

eolf-seql
SEQUENCE LISTING

<110> Merz Pharma GmbH & Co.KGaA

<120> Methods for Enhancing the specific Uptake of Botulinum Neurotoxins into Cells

<130> MP12983PC

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<170> PatentIn version 3.5

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<212> DNA

<213> Clostridium botulinum

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 145 150 155 160

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Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr
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Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly
325 330 335

Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu
340 345 350

eolf-seql

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

eolf-seql

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

eolf-seql

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

eolf-seql

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
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Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly
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Glu Ile Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe
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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

eolf-seql

Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	Arg	Ser	Lys	Tyr	Asn
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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
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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			
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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			
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eolf-seql

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eolf-seq1

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attaatgaat atttcaatag tattaatgat tcaaaaattt tgagcttaca aaacaaaaaa	2640
aatgcttttag tggatacatc aggatataat gcagaagtga ggctagaagg tgatgttcaa	2700

eolf-seql

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Pro Glu Lys Ala Phe Arg Ile Ile Gly Asn Ile Trp Val Ile Pro Asp
35 40 45

Arg Phe Ser Arg Asp Ser Asn Pro Asn Leu Asn Lys Pro Pro Arg Val
50 55 60

Thr Ser Pro Lys Ser Gly Tyr Tyr Asp Pro Asn Tyr Leu Ser Thr Asp
65 70 75 80

Ser Glu Lys Asp Thr Phe Leu Lys Glu Ile Ile Lys Leu Phe Lys Arg
85 90 95

Ile Asn Ser Arg Glu Ile Gly Glu Glu Leu Ile Tyr Arg Leu Ala Thr
100 105 110

Asp Ile Pro Phe Pro Gly Asn Asn Asn Thr Pro Ile Asn Thr Phe Asp
115 120 125

Phe Asp Val Asp Phe Asn Ser Val Asp Val Lys Thr Arg Gln Gly Asn
130 135 140

Asn Trp Val Lys Thr Gly Ser Ile Asn Pro Ser Val Ile Ile Thr Gly
145 150 155 160

Pro Arg Glu Asn Ile Ile Asp Pro Glu Thr Ser Thr Phe Lys Leu Thr
165 170 175

Asn Asn Thr Phe Ala Ala Gln Glu Gly Phe Gly Ala Leu Ser Ile Ile
180 185 190

eolf-seql

Ser Ile Ser Pro Arg Phe Met Leu Thr Tyr Ser Asn Ala Thr Asn Asn
195 200 205

Val Gly Glu Gly Arg Phe Ser Lys Ser Glu Phe Cys Met Asp Pro Ile
210 215 220

Leu Ile Leu Met His Glu Leu Asn His Ala Met His Asn Leu Tyr Gly
225 230 235 240

Ile Ala Ile Pro Asn Asp Gln Arg Ile Ser Ser Val Thr Ser Asn Ile
245 250 255

Phe Tyr Ser Gln Tyr Lys Val Lys Leu Glu Tyr Ala Glu Ile Tyr Ala
260 265 270

Phe Gly Gly Pro Thr Ile Asp Leu Ile Pro Lys Ser 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 Ala Val Asp Arg Asn Lys Phe Ala Glu Leu Tyr Lys
340 345 350

Glu Leu Thr Gln Ile Phe Thr Glu Phe Asn Tyr Ala Lys Ile Tyr Asn
355 360 365

Val Gln Asn Arg Lys Ile Tyr Leu Ser Asn Val Tyr Thr Pro Val Thr
370 375 380

eolf-seql

Ala Asn Ile Leu Asp Asp Asn Val Tyr Asp Ile Gln Asn Gly Phe Asn
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Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu Ser
405 410 415

Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr Leu
420 425 430

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

Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro
450 455 460

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

Asp Ile Asn Glu Glu Thr Glu Val Ile Asp Tyr Pro Asp Asn Val Ser
485 490 495

Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu
500 505 510

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

Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu
545 550 555 560

Asp Phe Thr Phe Thr Thr Ser Ile Glu Glu Ala Leu Asp Asn Ser Gly
565 570 575

eolf-seql

Lys Val Tyr Thr Tyr Phe Pro Lys Leu Ala Asp Lys Val Asn Thr 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 Gln Glu Phe Thr Ile Pro Ala Leu Gly
660 665 670

Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys
675 680 685

Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser
690 695 700

Tyr Glu Trp Met Ile Gly Thr Trp Leu Ser Arg Ile Thr Thr Gln Phe
705 710 715 720

Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Asp
725 730 735

Ala Ile Lys Asp Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser
740 745 750

Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu
755 760 765

eolf-seql

Asp Ile Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg
770 775 780

Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile
785 790 795 800

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

Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu
820 825 830

Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Ile Pro Phe Asn Ile
835 840 845

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

Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys
865 870 875 880

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

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

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

Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser
930 935 940

Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile
945 950 955 960

eolf-seql

Lys Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu
965 970 975

Trp Ile Leu Gln Asp Ile Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp
980 985 990

Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe
995 1000 1005

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

Asn Gly Glu Leu Lys Gln Ser Glu Arg Ile Glu Asp Leu Asn Glu
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Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
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Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser
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Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
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Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys
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Phe Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg
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Tyr Ile Ala Pro Lys Ser Asn Ile Leu Val Leu Val Gln Tyr Pro
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Asp Arg Ser Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser
1130 1135 1140

eolf-seql

Val Ser Asp Lys Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn
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Ile Met Phe His Met Leu Tyr Asn Ser Gly Lys Tyr Met Ile Ile
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Arg Asp Thr Asp Thr Ile Tyr Ala Ile Glu Gly Arg Glu Cys Ser
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Lys Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn Leu Gly Asn
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Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Met Lys Asn Thr Met
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Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Glu Asn
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Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu
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gagttttaca tacctgcact cggtgtattt accttttata gttctattca agaaagagag	2040
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cagaatgaaa atattgtata taatgctatg tatgaaagtt ttagtattag tttttggatt	2820
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eolf-seql

gaaaatagtg aacaagatat aaacttttagt tatgatatat caaagaatgc tgcgggatat 3000
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aatggaaaat taatagatac tataaaaagtt aaagagttaa ctggaattaa ttttagcaaa 3120
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<211> 1285

<212> PRT

<213> Clostridium botulinum

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Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile Thr Thr
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eolf-seql

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

eolf-seql

Ile Ala Leu Met His Glu Leu Thr His Ser Leu His Gln Leu Tyr Gly
225 230 235 240

Ile Asn Ile Pro Ser Asp Lys Arg Ile Arg Pro Gln Val Ser Glu Gly
245 250 255

Phe Phe Ser Gln Asp Gly Pro Asn Val Gln Phe Glu Glu Leu Tyr Thr
260 265 270

Phe Gly Gly Ser Asp Val Glu Ile Ile Pro Gln Ile Glu Arg Leu Gln
275 280 285

Leu Arg Glu Lys Ala Leu Gly His Tyr Lys Asp Ile Ala Lys Arg Leu
290 295 300

Asn Asn Ile Asn Lys Thr Ile Pro Ser Ser Trp Ser Ser Asn Ile Asp
305 310 315 320

Lys Tyr Lys Lys Ile Phe Ser Glu Lys Tyr Asn Phe Asp Lys Asp Asn
325 330 335

Thr Gly Asn Phe Val Val Asn Ile Asp Lys Phe Asn Ser Leu Tyr Ser
340 345 350

Asp Leu Thr Asn Val Met Ser Glu Val Val Tyr Ser Ser Gln Tyr Asn
355 360 365

Val Lys Asn Arg Thr His Tyr Phe Ser Lys His Tyr Leu Pro Val Phe
370 375 380

Ala Asn Ile Leu Asp Asp Asn Ile Tyr Thr Ile Ile Asn Gly Phe Asn
385 390 395 400

Leu Thr Thr Lys Gly Phe Asn Ile Glu Asn Ser Gly Gln Asn Ile Glu
405 410 415

eolf-seq1

Arg Asn Pro Ala Leu Gln Lys Leu Ser Ser Glu Ser Val Val Asp Leu
420 425 430

Phe Thr Lys Val Cys Leu Arg Leu Thr Arg Asn Ser Arg Asp Asp Ser
435 440 445

Thr Cys Ile Gln Val Lys Asn Asn Thr Leu Pro Tyr Val Ala Asp Lys
450 455 460

Asp Ser Ile Ser Gln Glu Ile Phe Glu Ser Gln Ile Ile Thr Asp Glu
465 470 475 480

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

Leu Asp Ala Lys Val Pro Thr Asn Pro Glu Ala Val Asp Pro Leu Leu
500 505 510

Pro Asn Val Asn Met Glu Pro Leu Asn Val Pro Gly Glu Glu Glu Val
515 520 525

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

Tyr Leu Glu Ala Gln Lys Leu Ser Asn Asn Val Glu Asn Ile Thr Leu
545 550 555 560

Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys Ile Tyr Thr
565 570 575

Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val Gln Ala Gly
580 585 590

Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe Thr Thr Asn
595 600 605

eolf-seq1

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

Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser Ala Leu Arg
625 630 635 640

Gly Asn Phe Lys Gln Ala Phe Ala Thr Ala Gly Val Ala Phe Leu Leu
645 650 655

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

Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr Ile Glu Asn
675 680 685

Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr Gln Trp Met
690 695 700

Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Arg Phe Asn His Ile Ser
705 710 715 720

Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala Ile Lys Ala
725 730 735

Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn
740 745 750

Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile
755 760 765

Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val
770 775 780

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

eolf-seql

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

His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys Ala Lys Val
820 825 830

Asn Glu Ser Phe Glu Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr
835 840 845

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

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

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

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

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

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

Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn
945 950 955 960

Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr
965 970 975

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

eolf-seql

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

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

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

Ser Lys Thr Ile Thr Phe Gln Met Asn Lys Ile Pro Asn Thr Gly
 1040 1045 1050

Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp
 1055 1060 1065

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

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

Gly Asn Asp Leu Arg Tyr Asp Lys Glu Tyr Tyr Met Ile Asn Val
 1100 1105 1110

Asn Tyr Met Asn Arg Tyr Met Ser Lys Lys Gly Asn Gly Ile Val
 1115 1120 1125

Phe Asn Thr Arg Lys Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys
 1130 1135 1140

Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg Val
 1145 1150 1155

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

eolf-seql

Gln Tyr Ser Leu Gly Met Tyr Lys Pro Ser Arg Asn Leu Gly Thr
1175 1180 1185

Asp Leu Val Pro Leu Gly Ala Leu Asp Gln Pro Met Asp Glu Ile
1190 1195 1200

Arg Lys Tyr Gly Ser Phe Ile Ile Gln Pro Cys Asn Thr Phe Asp
1205 1210 1215

Tyr Tyr Ala Ser Gln Leu Phe Leu Ser Ser Asn Ala Thr Thr Asn
1220 1225 1230

Arg Leu Gly Ile Leu Ser Ile Gly Ser Tyr Ser Phe Lys Leu Gly
1235 1240 1245

Asp Asp Tyr Trp Phe Asn His Glu Tyr Leu Ile Pro Val Ile Lys
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Ile Glu His Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp
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Val Phe Val Pro Ala Ser Glu
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<212> DNA

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ataattccag agagaaatgt aattggtaca accccccaag attttcatcc gcctacttca 180

ttaaaaaatg gagatagtag ttattatgac cctaattatt tacaaagtga tgaagaaaag 240

gatagatttt taaaaatagt cacaaaaata tttaatagaa taaataataa tctttcagga 300

eolf-seq1

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eolf-seq1

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ttaattccta caatttttagt attcacgata aaatcttttt taggttcatc tgataataaa	1980
aataaagtta ttaaagcaat aaataatgca ttgaaagaaa gagatgaaaa atggaaagaa	2040
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eolf-seql

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<212> PRT

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Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
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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

eolf-seql

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

eolf-seq1

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
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Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr
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eolf-seq1

Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala
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Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala
485 490 495

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

Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val
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

eolf-seq1

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

eolf-seq1

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

Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
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

eolf-seql

Thr	Arg	Tyr	Ile	Gly	Ile	Arg	Tyr	Phe	Asn	Ile	Phe	Asp	Lys	Glu
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eolf-seql

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seql

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eolf-seql

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eolf-seql

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eolf-seql

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3894

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 <212> PRT
 <213> Clostridium botulinum

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<400> 14

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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			

eolf-seql

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

eolf-seql

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

eolf-seql

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

eolf-seq1

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

eolf-seql

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

eolf-seql

Trp	Ile	Gln	Ser	Ser	Thr	Asn	Thr	Leu	Lys	Asp	Phe	Trp	Gly	Asn
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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
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eolf-seql

Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
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Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu
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Gly Trp Thr Glu
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<212> DNA

<213> Clostridium tetani

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eolf-seq1

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eolf-seq1

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eolf-seql

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<400> 16

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 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

eolf-seql

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

eolf-seql

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

eolf-seql

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

eolf-seql

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

eolf-seql

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
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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
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Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn
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Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys
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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

eolf-seql

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

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1145 1150 1155

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

eolf-seql

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