lys Leu
1085 1090 1095

Tyr Asn Tyr Tyr Phe Asn Ser Asn Tyr Ile Arg Asp Ile Trp Gly

1100 1105 1110

Asn Pro Leu Gln Tyr Asn Lys Lys Tyr Tyr Leu Gln Thr Gln Asp
1115 1120 1125

Lys Pro Gly Lys Gly Leu Ile Arg Glu Tyr Trp Ser Ser Phe Gly
1130 1135 1140

Tyr Asp Tyr Val Ile Leu Ser Asp Ser Lys Thr Ile Thr Phe Pro
1145 1150 1155

Asn Asn Ile Arg Tyr Gly Ala Leu Tyr Asn Gly Ser Lys Val Leu
1160 1165 1170

Ile Lys Asn Ser Lys Lys Leu Asp Gly Leu Val Arg Asn Lys Asp
1175 1180 1185

Phe Ile Gln Leu Glu Ile Asp Gly Tyr Asn Met Gly Ile Ser Ala
1190 1195 1200

Asp Arg Phe Asn Glu Asp Thr Asn Tyr Ile Gly Thr Thr Tyr Gly
1205 1210 1215

Thr Thr His Asp Leu Thr Thr Asp Phe Glu Ile Ile Gln Arg Gln
1220 1225 1230

Glu Lys Tyr Arg Asn Tyr Cys Gln Leu Lys Thr Pro Tyr Asn Ile
1235 1240 1245

Phe His Lys Ser Gly Leu Met Ser Thr Glu Thr Ser Lys Pro Thr
1250 1255 1260

Phe His Asp Tyr Arg Asp Trp Val Tyr Ser Ser Ala Trp Tyr Phe
1265 1270 1275

Gln Asn Tyr Glu Asn Leu Asn Leu Arg Lys His Thr Lys Thr Asn
1280 1285 1290

Trp Tyr Phe Ile Pro Lys Asp Glu Gly Trp Asp Glu Asp Leu Glu
1295 1300 1305

Val Leu Phe Gln Gly Pro His His His His His His His His His
1310 1315 1320

His

<210> 35
<211> 1296
<212> PRT
<213> Clostridium botulinum

<400> 35

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 Val 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

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
1010 1015 1020

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

Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
1040 1045 1050

Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp
1055 1060 1065

Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
1070 1075 1080

Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
1085 1090 1095

Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met
1100 1105 1110

Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
1115 1120 1125

Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val
1130 1135 1140

Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr
1145 1150 1155

Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
1160 1165 1170

Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1175 1180 1185

Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu
1190 1195 1200

Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser
1205 1210 1215

Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
1220 1225 1230

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
1250 1255 1260

Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
1265 1270 1275

Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
1280 1285 1290

Arg Pro Leu
1295

<210> 36
<211> 1291
<212> PRT
<213> Clostridium botulinum

<400> 36

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

Asn 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

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 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

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
865 870 875 880

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
1010 1015 1020

Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly
1025 1030 1035

Glu Ile Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe
1040 1045 1050

Ile Trp Met Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln
1055 1060 1065

Ser Asn Ile Glu Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr
1070 1075 1080

Leu Lys Asp Phe Trp Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr
1085 1090 1095

Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys
1100 1105 1110

Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser Lys Tyr Asn
1115 1120 1125

Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile Gly Glu
1130 1135 1140

Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp
1145 1150 1155

Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn
1160 1165 1170

Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys
1175 1180 1185

Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
1190 1195 1200

Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr
1205 1210 1215

Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
1220 1225 1230

Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile
1235 1240 1245

Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr
1250 1255 1260

Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys
1265 1270 1275

Asn Trp Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
1280 1285 1290

<210> 37
<211> 1291
<212> PRT
<213> Clostridium botulinum

<400> 37

Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn
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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 Pro 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

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
1010 1015 1020

Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr
1025 1030 1035

Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile
1040 1045 1050

Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met
1055 1060 1065

Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys
1070 1075 1080

Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val Val
1085 1090 1095

Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
1100 1105 1110

Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser
1115 1120 1125

Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
1130 1135 1140

Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn
1145 1150 1155

Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr
1160 1165 1170

Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met
1175 1180 1185

Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu

1190 1195 1200

Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile
1205 1210 1215

Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
1220 1225 1230

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
1250 1255 1260

Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu
1265 1270 1275

Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
1280 1285 1290

<210> 38
<211> 1276
<212> PRT
<213> Clostridium botulinum

<400> 38

Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp
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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

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

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
1010 1015 1020

Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp Glu Val Lys Leu Asp
1025 1030 1035

Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn Gln
1040 1045 1050

Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser
1055 1060 1065

Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn
1070 1075 1080

Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu
1085 1090 1095

Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
1100 1105 1110

Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser Lys
1115 1120 1125

Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
1130 1135 1140

Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His
1145 1150 1155

Met Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp
1160 1165 1170

Thr Ile Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val
1175 1180 1185

Tyr Ala Leu Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly
1190 1195 1200

Ile Phe Ser Ile Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser
1205 1210 1215

Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr Met Leu Leu Ala Asp
1220 1225 1230

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
1250 1255 1260

Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu
1265 1270 1275

<210> 39
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<212> PRT
<213> Clostridium botulinum

<400> 39

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 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

Arg Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190

Arg Phe Asn Asp Asn Cys 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 Arg 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

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 Ile 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 Phe Glu Asp Asn Arg 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
1010 1015 1020

His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr
1025 1030 1035

Thr Arg Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu
1040 1045 1050

Leu Asp Glu Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn
1055 1060 1065

Thr Asn Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp
1070 1075 1080

Lys Glu Tyr Tyr Leu Leu Asn Val Leu Lys Pro Asn Asn Phe Ile
1085 1090 1095

Asp Arg Arg Lys Asp Ser Thr Leu Ser Ile Asn Asn Ile Arg Ser
1100 1105 1110

Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser Gly Ile Lys Val Lys
1115 1120 1125

Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp Asn Leu Val Arg
1130 1135 1140

Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser Lys Thr His
1145 1150 1155

Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys Glu Lys
1160 1165 1170

Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val Val
1175 1180 1185

Val Met Asn Ser Val Gly Asn Cys Thr Met Asn Phe Lys Asn Asn
1190 1195 1200

Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
1205 1210 1215

Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn
1220 1225 1230

Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
1235 1240 1245

Gln Glu Lys
1250

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<211> 1278
<212> PRT
<213> Clostridium botulinum

<400> 40

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

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

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
1010 1015 1020

Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
1025 1030 1035

Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly
1040 1045 1050

Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
1055 1060 1065

Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp
1070 1075 1080

Glu Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu
1085 1090 1095

Leu Tyr Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp
1100 1105 1110

Lys Ser Ile Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln
1115 1120 1125

Arg Gly Val Tyr Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu
1130 1135 1140

Tyr Thr Gly Val Glu Val Ile Ile Arg Lys Asn Gly Ser Thr Asp
1145 1150 1155

Ile Ser Asn Thr Asp Asn Phe Val Arg Lys Asn Asp Leu Ala Tyr
1160 1165 1170

Ile Asn Val Val Asp Arg Asp Val Glu Tyr Arg Leu Tyr Ala Asp
1175 1180 1185

Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys Leu Ile Arg Thr
1190 1195 1200

Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val Met Asp Ser
1205 1210 1215

Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly Gly
1220 1225 1230

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
1250 1255 1260

Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
1265 1270 1275

<210> 41
<211> 1297
<212> PRT
<213> Clostridium botulinum

<220>
<221> SITE
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 41

Met Pro Val Asn Ile Lys Xaa Phe Asn Tyr Asn Asp Pro Ile Asn Asn
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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
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
995 1000 1005

Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn
1010 1015 1020

Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
1025 1030 1035

Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile
1040 1045 1050

Asn Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn
1055 1060 1065

Ile Phe Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr
1070 1075 1080

Trp Ile Gln Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn
1085 1090 1095

Pro Leu Arg Tyr Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met
1100 1105 1110

Gln Asn Ile Tyr Ile Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu
1115 1120 1125

Thr Ala Pro Arg Thr Asn Phe Asn Asn Ala Ala Ile Asn Tyr Gln
1130 1135 1140

Asn Leu Tyr Leu Gly Leu Arg Phe Ile Ile Lys Lys Ala Ser Asn
1145 1150 1155

Ser Arg Asn Ile Asn Asn Asp Asn Ile Val Arg Glu Gly Asp Tyr
1160 1165 1170

Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu Ser Tyr Arg Val
1175 1180 1185

Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln Leu Phe Leu
1190 1195 1200

Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu Gln Ile
1205 1210 1215

Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu Cys
1220 1225 1230

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
1250 1255 1260

Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
1265 1270 1275

Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu
1280 1285 1290

Gly Trp Thr Glu
1295

<210> 42
<211> 1315
<212> PRT
<213> Clostridium tetani

<400> 42

Met Pro Ile Thr Ile Asn Asn Phe Arg Tyr Ser Asp Pro Val Asn Asn
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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
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
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
1010 1015 1020

Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
1025 1030 1035

Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met
1040 1045 1050

Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn
1055 1060 1065

Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr
1070 1075 1080

Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro
1085 1090 1095

Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe
1100 1105 1110

Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr
1115 1120 1125

Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys
1130 1135 1140

Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr
1145 1150 1155

Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu
1160 1165 1170

Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser
1175 1180 1185

Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn
1190 1195 1200

Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe
1205 1210 1215

Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly
1220 1225 1230

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
1250 1255 1260

Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp
1265 1270 1275

Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His
1280 1285 1290

Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr
1295 1300 1305

Asp Glu Gly Trp Thr Asn Asp
1310 1315

<210> 43

<211> 2634
<212> DNA
<213> Artificial Sequence

<220>
<223> LHN/A1 with an EK Cleavage Site

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tacatcaaaa tcccgaacgc tggccagatg cagccggtaa aggcattcaa aatccacaac 120

aaaatctggg ttatcccgga acgtgatacc tttactaacc cggaagaagg tgacctgaac 180

ccgccaccgg aagcgaaaca ggtgccggta tcttactatg actccaccta cctgtctacc 240

gataacgaaa aggacaacta cctgaaaggt gttactaaac tgttcgagcg tatttactcc 300

accgacctgg gccgtatgct gctgactagc atcgttcgcg gtatcccgtt ctggggcggt 360

tctaccatcg ataccgaact gaaagtaatc gacactaact gcatcaacgt tattcagccg 420

gacggttcct atcgttccga agaactgaac ctggtgatca tcggcccgtc tgctgatatc 480

atccagttcg agtgtaagag ctttggtcac gaagttctga acctcacccg taacggctac 540

ggttccactc agtacatccg tttctctccg gacttcacct tcggttttga agaatccctg 600

gaagtagaca cgaacccact gctgggcgct ggtaaattcg caactgatcc tgcggttacc 660

ctggctcacg aactgattca tgcaggccac cgcctgtacg gtatcgccat caatccgaac 720

cgtgtcttca aagttaacac caacgcgtat tacgagatgt ccggtctgga agttagcttc 780

gaagaactgc gtacttttgg cggtcacgac gctaaattca tcgactctct gcaagaaaac 840

gagttccgtc tgtactacta taacaagttc aaagatatcg catccaccct gaacaaagcg 900

aaatccatcg tgggtaccac tgcttctctc cagtacatga agaacgtttt taaagaaaaa 960

tacctgctca gcgaagacac ctccggcaaa ttctctgtag acaagttgaa attcgataaa 1020

ctttacaaaa tgctgactga aatttacacc gaagacaact tcgttaagtt ctttaaagtt 1080

ctgaaccgca aaacctatct gaacttcgac aaggcagtat tcaaaatcaa catcgtgccg 1140

aaagttaact acactatcta cgatggtttc aacctgcgta acaccaacct ggctgctaat 1200

tttaacggcc agaacacgga aatcaacaac atgaacttca caaaactgaa aaacttcact 1260

ggtctgttcg agttttacaa gctgctgtgc gtcgacggca tcattacctc caaaactaaa 1320

tctgacgatg acgataaaaa caaagcgctg aacctgcagt gtatcaaggt taacaactgg 1380

gatttattct tcagcccgag tgaagacaac ttcaccaacg acctgaacaa aggtgaagaa 1440

atcacctcag atactaacat cgaagcagcc gaagaaaaca tctcgctgga cctgatccag 1500

cagtactacc tgacctttaa tttcgacaac gagccggaaa acatttctat cgaaaacctg 1560

agctctgata tcatcggcca gctggaactg atgccgaaca tcgaacgttt cccaaacggt 1620

aaaaagtacg agctggacaa atataccatg ttccactacc tgcgcgcgca ggaatttgaa 1680

cacggcaaat cccgtatcgc actgactaac tccgttaacg aagctctgct caacccgtcc 1740

cgtgtataca ccttcttctc tagcgactac gtgaaaaagg tcaacaaagc gactgaagct 1800

gcaatgttct tgggttgggt tgaacagctt gtttatgatt ttaccgacga gacgtccgaa 1860

gtatctacta ccgacaaaat tgcggatatc actatcatca tcccgtacat cggtccggct 1920

ctgaacattg gcaacatgct gtacaaagac gacttcgttg gcgcactgat cttctccggt 1980

gcggtgatcc tgctggagtt catcccggaa atcgccatcc cggtactggg caccttgct 2040

ctggtttctt acattgcaaa caaggttctg actgtacaaa ccatcgacaa cgcgctgagc 2100

aaacgtaacg aaaaatggga tgaagtttac aaatatatcg tgaccaactg gctggctaag 2160

gttaatactc agatcgacct catccgcaaa aaaatgaaag aagcactgga aaaccaggcg 2220

gaagctacca aggcaatcat taactaccag tacaaccagt acaccgagga agaaaaaaac 2280

aacatcaact tcaacatcga cgatctgtcc tctaaactga acgaatccat caacaaagct 2340

atgatcaaca tcaacaagtt cctgaaccag tgctctgtaa gctatctgat gaactccatg 2400

atcccgtacg gtgttaaacg tctggaggac ttcgatgcgt ctctgaaaga cgccctgctg 2460

aaatacattt acgacaaccg tggcactctg atcggtcagg ttgatcgtct gaaggacaaa 2520

gtgaacaata ccttatcgac cgacatccct tttcagctca gtaaatatgt cgataaccaa 2580

cgccttttgt ccactctaga agcacaccat catcaccacc atcaccatca ccat 2634

<210> 44
<211> 878
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/A1 with an EK Cleavage Site

<400> 44

Met Glu 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 Asp
420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Asp Asp Asp Asp Lys Asn Lys
435 440 445

Ala Leu Asn Leu Gln 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

Thr Leu Glu Ala His His His His His His His His His His
865 870 875

<210> 45
<211> 3996
<212> DNA

<213> Clostridium botulinum

<400> 45
atgaaactgg aaatcaacaa attcaactac aacgatccga tcgatggcat taatgttatt 60

accatgcgtc cgcctcgtca tagcgataaa atcaataaag gtaaaggtcc gttcaaagcc 120

tttcaggtga ttaaaaacat ttggattgtg ccggaacgct acaactttac caataatacc 180

aacgatctga acattccgag cgaaccgatt atggaagcag atgccattta taacccgaac 240

tatctgaata ccccgagcga aaaagatgaa tttctgcagg gtgttatcaa agtgctggaa 300

cgcattaaaa gcaaaccgga aggtgaaaaa ctgctggaac tgattagcag cagcattccg 360

ctgccgctgg ttagcaatgg tgcactgacc ctgagcgata atgaaaccat tgcatatcaa 420

gagaacaaca acattgtgag caatctgcag gcaaacctgg ttatttatgg tccgggtcct 480

gatattgcaa ataatgcaac ctatggtctg tatagcaccc cgattagtaa tggtgaaggt 540

acactgagcg aagttagctt tagcccgttt tatctgaaac cgtttgatga aagctatggc 600

aattatcgta gcctggtgaa tatcgtgaac aaattcgtga aacgtgaatt tgcacctgat 660

ccggcaagca ccctgatgca tgaactggtt catgttaccc ataatctgta tggtattagc 720

aaccgcaact tctactataa ctttgacacc ggcaaaattg aaaccagccg tcagcagaat 780

agcctgattt ttgaagaact gctgaccttt ggtggcattg atagcaaagc aattagcagc 840

ctgatcatca agaaaattat cgaaaccgcc aagaacaact ataccacgct gattagcgaa 900

cgcctgaata ccgttaccgt tgaaaatgat ctgctgaaat atatcaaaaa caaaatcccg 960

gttcagggtc gtctgggtaa ctttaaactg gataccgcag aattcgagaa aaagctgaat 1020

accattctgt ttgtgctgaa cgaaagcaat ctggcacagc gttttagcat tctggttcgt 1080

aaacattacc tgaaagaacg tccgattgat ccgatttatg tgaacattct ggatgacaat 1140

agctacagca ccctggaagg ttttaacatt agcagtcagg gtagcaatga tttccaaggt 1200

cagctgctgg aaagcagcta ttttgaaaaa attgaaagca atgccctgcg tgccttcatt 1260

aaaatctgtc cgcgtaatgg tctgctgtat aatgccattt atcgcaacag caaaaatctg 1320

gaagttctgt ttcagggtcc gcatcatcac caccatcacc atcatcatca cctggaagtg 1380

ttatttcagg gaccgtatct gaataacatt gatctggaag ataaaaagac cacgagcaaa 1440

accaatgtta gctatccgtg tagcctgctg aatggttgta ttgaagttga aaacaaagac 1500

ctgttcctga ttagcaacaa agatagcctg aacgatatta acctgagcga agaaaaaatc 1560

aaaccggaaa ccaccgtgtt cttcaaagat aaactgcctc cgcaggatat tacgctgagc 1620

aattatgatt ttaccgaagc caatagcatt ccgagcatta gccagcagaa cattctggaa 1680

cgtaatgaag aactgtatga accgattcgc aatagcctgt ttgaaatcaa aaccatctat 1740

gtggataagc tgaccacctt tcattttctg gaagcccaga atattgatga gagcattgat 1800

agcagcaaaa ttcgtgttga actgaccgat agcgttgatg aagcactgag caatccgaat 1860

aaagtttata gcccgttcaa gaacatgagc aacaccatta atagcattga aaccggtatt 1920

accagcacct acatctttta tcagtggctg cgtagcatcg tgaaagattt tagtgatgaa 1980

accggcaaaa tcgacgtgat tgataaaagc agcgataccc tggcaattgt tccgtatatt 2040

ggtccgctgc tgaatattgg taatgatatt cgtcatggcg attttgtggg tgcaattgaa 2100

ctggcaggca ttaccgcact gctggaatat gttccggaat ttaccattcc gattctggtt 2160

ggtctggaag tgattggtgg cgaactggca cgtgaacagg ttgaagcaat tgttaataat 2220

gccctggata aacgcgatca gaaatgggca gaagtttaca atattaccaa agcacagtgg 2280

tggggcacca ttcatttaca gattaatacc cgtctggccc atacctataa agccctgagc 2340

cgtcaggcaa atgccattaa aatgaatatg gaatttcagc tggccaacta caaaggcaac 2400

attgatgata aagccaagat caaaaacgcc atcagcgaaa ccgaaattct gctgaacaaa 2460

agcgttgaac aggccatgaa aaacaccgag aaattcatga ttaaactgag caacagctac 2520

ctgaccaaag aaatgattcc gaaagttcag gacaacctga aaaactttga cctggaaacc 2580

aaaaaaaccc tggacaagtt catcaaagag aaagaagata tcctgggcac caatctgagc 2640

agcagcctgc gtcgtaaagt tagcattcgt ctgaataaaa acattgcctt cgacatcaac 2700

gatatcccgt ttagcgaatt tgatgatctg atcaaccagt acaaaaacga gatcgaagat 2760

tatgaagtgc tgaatctggg tgcagaagat ggcaaaatca aagatctgag cggtacaacc 2820

agcgatatca atattggttc agatatcgaa ctggccgatg gtcgtgaaaa taaagccatt 2880

aagattaaag gcagcgagaa cagcaccatc aaaattgcaa tgaacaaata tctgcgtttt 2940

agcgccaccg ataactttag cattagcttt tggatcaaac atccgaaacc gaccaatctg 3000

cttaataacg gtattgaata taccctggtc gagaacttta atcagcgtgg ttggaaaatt 3060

agcatccagg atagcaaact gatttggtat ctgcgcgatc acaataacag catcaaaatc 3120

gttacaccgg attatattgc gtttaatggc tggaacctga tcaccattac gaataatcgt 3180

agcaaaggca gcatcgtgta tgtgaatggt agcaaaattg aagagaagga cattagcagc 3240

atttggaata ccgaagtgga tgatccgatt atcttccgcc tgaaaaataa ccgtgatacc 3300

caggcattta ccctgctgga tcagtttagc atttatcgga aagaactgaa ccagaacgaa 3360

gtggtgaaac tgtataacta ctacttcaac agcaactaca ttcgcgatat ttggggtaat 3420

ccgctgcagt acaacaaaaa atactatctg cagacccagg acaaacctgg taaaggtctg 3480

atccgcgaat attggagcag ctttggttat gattatgtga ttctgagcga tagcaagacg 3540

attacctttc cgaacaatat ccgttatggt gccctgtata acggtagcaa agttctgatc 3600

aagaacagca agaaattaga tggtctggtg cgcaataaag atttcattca gctggaaatc 3660

gatggctata atatgggtat tagcgcagat cgctttaacg aggataccaa ctatattggc 3720

accacctatg gtacaaccca tgatctgacc accgattttg aaattattca gcgccaagag 3780

aaataccgca attattgtca gctgaaaacc ccgtataaca tctttcataa aagcggtctg 3840

atgagcaccg aaaccagcaa accgaccttc catgattatc gcgattgggt ttatagcagc 3900

gcatggtatt ttcagaacta tgaaaatctg aacctgcgca aacataccaa aaccaactgg 3960

tattttatcc cgaaagatga aggttgggac gaagat 3996

<210> 46
<211> 1332
<212> PRT
<213> Clostridium botulinum

<400> 46

Met Lys Leu Glu Ile Asn Lys Phe Asn Tyr Asn Asp Pro Ile Asp Gly
1 5 10 15

Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
20 25 30

Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser
225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys Pro Arg Asn Gly Leu Leu Tyr Asn Ala
420 425 430

Ile Tyr Arg Asn Ser Lys Asn Leu Glu Val Leu Phe Gln Gly Pro His
435 440 445

His His His His His His His His His Leu Glu Val Leu Phe Gln Gly
450 455 460

Pro Tyr Leu Asn Asn Ile Asp Leu Glu Asp Lys Lys Thr Thr Ser Lys
465 470 475 480

Thr Asn Val Ser Tyr Pro Cys Ser Leu Leu Asn Gly Cys Ile Glu Val
485 490 495

Glu Asn Lys Asp Leu Phe Leu Ile Ser Asn Lys Asp Ser Leu Asn Asp
500 505 510

Ile Asn Leu Ser Glu Glu Lys Ile Lys Pro Glu Thr Thr Val Phe Phe
515 520 525

Lys Asp Lys Leu Pro Pro Gln Asp Ile Thr Leu Ser Asn Tyr Asp Phe
530 535 540

Thr Glu Ala Asn Ser Ile Pro Ser Ile Ser Gln Gln Asn Ile Leu Glu
545 550 555 560

Arg Asn Glu Glu Leu Tyr Glu Pro Ile Arg Asn Ser Leu Phe Glu Ile
565 570 575

Lys Thr Ile Tyr Val Asp Lys Leu Thr Thr Phe His Phe Leu Glu Ala
580 585 590

Gln Asn Ile Asp Glu Ser Ile Asp Ser Ser Lys Ile Arg Val Glu Leu
595 600 605

Thr Asp Ser Val Asp Glu Ala Leu Ser Asn Pro Asn Lys Val Tyr Ser
610 615 620

Pro Phe Lys Asn Met Ser Asn Thr Ile Asn Ser Ile Glu Thr Gly Ile
625 630 635 640

Thr Ser Thr Tyr Ile Phe Tyr Gln Trp Leu Arg Ser Ile Val Lys Asp
645 650 655

Phe Ser Asp Glu Thr Gly Lys Ile Asp Val Ile Asp Lys Ser Ser Asp
660 665 670

Thr Leu Ala Ile Val Pro Tyr Ile Gly Pro Leu Leu Asn Ile Gly Asn
675 680 685

Asp Ile Arg His Gly Asp Phe Val Gly Ala Ile Glu Leu Ala Gly Ile
690 695 700

Thr Ala Leu Leu Glu Tyr Val Pro Glu Phe Thr Ile Pro Ile Leu Val
705 710 715 720

Gly Leu Glu Val Ile Gly Gly Glu Leu Ala Arg Glu Gln Val Glu Ala
725 730 735

Ile Val Asn Asn Ala Leu Asp Lys Arg Asp Gln Lys Trp Ala Glu Val

740 745 750

Tyr Asn Ile Thr Lys Ala Gln Trp Trp Gly Thr Ile His Leu Gln Ile
755 760 765

Asn Thr Arg Leu Ala His Thr Tyr Lys Ala Leu Ser Arg Gln Ala Asn
770 775 780

Ala Ile Lys Met Asn Met Glu Phe Gln Leu Ala Asn Tyr Lys Gly Asn
785 790 795 800

Ile Asp Asp Lys Ala Lys Ile Lys Asn Ala Ile Ser Glu Thr Glu Ile
805 810 815

Leu Leu Asn Lys Ser Val Glu Gln Ala Met Lys Asn Thr Glu Lys Phe
820 825 830

Met Ile Lys Leu Ser Asn Ser Tyr Leu Thr Lys Glu Met Ile Pro Lys
835 840 845

Val Gln Asp Asn Leu Lys Asn Phe Asp Leu Glu Thr Lys Lys Thr Leu
850 855 860

Asp Lys Phe Ile Lys Glu Lys Glu Asp Ile Leu Gly Thr Asn Leu Ser
865 870 875 880

Ser Ser Leu Arg Arg Lys Val Ser Ile Arg Leu Asn Lys Asn Ile Ala
885 890 895

Phe Asp Ile Asn Asp Ile Pro Phe Ser Glu Phe Asp Asp Leu Ile Asn
900 905 910

Gln Tyr Lys Asn Glu Ile Glu Asp Tyr Glu Val Leu Asn Leu Gly Ala
915 920 925

Glu Asp Gly Lys Ile Lys Asp Leu Ser Gly Thr Thr Ser Asp Ile Asn
930 935 940

Ile Gly Ser Asp Ile Glu Leu Ala Asp Gly Arg Glu Asn Lys Ala Ile
945 950 955 960

Lys Ile Lys Gly Ser Glu Asn Ser Thr Ile Lys Ile Ala Met Asn Lys
965 970 975

Tyr Leu Arg Phe Ser Ala Thr Asp Asn Phe Ser Ile Ser Phe Trp Ile
980 985 990

Lys His Pro Lys Pro Thr Asn Leu Leu Asn Asn Gly Ile Glu Tyr Thr
995 1000 1005

Leu Val Glu Asn Phe Asn Gln Arg Gly Trp Lys Ile Ser Ile Gln
1010 1015 1020

Asp Ser Lys Leu Ile Trp Tyr Leu Arg Asp His Asn Asn Ser Ile
1025 1030 1035

Lys Ile Val Thr Pro Asp Tyr Ile Ala Phe Asn Gly Trp Asn Leu
1040 1045 1050

Ile Thr Ile Thr Asn Asn Arg Ser Lys Gly Ser Ile Val Tyr Val
1055 1060 1065

Asn Gly Ser Lys Ile Glu Glu Lys Asp Ile Ser Ser Ile Trp Asn
1070 1075 1080

Thr Glu Val Asp Asp Pro Ile Ile Phe Arg Leu Lys Asn Asn Arg
1085 1090 1095

Asp Thr Gln Ala Phe Thr Leu Leu Asp Gln Phe Ser Ile Tyr Arg
1100 1105 1110

Lys Glu Leu Asn Gln Asn Glu Val Val Lys Leu Tyr Asn Tyr Tyr
1115 1120 1125

Phe Asn Ser Asn Tyr Ile Arg Asp Ile Trp Gly Asn Pro Leu Gln
1130 1135 1140

Tyr Asn Lys Lys Tyr Tyr Leu Gln Thr Gln Asp Lys Pro Gly Lys
1145 1150 1155

Gly Leu Ile Arg Glu Tyr Trp Ser Ser Phe Gly Tyr Asp Tyr Val
1160 1165 1170

Ile Leu Ser Asp Ser Lys Thr Ile Thr Phe Pro Asn Asn Ile Arg
1175 1180 1185

Tyr Gly Ala Leu Tyr Asn Gly Ser Lys Val Leu Ile Lys Asn Ser
1190 1195 1200

Lys Lys Leu Asp Gly Leu Val Arg Asn Lys Asp Phe Ile Gln Leu
1205 1210 1215

Glu Ile Asp Gly Tyr Asn Met Gly Ile Ser Ala Asp Arg Phe Asn
1220 1225 1230

Glu Asp Thr Asn Tyr Ile Gly Thr Thr Tyr Gly Thr Thr His Asp
1235 1240 1245

Leu Thr Thr Asp Phe Glu Ile Ile Gln Arg Gln Glu Lys Tyr Arg
1250 1255 1260

Asn Tyr Cys Gln Leu Lys Thr Pro Tyr Asn Ile Phe His Lys Ser
1265 1270 1275

Gly Leu Met Ser Thr Glu Thr Ser Lys Pro Thr Phe His Asp Tyr
1280 1285 1290

Arg Asp Trp Val Tyr Ser Ser Ala Trp Tyr Phe Gln Asn Tyr Glu
1295 1300 1305

Asn Leu Asn Leu Arg Lys His Thr Lys Thr Asn Trp Tyr Phe Ile
1310 1315 1320

Pro Lys Asp Glu Gly Trp Asp Glu Asp
1325 1330

<210> 47
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Trypsin

<400> 47

Met His Pro Leu Leu Ile Leu Ala Phe Val Gly Ala Ala Val Ala Phe
1 5 10 15

Pro Ser Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Thr Cys Ala Glu
20 25 30

Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ala Gly Tyr His Phe Cys
35 40 45

Gly Gly Ser Leu Ile Asn Asp Gln Trp Val Val Ser Ala Ala His Cys
50 55 60

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

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

Pro Lys Tyr Ser Ser Trp Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys
100 105 110

Leu Ser Thr Pro Ala Val Ile Asn Ala Arg Val Ser Thr Leu Ala Leu
115 120 125

Pro Ser Ala Cys Ala Ser Gly Ser Thr Glu Cys Leu Ile Ser Gly Trp
130 135 140

Gly Asn Thr Leu Ser Ser Gly Val Asn Tyr Pro Asp Leu Leu Gln Cys
145 150 155 160

Leu Glu Ala Pro Leu Leu Ser His Ala Asp Cys Glu Ala Ser Tyr Pro
165 170 175

Gly Glu Ile Thr Asn Asn Met Ile Cys Ala Gly Phe Leu Glu Gly Gly
180 185 190

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Ala Cys Asn Gly
195 200 205

Gln Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Gly
210 215 220

Lys Pro Gly Val Tyr Thr Lys Val Cys Asn Tyr Val Asp Trp Ile Gln
225 230 235 240

Glu Thr Ile Ala Ala Asn Ser
245

<210> 48
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Lys-C

<400> 48

Gly Val Ser Gly Ser Cys Asn Ile Asp Val Val Cys Pro Glu Gly Asn
1 5 10 15

Gly His Arg Asp Val Ile Arg Ser Val Ala Ala Tyr Ser Lys Gln Gly
20 25 30

Thr Met Trp Cys Thr Gly Ser Leu Val Asn Asn Ser Ala Asn Asp Lys
35 40 45

Lys Met Tyr Phe Leu Thr Ala Asn His Cys Gly Met Thr Thr Ala Ala
50 55 60

Ile Ala Ser Ser Met Val Val Tyr Trp Asn Tyr Gln Asn Ser Thr Cys
65 70 75 80

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

Ala Gln Ser Gln Thr Gly Ala Val Val Arg Ala Thr Asn Ala Ala Ser
100 105 110

Asp Phe Thr Leu Leu Glu Leu Asn Thr Ala Ala Asn Pro Ala Tyr Asn
115 120 125

Leu Phe Trp Ala Gly Trp Asp Arg Arg Asp Gln Asn Phe Ala Gly Ala
130 135 140

Thr Ala Ile His His Pro Asn Val Ala Glu Lys Arg Ile Ser His Ser
145 150 155 160

Thr Val Ala Thr Glu Ile Ser Gly Tyr Asn Gly Ala Thr Gly Thr Ser
165 170 175

His Leu His Val Phe Trp Gln Ala Ser Gly Gly Val Thr Glu Pro Gly
180 185 190

Ser Ser Gly Ser Pro Ile Tyr Ser Pro Glu Lys Arg Val Leu Gly Gln
195 200 205

Leu His Gly Gly Pro Ser Ser Cys Ser Ala Thr Gly Ala Asp Arg Ser
210 215 220

Asp Tyr Tyr Gly Arg Val Phe Thr Ser Trp Thr Gly Gly Gly Thr Ser
225 230 235 240

Ala Thr Arg Leu Ser Asp Trp Leu Asp Ala Ala Gly Thr Gly Ala Gln
245 250 255

Phe Ile Asp Gly Leu Asp Ser Thr Gly Thr Pro Pro Val
260 265

<210> 49
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Enterokinase Light Chain

<400> 49

Ile Val Gly Gly Ser Asp Ser Arg Glu Gly Ala Trp Pro Trp Val Val
1 5 10 15

Ala Leu Tyr Phe Asp Asp Gln Gln Val Cys Gly Ala Ser Leu Val Ser
20 25 30

Arg Asp Trp Leu Val Ser Ala Ala His Cys Val Tyr Gly Arg Asn Met
35 40 45

Glu Pro Ser Lys Trp Lys Ala Val Leu Gly Leu His Met Ala Ser Asn

50 55 60

Leu Thr Ser Pro Gln Ile Glu Thr Arg Leu Ile Asp Gln Ile Val Ile
65 70 75 80

Asn Arg His Tyr Asn Lys Arg Arg Lys Asn Asn Asp Ile Ala Met Met
85 90 95

His Leu Glu Met Lys Val Asn Tyr Thr Asp Tyr Ile Gln Pro Ile Cys
100 105 110

Leu Pro Glu Glu Asn Gln Val Phe Pro Pro Gly Arg Ile Cys Ser Ile
115 120 125

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

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

Met Pro Glu Tyr Asn Ile Thr Glu Asn Met Val Cys Ala Gly Tyr Asp
165 170 175

Ala Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met
180 185 190

Cys Gln Glu Asn Asn Arg Trp Leu Leu Ala Gly Val Thr Ser Phe Gly
195 200 205

Tyr Gln Cys Ala Leu Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Pro
210 215 220

Arg Phe Thr Glu Trp Ile Gln Ser Phe Leu His
225 230 235

<210> 50
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Factor Xa Heavy Chain

<400> 50

Ile Val Gly Gly Arg Asp Cys Ala Glu Gly Glu Cys Pro Trp Gln Ala
1 5 10 15

Leu Leu Val Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu
20 25 30

Asn Glu Phe Tyr Val Leu Thr Ala Ala His Cys Leu His Gln Ala Lys
35 40 45

Arg Phe Thr Val Arg Val Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly
50 55 60

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

Val Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr
85 90 95

Pro Ile Arg Phe Arg Arg Asn Val Ala Pro Ala Cys Leu Pro Glu Lys
100 105 110

Asp Trp Ala Glu Ala Thr Leu Met Thr Gln Lys Thr Gly Ile Val Ser
115 120 125

Gly Phe Gly Arg Thr His Glu Lys Gly Arg Leu Ser Ser Thr Leu Lys
130 135 140

Met Leu Glu Val Pro Tyr Val Asp Arg Ser Thr Cys Lys Leu Ser Ser
145 150 155 160

Ser Phe Thr Ile Thr Pro Asn Met Phe Cys Ala Gly Tyr Asp Thr Gln
165 170 175

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

Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val Ser Trp Gly Glu Gly
195 200 205

Cys Ala Arg Lys Gly Lys Phe Gly Val Tyr Thr Lys Val Ser Asn Phe

210 215 220

Leu Lys Trp Ile Asp Lys Ile Met Lys Ala Arg Ala Gly Ala Ala Gly
225 230 235 240

Ser Arg Gly His Ser Glu Ala Pro Ala Thr Trp Thr Val Pro Pro Pro
245 250 255

Leu Pro Leu

<210> 51
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Factor Xa Light Chain

<400> 51

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

Cys Leu Glu Glu Ala Cys Ser Leu Glu Glu Ala Arg Glu Val Phe Glu
20 25 30

Asp Ala Glu Gln Thr Asp Glu Phe Trp Ser Lys Tyr Lys Asp Gly Asp
35 40 45

Gln Cys Glu Gly His Pro Cys Leu Asn Gln Gly His Cys Lys Asp Gly
50 55 60

Ile Gly Asp Tyr Thr Cys Thr Cys Ala Glu Gly Phe Glu Gly Lys Asn
65 70 75 80

Cys Glu Phe Ser Thr Arg Glu Ile Cys Ser Leu Asp Asn Gly Gly Cys
85 90 95

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

His Gly Tyr Val Leu Gly Asp Asp Ser Lys Ser Cys Val Ser Thr Glu
115 120 125

Arg Phe Pro Cys Gly Lys Phe Thr Gln Gly Arg Ser
130 135 140

<210> 52
<211> 764
<212> PRT
<213> Bacillus anthracis

<400> 52

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
1 5 10 15

Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
20 25 30

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
35 40 45

Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
50 55 60

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

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
85 90 95

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

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
145 150 155 160

Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
165 170 175

Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
195 200 205

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

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
245 250 255

Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
305 310 315 320

Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
325 330 335

Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr

385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755 760

<210> 53
<211> 863
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/A with a C1 Activation Loop

<400> 53

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 Val 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 His Lys
420 425 430

Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp Cys Ile Lys
435 440 445

Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
450 455 460

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

Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu
485 490 495

Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu
500 505 510

Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg
515 520 525

Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His
530 535 540

Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu
545 550 555 560

Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr
565 570 575

Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala
580 585 590

Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp
595 600 605

Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr Ile
610 615 620

Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met Leu Tyr
625 630 635 640

Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu
645 650 655

Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala
660 665 670

Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr Ile Asp
675 680 685

Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr Lys Tyr
690 695 700

Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp Leu Ile
705 710 715 720

Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys
725 730 735

Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn
740 745 750

Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser
755 760 765

Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser
770 775 780

Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu
785 790 795 800

Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr
805 810 815

Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys
820 825 830

Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr
835 840 845

Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys
850 855 860

<210> 54
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/B with a C1 Activation Loop

<400> 54

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

Asn 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

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 His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn

435 440 445

Lys Thr Leu Asp Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe Ile
450 455 460

Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg Ile
465 470 475 480

Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile Asn
485 490 495

Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser
500 505 510

Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr
515 520 525

Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile
530 535 540

Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp Ile
545 550 555 560

Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val
565 570 575

Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val Val
580 585 590

Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe
595 600 605

Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp Ile
610 615 620

Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu
625 630 635 640

Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser
645 650 655

Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly Ala
660 665 670

Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr
675 680 685

Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr
690 695 700

Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
705 710 715 720

Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala
725 730 735

Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu
740 745 750

Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu Asn
755 760 765

Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn Gly
770 775 780

Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
785 790 795 800

Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn Tyr
805 810 815

Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu Lys
820 825 830

Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu Ser
835 840 845

Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe Asn Lys Tyr Asn
850 855 860

Ser
865

<210> 55
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/D with a C1 Activation Loop

<400> 55

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

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 His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn
435 440 445

Lys Thr Leu Asp Cys Ile Lys Val Lys Asn Asn Arg Leu Pro Tyr Val
450 455 460

Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe Glu Asn Lys Ile Ile
465 470 475 480

Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp Lys Phe Ser Leu Asp
485 490 495

Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn Pro Glu Ile Val Asp
500 505 510

Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu Asn Leu Pro Gly Glu
515 520 525

Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr Val Asp Tyr Leu Asn
530 535 540

Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asn Asn Val Glu Asn
545 550 555 560

Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys
565 570 575

Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val
580 585 590

Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe
595 600 605

Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp Lys Ile Ser Asp Val
610 615 620

Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser
625 630 635 640

Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala Thr Ala Gly Val Ala
645 650 655

Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Val
660 665 670

Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr
675 680 685

Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr
690 695 700

Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Gln Phe Asn
705 710 715 720

His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala
725 730 735

Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp
740 745 750

Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp
755 760 765

Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu
770 775 780

Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp
785 790 795 800

Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr Glu Leu Ile Asn Leu
805 810 815

Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys
820 825 830

Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro Phe Asn Ile Phe

835 840 845

Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe
850 855 860

Asn
865

<210> 56
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/E with a C1 Activation Loop

<400> 56

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

Arg Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190

Arg Phe Asn Asp Asn Cys 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 Arg 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 His Lys Ala Ile
405 410 415

Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp Cys Ile Glu Ile Asn
420 425 430

Asn Gly Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp
435 440 445

Asn Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn
450 455 460

Asn Tyr Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu
465 470 475 480

Ser Ala Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn
485 490 495

Asp Ala Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu
500 505 510

Gln His Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln
515 520 525

Lys Val Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp
530 535 540

Thr Ala Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu
545 550 555 560

Phe Ile Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser
565 570 575

Trp Ile Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys
580 585 590

Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile
595 600 605

Gly Leu Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys
610 615 620

Asp Ala Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro
625 630 635 640

Glu Leu Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu
645 650 655

Gly Ser Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala
660 665 670

Leu Lys Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val
675 680 685

Ser Asn Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu
690 695 700

Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile
705 710 715 720

Ile Glu Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu
725 730 735

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

Val Ser Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser
755 760 765

Ile Ser Tyr Leu Met Lys Ile Ile Asn Glu Val Lys Ile Asn Lys Leu
770 775 780

Arg Glu Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile
785 790 795 800

Gln His Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met
805 810 815

Val Thr Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr
820 825 830

Thr Asp Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys
835 840 845

<210> 57
<211> 864
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/F with a C1 Activation Loop

<400> 57

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

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 His Lys Ala
420 425 430

Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp 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

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

<210> 58
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/G with a C1 Activation Loop

<220>
<221> SITE
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 58

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 His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys
435 440 445

Thr Leu Asp Cys Ile Ile Val Asn Asn Glu Asp Leu Phe Phe Ile Ala
450 455 460

Asn Lys Asp Ser Phe Ser Lys Asp Leu Ala Lys Ala Glu Thr Ile Ala
465 470 475 480

Tyr Asn Thr Gln Asn Asn Thr Ile Glu Asn Asn Phe Ser Ile Asp Gln
485 490 495

Leu Ile Leu Asp Asn Asp Leu Ser Ser Gly Ile Asp Leu Pro Asn Glu
500 505 510

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

Ile Lys Gln Ser Ala Leu Lys Lys Ile Phe Val Asp Gly Asp Ser Leu
530 535 540

Phe Glu Tyr Leu His Ala Gln Thr Phe Pro Ser Asn Ile Glu Asn Leu
545 550 555 560

Gln Leu Thr Asn Ser Leu Asn Asp Ala Leu Arg Asn Asn Asn Lys Val
565 570 575

Tyr Thr Phe Phe Ser Thr Asn Leu Val Glu Lys Ala Asn Thr Val Val
580 585 590

Gly Ala Ser Leu Phe Val Asn Trp Val Lys Gly Val Ile Asp Asp Phe
595 600 605

Thr Ser Glu Ser Thr Gln Lys Ser Thr Ile Asp Lys Val Ser Asp Val
610 615 620

Ser Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Val Gly Asn Glu
625 630 635 640

Thr Ala Lys Glu Asn Phe Lys Asn Ala Phe Glu Ile Gly Gly Ala Ala
645 650 655

Ile Leu Met Glu Phe Ile Pro Glu Leu Ile Val Pro Ile Val Gly Phe
660 665 670

Phe Thr Leu Glu Ser Tyr Val Gly Asn Lys Gly His Ile Ile Met Thr
675 680 685

Ile Ser Asn Ala Leu Lys Lys Arg Asp Gln Lys Trp Thr Asp Met Tyr
690 695 700

Gly Leu Ile Val Ser Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
705 710 715 720

Thr Ile Lys Glu Arg Met Tyr Asn Ala Leu Asn Asn Gln Ser Gln Ala
725 730 735

Ile Glu Lys Ile Ile Glu Asp Gln Tyr Asn Arg Tyr Ser Glu Glu Asp

740 745 750

Lys Met Asn Ile Asn Ile Asp Phe Asn Asp Ile Asp Phe Lys Leu Asn
755 760 765

Gln Ser Ile Asn Leu Ala Ile Asn Asn Ile Asp Asp Phe Ile Asn Gln
770 775 780

Cys Ser Ile Ser Tyr Leu Met Asn Arg Met Ile Pro Leu Ala Val Lys
785 790 795 800

Lys Leu Lys Asp Phe Asp Asp Asn Leu Lys Arg Asp Leu Leu Glu Tyr
805 810 815

Ile Asp Thr Asn Glu Leu Tyr Leu Leu Asp Glu Val Asn Ile Leu Lys
820 825 830

Ser Lys Val Asn Arg His Leu Lys Asp Ser Ile Pro Phe Asp Leu Ser
835 840 845

Leu Tyr Thr Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
850 855 860

Ser
865

<210> 59
<211> 867
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/TeNT with a C1 Activation Loop

<400> 59

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
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 His Lys Ala Ile Asp Gly Arg Ser Leu
435 440 445

Tyr Asn Lys Thr Leu Asp Cys Ile Lys Ile Lys Asn Glu Asp Leu Thr
450 455 460

Phe Ile Ala Glu Lys Asn Ser Phe Ser Glu Glu Pro Phe Gln Asp Glu
465 470 475 480

Ile Val Ser Tyr Asn Thr Lys Asn Lys Pro Leu Asn Phe Asn Tyr Ser
485 490 495

Leu Asp Lys Ile Ile Val Asp Tyr Asn Leu Gln Ser Lys Ile Thr Leu
500 505 510

Pro Asn Asp Arg Thr Thr Pro Val Thr Lys Gly Ile Pro Tyr Ala Pro
515 520 525

Glu Tyr Lys Ser Asn Ala Ala Ser Thr Ile Glu Ile His Asn Ile Asp
530 535 540

Asp Asn Thr Ile Tyr Gln Tyr Leu Tyr Ala Gln Lys Ser Pro Thr Thr
545 550 555 560

Leu Gln Arg Ile Thr Met Thr Asn Ser Val Asp Asp Ala Leu Ile Asn
565 570 575

Ser Thr Lys Ile Tyr Ser Tyr Phe Pro Ser Val Ile Ser Lys Val Asn
580 585 590

Gln Gly Ala Gln Gly Ile Leu Phe Leu Gln Trp Val Arg Asp Ile Ile
595 600 605

Asp Asp Phe Thr Asn Glu Ser Ser Gln Lys Thr Thr Ile Asp Lys Ile
610 615 620

Ser Asp Val Ser Thr Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile
625 630 635 640

Val Lys Gln Gly Tyr Glu Gly Asn Phe Ile Gly Ala Leu Glu Thr Thr
645 650 655

Gly Val Val Leu Leu Leu Glu Tyr Ile Pro Glu Ile Thr Leu Pro Val
660 665 670

Ile Ala Ala Leu Ser Ile Ala Glu Ser Ser Thr Gln Lys Glu Lys Ile
675 680 685

Ile Lys Thr Ile Asp Asn Phe Leu Glu Lys Arg Tyr Glu Lys Trp Ile
690 695 700

Glu Val Tyr Lys Leu Val Lys Ala Lys Trp Leu Gly Thr Val Asn Thr
705 710 715 720

Gln Phe Gln Lys Arg Ser Tyr Gln Met Tyr Arg Ser Leu Glu Tyr Gln
725 730 735

Val Asp Ala Ile Lys Lys Ile Ile Asp Tyr Glu Tyr Lys Ile Tyr Ser
740 745 750

Gly Pro Asp Lys Glu Gln Ile Ala Asp Glu Ile Asn Asn Leu Lys Asn
755 760 765

Lys Leu Glu Glu Lys Ala Asn Lys Ala Met Ile Asn Ile Asn Ile Phe
770 775 780

Met Arg Glu Ser Ser Arg Ser Phe Leu Val Asn Gln Met Ile Asn Glu
785 790 795 800

Ala Lys Lys Gln Leu Leu Glu Phe Asp Thr Gln Ser Lys Asn Ile Leu
805 810 815

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

Lys Lys Leu Glu Ser Lys Ile Asn Lys Val Phe Ser Thr Pro Ile Pro
835 840 845

Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp
850 855 860

Ile Asp Val
865

<210> 60
<211> 896
<212> PRT
<213> Artificial Sequence

<220>
<223> LHN/X with a C1 Activation Loop

<400> 60

Met Lys Leu Glu Ile Asn Lys Phe Asn Tyr Asn Asp Pro Ile Asp Gly
1 5 10 15

Ile Asn Val Ile Thr Met Arg Pro Pro Arg His Ser Asp Lys Ile Asn
20 25 30

Lys Gly Lys Gly Pro Phe Lys Ala Phe Gln Val Ile Lys Asn Ile Trp
35 40 45

Ile Val Pro Glu Arg Tyr Asn Phe Thr Asn Asn Thr Asn Asp Leu Asn
50 55 60

Ile Pro Ser Glu Pro Ile Met Glu Ala Asp Ala Ile Tyr Asn Pro Asn
65 70 75 80

Tyr Leu Asn Thr Pro Ser Glu Lys Asp Glu Phe Leu Gln Gly Val Ile
85 90 95

Lys Val Leu Glu Arg Ile Lys Ser Lys Pro Glu Gly Glu Lys Leu Leu
100 105 110

Glu Leu Ile Ser Ser Ser Ile Pro Leu Pro Leu Val Ser Asn Gly Ala
115 120 125

Leu Thr Leu Ser Asp Asn Glu Thr Ile Ala Tyr Gln Glu Asn Asn Asn
130 135 140

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

Asp Ile Ala Asn Asn Ala Thr Tyr Gly Leu Tyr Ser Thr Pro Ile Ser
165 170 175

Asn Gly Glu Gly Thr Leu Ser Glu Val Ser Phe Ser Pro Phe Tyr Leu
180 185 190

Lys Pro Phe Asp Glu Ser Tyr Gly Asn Tyr Arg Ser Leu Val Asn Ile
195 200 205

Val Asn Lys Phe Val Lys Arg Glu Phe Ala Pro Asp Pro Ala Ser Thr
210 215 220

Leu Met His Glu Leu Val His Val Thr His Asn Leu Tyr Gly Ile Ser
225 230 235 240

Asn Arg Asn Phe Tyr Tyr Asn Phe Asp Thr Gly Lys Ile Glu Thr Ser
245 250 255

Arg Gln Gln Asn Ser Leu Ile Phe Glu Glu Leu Leu Thr Phe Gly Gly
260 265 270

Ile Asp Ser Lys Ala Ile Ser Ser Leu Ile Ile Lys Lys Ile Ile Glu
275 280 285

Thr Ala Lys Asn Asn Tyr Thr Thr Leu Ile Ser Glu Arg Leu Asn Thr
290 295 300

Val Thr Val Glu Asn Asp Leu Leu Lys Tyr Ile Lys Asn Lys Ile Pro
305 310 315 320

Val Gln Gly Arg Leu Gly Asn Phe Lys Leu Asp Thr Ala Glu Phe Glu
325 330 335

Lys Lys Leu Asn Thr Ile Leu Phe Val Leu Asn Glu Ser Asn Leu Ala
340 345 350

Gln Arg Phe Ser Ile Leu Val Arg Lys His Tyr Leu Lys Glu Arg Pro
355 360 365

Ile Asp Pro Ile Tyr Val Asn Ile Leu Asp Asp Asn Ser Tyr Ser Thr
370 375 380

Leu Glu Gly Phe Asn Ile Ser Ser Gln Gly Ser Asn Asp Phe Gln Gly
385 390 395 400

Gln Leu Leu Glu Ser Ser Tyr Phe Glu Lys Ile Glu Ser Asn Ala Leu
405 410 415

Arg Ala Phe Ile Lys Ile Cys His Lys Ala Ile Asp Gly Arg Ser Leu
420 425 430

Tyr Asn Lys Thr Leu Asp Cys Ile Glu Val Glu Asn Lys Asp Leu Phe
435 440 445

Leu Ile Ser Asn Lys Asp Ser Leu Asn Asp Ile Asn Leu Ser Glu Glu
450 455 460

Lys Ile Lys Pro Glu Thr Thr Val Phe Phe Lys Asp Lys Leu Pro Pro
465 470 475 480

Gln Asp Ile Thr Leu Ser Asn Tyr Asp Phe Thr Glu Ala Asn Ser Ile
485 490 495

Pro Ser Ile Ser Gln Gln Asn Ile Leu Glu Arg Asn Glu Glu Leu Tyr
500 505 510

Glu Pro Ile Arg Asn Ser Leu Phe Glu Ile Lys Thr Ile Tyr Val Asp
515 520 525

Lys Leu Thr Thr Phe His Phe Leu Glu Ala Gln Asn Ile Asp Glu Ser
530 535 540

Ile Asp Ser Ser Lys Ile Arg Val Glu Leu Thr Asp Ser Val Asp Glu
545 550 555 560

Ala Leu Ser Asn Pro Asn Lys Val Tyr Ser Pro Phe Lys Asn Met Ser
565 570 575

Asn Thr Ile Asn Ser Ile Glu Thr Gly Ile Thr Ser Thr Tyr Ile Phe
580 585 590

Tyr Gln Trp Leu Arg Ser Ile Val Lys Asp Phe Ser Asp Glu Thr Gly
595 600 605

Lys Ile Asp Val Ile Asp Lys Ser Ser Asp Thr Leu Ala Ile Val Pro
610 615 620

Tyr Ile Gly Pro Leu Leu Asn Ile Gly Asn Asp Ile Arg His Gly Asp
625 630 635 640

Phe Val Gly Ala Ile Glu Leu Ala Gly Ile Thr Ala Leu Leu Glu Tyr
645 650 655

Val Pro Glu Phe Thr Ile Pro Ile Leu Val Gly Leu Glu Val Ile Gly

660 665 670

Gly Glu Leu Ala Arg Glu Gln Val Glu Ala Ile Val Asn Asn Ala Leu
675 680 685

Asp Lys Arg Asp Gln Lys Trp Ala Glu Val Tyr Asn Ile Thr Lys Ala
690 695 700

Gln Trp Trp Gly Thr Ile His Leu Gln Ile Asn Thr Arg Leu Ala His
705 710 715 720

Thr Tyr Lys Ala Leu Ser Arg Gln Ala Asn Ala Ile Lys Met Asn Met
725 730 735

Glu Phe Gln Leu Ala Asn Tyr Lys Gly Asn Ile Asp Asp Lys Ala Lys
740 745 750

Ile Lys Asn Ala Ile Ser Glu Thr Glu Ile Leu Leu Asn Lys Ser Val
755 760 765

Glu Gln Ala Met Lys Asn Thr Glu Lys Phe Met Ile Lys Leu Ser Asn
770 775 780

Ser Tyr Leu Thr Lys Glu Met Ile Pro Lys Val Gln Asp Asn Leu Lys
785 790 795 800

Asn Phe Asp Leu Glu Thr Lys Lys Thr Leu Asp Lys Phe Ile Lys Glu
805 810 815

Lys Glu Asp Ile Leu Gly Thr Asn Leu Ser Ser Ser Leu Arg Arg Lys
820 825 830

Val Ser Ile Arg Leu Asn Lys Asn Ile Ala Phe Asp Ile Asn Asp Ile
835 840 845

Pro Phe Ser Glu Phe Asp Asp Leu Ile Asn Gln Tyr Lys Asn Glu Ile
850 855 860

Glu Asp Tyr Glu Val Leu Asn Leu Gly Ala Glu Asp Gly Lys Ile Lys
865 870 875 880

Asp Leu Ser Gly Thr Thr Ser Asp Ile Asn Ile Gly Ser Asp Ile Glu
885 890 895

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> BoNT/DC Activation Loop

<400> 61

Cys Leu Arg Leu Thr Arg Asn Ser Arg Asp Asp Ser Thr Cys
1 5 10

<210> 62
<211> 25
<212> PRT
<213> Clostridium botulinum

<400> 62

Cys Val Arg Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly
1 5 10 15

Tyr Asn Lys Ala Leu Asn Glu Leu Cys
20 25

<210> 63
<211> 25
<212> PRT
<213> Clostridium botulinum

<400> 63

Cys Val Arg Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly
1 5 10 15

Tyr Asn Lys Ala Leu Asn Asp Leu Cys
20 25

<210> 64
<211> 25
<212> PRT
<213> Clostridium botulinum

<400> 64

Cys Val Arg Gly Ile Ile Pro Phe Lys Thr Lys Ser Leu Asp Glu Gly
1 5 10 15

Tyr Asn Lys Ala Leu Asn Tyr Leu Cys
20 25

<210> 65
<211> 25
<212> PRT
<213> Clostridium botulinum

<400> 65

Cys Val Arg Gly Ile Ile Pro Phe Lys Thr Lys Ser Leu Asp Glu Gly
1 5 10 15

Tyr Asn Lys Ala Leu Asn Asp Leu Cys
20 25

<210> 66
<211> 11
<212> PRT
<213> Clostridium botulinum

<400> 66

Cys Ser Asn Ser Asn Thr Lys Asn Ser Leu Cys
1 5 10

<210> 67
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 67

Cys Thr Asn Ile Phe Ser Pro Lys Gly Ile Arg Lys Ser Ile Cys
1 5 10 15

<210> 68
<211> 15
<212> PRT
<213> Clostridium botulinum

<400> 68

Cys Lys Asn Ile Val Phe Ser Lys Gly Ile Thr Lys Ser Ile Cys
1 5 10 15

<210> 69
<211> 15
<212> PRT
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<400> 69

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Asp Asp Asp Asp Lys
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<400> 76

Xaa Glu Xaa Xaa Xaa Ile Leu
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Xaa Glu Xaa Xaa Xaa Leu Met
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<210> 78
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Tyr Xaa Xaa Xaa
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Glu Asn Leu Tyr Phe Gln Gly
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Leu Val Pro Arg Gly Ser
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<210> 81

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Leu Glu Val Leu Phe Gln Gly Pro
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