

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS FOR INDUCING IMMUNE RESPONSES AGAINST
CLOSTRIDIUM DIFFICILE

<130> NOV-058/02WO

<150> US 62/474,434
<151> 2017-03-21

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<151> 2017-03-16

<160> 28

<170> PatentIn version 3.5

<210> 1
<211> 1813
<212> PRT
<213> Artificial Sequence

<220>
<223> Triple toxin vaccine BV1470

<220>
<221> misc_feature
<222> (588)..(588)
<223> Xaa can be any naturally occurring amino acid

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp	Val	Leu	Met	Gln	Val	Asn	Thr	Glu	Ser	Thr	Ile	Ser	Asn	Thr	Leu
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Lys	Val	Asn	Met	Lys	Lys	Gly	Lys	Glu	Tyr	Lys	Val	Arg	Ile	Glu	Leu
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Gln	Asp	Lys	Asn	Leu	Gly	Ser	Ile	Asp	Asn	Leu	Ser	Ser	Pro	Asn	Leu
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Tyr	Trp	Glu	Leu	Asp	Gly	Met	Lys	Lys	Ile	Ile	Pro	Glu	Glu	Asn	Leu
	130					135					140				
Phe	Leu	Arg	Asp	Tyr	Ser	Asn	Ile	Glu	Lys	Asp	Asp	Pro	Phe	Ile	Pro
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Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu
				165					170					175	
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn
			180					185					190		
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe
		195					200					205			
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn
	210					215					220				
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe
225					230					235					240
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr
				245					250					255	
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu
			260					265					270		
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn
		275					280					285			
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr
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Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
 305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
 325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
 340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
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Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
 370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
 385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
 405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
 420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
 450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
 465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
 485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
 500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
 515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
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Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr
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Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

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

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser
835 840 845

Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val
850 855 860

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

Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn
885 890 895

Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe
900 905 910

Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu
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Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr
930 935 940

Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly
945 950 955 960

Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu
965 970 975

Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met
980 985 990

Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp
995 1000 1005

Ser	Gly	Val	Met	Lys	Val	Gly	Tyr	Thr	Glu	Ile	Asp	Gly	Lys	His
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Phe	Tyr	Phe	Ala	Glu	Asn	Gly	Glu	Met	Gln	Ile	Gly	Val	Phe	Asn
1025						1030					1035			
Thr	Glu	Asp	Gly	Phe	Lys	Tyr	Phe	Ala	His	His	Asn	Glu	Asp	Leu
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Gly	Asn	Glu	Glu	Gly	Glu	Glu	Ile	Ser	Tyr	Ser	Gly	Ile	Leu	Asn
1055						1060					1065			
Phe	Asn	Asn	Lys	Ile	Tyr	Tyr	Phe	Asp	Asp	Ser	Phe	Thr	Ala	Val
1070						1075					1080			
Val	Gly	Trp	Lys	Asp	Leu	Glu	Asp	Gly	Ser	Lys	Tyr	Tyr	Phe	Asp
1085						1090					1095			
Glu	Asp	Thr	Ala	Glu	Ala	Tyr	Ile	Gly	Leu	Ser	Leu	Ile	Asn	Asp
1100						1105					1110			
Gly	Gln	Tyr	Tyr	Phe	Asn	Asp	Asp	Gly	Ile	Met	Gln	Val	Gly	Phe
1115						1120					1125			
Val	Thr	Ile	Asn	Asp	Lys	Val	Phe	Tyr	Phe	Ser	Asp	Ser	Gly	Ile
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Ile	Glu	Ser	Gly	Val	Gln	Asn	Ile	Asp	Asp	Asn	Tyr	Phe	Tyr	Ile
1145						1150					1155			
Asp	Asp	Asn	Gly	Ile	Val	Gln	Ile	Gly	Val	Phe	Asp	Thr	Ser	Asp
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Gly	Tyr	Lys	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Val	Asn	Asp	Asn	Ile
1175						1180					1185			
Tyr	Gly	Gln	Ala	Val	Glu	Tyr	Ser	Gly	Leu	Val	Arg	Val	Gly	Glu
1190						1195					1200			
Asp	Val	Tyr	Tyr	Phe	Gly	Glu	Thr	Tyr	Thr	Ile	Glu	Thr	Gly	Trp
1205						1210					1215			

Ile	Tyr	Asp	Met	Glu	Asn	Glu	Ser	Asp	Lys	Tyr	Tyr	Phe	Asn	Pro
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Glu	Thr	Lys	Lys	Ala	Cys	Lys	Gly	Ile	Asn	Leu	Ile	Asp	Asp	Ile
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Lys	Tyr	Tyr	Phe	Asp	Glu	Lys	Gly	Ile	Met	Arg	Thr	Gly	Leu	Ile
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Ser	Phe	Glu	Asn	Asn	Asn	Tyr	Tyr	Phe	Asn	Glu	Asn	Gly	Glu	Met
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Gln	Phe	Gly	Tyr	Ile	Asn	Ile	Glu	Asp	Lys	Met	Phe	Tyr	Phe	Gly
1280						1285					1290			
Glu	Asp	Gly	Val	Met	Gln	Ile	Gly	Val	Phe	Asn	Thr	Pro	Asp	Gly
1295						1300					1305			
Phe	Lys	Tyr	Phe	Ala	His	Gln	Asn	Thr	Leu	Asp	Glu	Asn	Phe	Glu
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Gly	Glu	Ser	Ile	Asn	Tyr	Thr	Gly	Trp	Leu	Asp	Leu	Asp	Glu	Lys
1325						1330					1335			
Arg	Tyr	Tyr	Phe	Thr	Asp	Glu	Tyr	Ile	Ala	Ala	Thr	Gly	Ser	Val
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Ile	Ile	Asp	Gly	Glu	Glu	Tyr	Tyr	Phe	Asp	Pro	Asp	Thr	Ala	Gln
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Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu
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Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp
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Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Phe
1475						1480					1485			
Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ser	Ile	Asn	Gly	Lys	His	Phe	Tyr
1490						1495					1500			
Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro
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Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn
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Ile	Glu	Gly	Gln	Ala	Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu
1535						1540					1545			
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1550						1555					1560			
Gly	Leu	Arg	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn
1565						1570					1575			
Thr	Ala	Val	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys
1580						1585					1590			
Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr
1595						1600					1605			
Ile	Ile	Ser	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met
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Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro	Asp	Gly	Phe	Glu	Tyr	Phe	Ala
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Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Arg
1640						1645					1650			

Tyr	Gln	Asn	Arg	Phe	Leu	Tyr	Leu	His	Asp	Asn	Ile	Tyr	Tyr	Phe
1655						1660					1665			
Gly	Asn	Asn	Ser	Lys	Ala	Ala	Thr	Gly	Trp	Val	Thr	Ile	Asp	Gly
1670						1675					1680			
Asn	Arg	Tyr	Tyr	Phe	Glu	Pro	Asn	Thr	Ala	Met	Gly	Ala	Asn	Gly
1685						1690					1695			
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1700						1705					1710			
Pro	Gln	Ile	Gly	Val	Phe	Lys	Gly	Ser	Asn	Gly	Phe	Glu	Tyr	Phe
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Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile
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1745						1750					1755			
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1775						1780					1785			
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Asp	Ile	Leu	Pro	Asn	Asn	Gly	Leu	Met	Gly	Tyr	Tyr	Phe	Thr	Asp
			10					15					20	Glu
His	Phe	Lys	Asp	Leu	Lys	Leu	Met	Ala	Pro	Ile	Lys	Asp	Gly	Asn
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Lys	Phe	Glu	Glu	Lys	Lys	Val	Asp	Lys	Leu	Leu	Asp	Lys	Asp	Lys
		40				45					50			Ser
Asp	Val	Lys	Ser	Ile	Arg	Trp	Thr	Gly	Arg	Ile	Ile	Pro	Ser	Lys
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Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp Asp Val Leu Met Gln Val
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Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu Lys Val Asn Met Lys Lys
90 95 100

Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu Gln Asp Lys Asn Leu Gly
105 110 115

Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu Tyr Trp Glu Leu Asp Gly
120 125 130

Met Lys Lys Ile Ile Pro Glu Glu Asn Leu Phe Leu Arg Asp Tyr Ser
135 140 145 150

Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro Asn Asn Asn Phe Phe Asp
155 160 165

Pro Lys Leu Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn
170 175 180

Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn Gly Tyr Thr Ile Lys Asp
185 190 195

Leu Ile Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys
200 205 210

Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr
215 220 225 230

Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe Asp Lys Ala Ile Lys Thr
235 240 245

Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly
250 255 260

Met Glu Lys Leu Ile Ile Ser Thr Asn Glu His Ala Ser Thr Asp Gln
265 270 275

Gly Lys Thr Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn
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Thr Ala Gly Val Ser Val Asn Val Gly Tyr Gln Asn Gly Phe Thr Ala
 295 300 305 310

Asn Val Thr Thr Asn Tyr Ser His Thr Thr Asp Asn Ser Thr Ala Val
 315 320 325

Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys
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Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val Arg Tyr Tyr Asn Thr Gly
 345 350 355

Thr Ala Pro Met Tyr Lys Val Thr Pro Thr Thr Asn Leu Val Leu Asp
 360 365 370

Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln Glu Asn Gln Ile Gly Asn
 375 380 385 390

Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys Lys Gly Leu Ser Pro Leu
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Ala Leu Asn Thr Met Asp Gln Phe Ser Ser Arg Leu Ile Pro Ile Asn
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Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly Lys Gln Ile Lys Leu Glu
 425 430 435

Thr Thr Gln Val Ser Gly Asn Phe Gly Thr Lys Asn Ser Ser Gly Gln
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Ile Val Thr Glu Gly Asn Ser Trp Ser Asp Tyr Ile Ser Gln Ile Asp
 455 460 465 470

Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr Glu Asn Glu Ser Tyr Glu
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Arg Arg Val Thr Ala Lys Asn Leu Gln Asp Pro Glu Asp Lys Thr Pro
 490 495 500

Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys Ala Phe Gly Ala Thr Lys
 505 510 515

Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile Pro Ile Asp Glu Ser Cys
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Val Glu Leu Ile Phe Asp Asp Asn Thr Ala Asn Lys Ile Lys Asp Ser
535 540 545 550

Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr Asn Val Lys Leu Glu Arg
555 560 565

Gly Met Asn Ile Leu Ile Lys Thr Pro Thr Tyr Phe Thr Asn Phe Asp
570 575 580

Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser Asn Val Asn Thr Thr Asn
585 590 595

Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys Leu Asn Gly Glu Thr Lys
600 605 610

Ile Lys Ile Pro Met Ser Glu Leu Lys Pro Tyr Lys Arg Tyr Val Phe
615 620 625 630

Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser Asn Ser Ile Ile Val Lys
635 640 645

Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr Leu Val Pro Glu Gln Gly
650 655 660

Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr Thr Glu Lys Asp Ser Ser
665 670 675

Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly Thr Thr Tyr Leu Asp Asn
680 685 690

Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro Glu Ile Leu Asp Glu Pro
695 700 705 710

Glu Val Lys Ile Pro Thr Asp Gln Glu Ile Met Asp Ala His Lys Ile
715 720 725

Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser Thr Gly Asn Thr Tyr Ile
730 735 740

Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr Asn Lys Glu Ala Leu Asp
745 750 755

Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr Leu Gln Tyr Ser Gly Phe
760 765 770

Lys Asp Ile Gly Thr Lys Asp Lys Glu Met Arg Asn Tyr Leu Gly Asp
775 780 785 790

Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn Leu Arg Ser Tyr Phe Thr
795 800 805

Gly Gly Glu Asn Ile Met Thr Tyr Lys Lys Leu Arg Ile Tyr Ala Ile
810 815 820

Thr Pro Asp Asp Arg Glu Leu Leu Val Leu Ser Val Asp Ala Ser Met
825 830 835

Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys Pro
840 845 850

Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp Lys
855 860 865 870

Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr
875 880 885

Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu Gln
890 895 900

Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala
905 910 915

Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly
920 925 930

Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr Arg
935 940 945 950

Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser
955 960 965

Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr
970 975 980

Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser
985 990 995

Ile	Asn	Asp	Asn	Lys	His	Tyr	Phe	Asp	Asp	Ser	Gly	Val	Met	Lys
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Val	Gly	Tyr	Thr	Glu	Ile	Asp	Gly	Lys	His	Phe	Tyr	Phe	Ala	Glu
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Asn	Gly	Glu	Met	Gln	Ile	Gly	Val	Phe	Asn	Thr	Glu	Asp	Gly	Phe
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Lys	Tyr	Phe	Ala	His	His	Asn	Glu	Asp	Leu	Gly	Asn	Glu	Glu	Gly
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Glu	Glu	Ile	Ser	Tyr	Ser	Gly	Ile	Leu	Asn	Phe	Asn	Asn	Lys	Ile
	1060					1065					1070			
Tyr	Tyr	Phe	Asp	Asp	Ser	Phe	Thr	Ala	Val	Val	Gly	Trp	Lys	Asp
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Leu	Glu	Asp	Gly	Ser	Lys	Tyr	Tyr	Phe	Asp	Glu	Asp	Thr	Ala	Glu
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Ala	Tyr	Ile	Gly	Leu	Ser	Leu	Ile	Asn	Asp	Gly	Gln	Tyr	Tyr	Phe
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Asn	Asp	Asp	Gly	Ile	Met	Gln	Val	Gly	Phe	Val	Thr	Ile	Asn	Asp
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Lys	Val	Phe	Tyr	Phe	Ser	Asp	Ser	Gly	Ile	Ile	Glu	Ser	Gly	Val
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Gln	Asn	Ile	Asp	Asp	Asn	Tyr	Phe	Tyr	Ile	Asp	Asp	Asn	Gly	Ile
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Val	Gln	Ile	Gly	Val	Phe	Asp	Thr	Ser	Asp	Gly	Tyr	Lys	Tyr	Phe
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Glu	Tyr	Ser	Gly	Leu	Val	Arg	Val	Gly	Glu	Asp	Val	Tyr	Tyr	Phe
	1195					1200					1205			

Gly	Glu	Thr	Tyr	Thr	Ile	Glu	Thr	Gly	Trp	Ile	Tyr	Asp	Met	Glu
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Cys	Lys	Gly	Ile	Asn	Leu	Ile	Asp	Asp	Ile	Lys	Tyr	Tyr	Phe	Asp
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Glu	Lys	Gly	Ile	Met	Arg	Thr	Gly	Leu	Ile	Ser	Phe	Glu	Asn	Asn
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1270						1275					1280			
Asn	Ile	Glu	Asp	Lys	Met	Phe	Tyr	Phe	Gly	Glu	Asp	Gly	Val	Met
1285						1290					1295			
Gln	Ile	Gly	Val	Phe	Asn	Thr	Pro	Asp	Gly	Phe	Lys	Tyr	Phe	Ala
1300						1305					1310			
His	Gln	Asn	Thr	Leu	Asp	Glu	Asn	Phe	Glu	Gly	Glu	Ser	Ile	Asn
1315						1320					1325			
Tyr	Thr	Gly	Trp	Leu	Asp	Leu	Asp	Glu	Lys	Arg	Tyr	Tyr	Phe	Thr
1330						1335					1340			
Asp	Glu	Tyr	Ile	Ala	Ala	Thr	Gly	Ser	Val	Ile	Ile	Asp	Gly	Glu
1345						1350					1355			
Glu	Tyr	Tyr	Phe	Asp	Pro	Asp	Thr	Ala	Gln	Leu	Val	Ile	Ser	Glu
1360						1365					1370			
Ser	Arg	Met	Val	Thr	Gly	Val	Phe	Lys	Gly	Pro	Asn	Gly	Phe	Glu
1375						1380					1385			
Tyr	Phe	Ala	Pro	Ala	Asn	Thr	His	Asn	Asn	Asn	Ile	Glu	Gly	Gln
1390						1395					1400			
Ala	Ile	Val	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys
1405						1410					1415			
Tyr	Tyr	Phe	Asp	Asn	Asp	Ser	Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr
1420						1425					1430			

Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala
	1435													
Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn
	1450													
Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly
	1465													
Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Phe	Ile	Ala	Ser	Thr	Gly
	1480													
Tyr	Thr	Ser	Ile	Asn	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly
	1495													
Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro	Asn	Gly	Phe	Glu	Tyr
	1510													
Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala
	1525													
Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys	Tyr
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Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly	Leu	Arg	Thr	Ile
	1555													
Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ala	Val	Ala	Val
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Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr
	1585													
Asn	Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile	Ile	Ser	Gly	Lys
	1600													
His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe
	1615													
Lys	Gly	Pro	Asp	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp
	1630													

Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Arg	Tyr	Gln	Asn	Arg	Phe
1645						1650					1655			
Leu	Tyr	Leu	His	Asp	Asn	Ile	Tyr	Tyr	Phe	Gly	Asn	Asn	Ser	Lys
1660						1665					1670			
Ala	Ala	Thr	Gly	Trp	Val	Thr	Ile	Asp	Gly	Asn	Arg	Tyr	Tyr	Phe
1675						1680					1685			
Glu	Pro	Asn	Thr	Ala	Met	Gly	Ala	Asn	Gly	Tyr	Lys	Thr	Ile	Asp
1690						1695					1700			
Asn	Lys	Asn	Phe	Tyr	Phe	Arg	Asn	Gly	Leu	Pro	Gln	Ile	Gly	Val
1705						1710					1715			
Phe	Lys	Gly	Ser	Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr
1720						1725					1730			
Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Arg	Tyr	Gln	Asn	Arg
1735						1740					1745			
Phe	Leu	His	Leu	Leu	Gly	Lys	Ile	Tyr	Tyr	Phe	Gly	Asn	Asn	Ser
1750						1755					1760			
Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Val	Tyr	Tyr
1765						1770					1775			
Phe	Met	Pro	Asp	Thr	Ala	Met	Ala	Ala	Ala	Gly	Gly	Leu	Phe	Glu
1780						1785					1790			
Ile	Asp	Gly	Val	Ile	Tyr	Phe	Phe	Gly	Val	Asp	Gly	Val	Lys	Ala
1795						1800					1805			
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1810														

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 <213> Clostridium difficile

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 <223> Xaa can be any naturally occurring amino acid

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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe
 225 230 235 240

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
 245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
 260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
 275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
 290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
 305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
 325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
 340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
 355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
 370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
 385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
 405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
 420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp

450		455		460
Tyr 465	Ile Ser Gln Ile Asp 470	Ser Ile Ser Ala Ser 475	Ile Ile Leu Asp 480	Thr
Glu	Asn Glu Ser Tyr 485	Glu Arg Arg Val Thr 490	Ala Lys Asn Leu Gln Asp 495	
Pro	Glu Asp Lys 500	Thr Pro Glu Leu Thr 505	Ile Gly Glu Ala Ile Glu Lys 510	
Ala	Phe Gly Ala Thr Lys Lys Asp 515	Gly Leu Leu Tyr Phe Asn Asp 520	Ile	
Pro	Ile Asp Glu Ser Cys 530	Val Glu Leu Ile Phe Asp 535	Asp Asn Thr Ala 540	
Asn 545	Lys Ile Lys Asp Ser 550	Leu Lys Thr Leu Ser Asp 555	Lys Lys Ile Tyr 560	
Asn	Val Lys Leu Glu 565	Arg Gly Met Asn 570	Ile Leu Ile Lys Thr Pro Thr 575	
Tyr	Phe Thr Asn 580	Phe Asp Asp Tyr Asn 585	Asn Tyr Xaa Ser Thr Trp Ser 590	
Asn	Val Asn Thr Thr Asn 595	Gln Asp Gly Leu Gln Gly 600	Ser Ala Asn Lys 605	
Leu	Asn Gly Glu Thr Lys 610	Ile Lys Ile Pro Met 615	Ser Glu Leu Lys Pro 620	
Tyr 625	Lys Arg Tyr Val Phe 630	Ser Gly Tyr Ser Lys 635	Asp Pro Leu Thr Ser 640	
Asn	Ser Ile Ile Val Lys 645	Ile Lys Ala Lys 650	Glu Glu Lys Thr Asp Tyr 655	
Leu	Val Pro Glu Gln Gly Tyr Thr 660	Lys Phe Ser Tyr Glu Phe Glu Thr 665		
Thr	Glu Lys Asp Ser Ser Asn 675	Ile Glu Ile Thr Leu Ile Gly Ser Gly 680		

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp
835

<210> 3
<211> 536
<212> PRT
<213> Clostridium difficile

<400> 3

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Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
35 40 45

Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
 275 280 285

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
 290 295 300

Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
 305 310 315 320

Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
 325 330 335

Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
 340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
 355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
 370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
 385 390 395 400

Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
 405 410 415

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
 420 425 430

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
 435 440 445

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
 450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
 465 470 475 480

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

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
 500 505 510

Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
515 520 525

Thr Ala Gln Leu Val Ile Ser Glu
530 535

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<211> 438
<212> PRT
<213> Clostridium difficile

<400> 4

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Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
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Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
35 40 45

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

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys

				165						170					175
Lys	Tyr	Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly	Leu	Arg	Thr
			180					185					190		
Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ala	Val	Ala	Val
		195					200					205			
Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn
	210					215					220				
Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile	Ile	Ser	Gly	Lys	His	Phe
225					230					235					240
Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro
				245					250					255	
Asp	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile
			260					265					270		
Glu	Gly	Gln	Ala	Ile	Arg	Tyr	Gln	Asn	Arg	Phe	Leu	Tyr	Leu	His	Asp
		275					280					285			
Asn	Ile	Tyr	Tyr	Phe	Gly	Asn	Asn	Ser	Lys	Ala	Ala	Thr	Gly	Trp	Val
	290					295					300				
Thr	Ile	Asp	Gly	Asn	Arg	Tyr	Tyr	Phe	Glu	Pro	Asn	Thr	Ala	Met	Gly
305					310					315					320
Ala	Asn	Gly	Tyr	Lys	Thr	Ile	Asp	Asn	Lys	Asn	Phe	Tyr	Phe	Arg	Asn
				325					330					335	
Gly	Leu	Pro	Gln	Ile	Gly	Val	Phe	Lys	Gly	Ser	Asn	Gly	Phe	Glu	Tyr
			340					345					350		
Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile
		355					360					365			
Arg	Tyr	Gln	Asn	Arg	Phe	Leu	His	Leu	Leu	Gly	Lys	Ile	Tyr	Tyr	Phe
	370					375					380				
Gly	Asn	Asn	Ser	Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys
385					390					395					400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
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Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys
420 425 430

Ala Pro Gly Ile Tyr Gly
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<220>
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<223> n is a, c, g, or t

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gttgctgtga ccggctggca gactatcaac ggaaagaagt attatttcaa taccaacact	4800
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<210> 6
 <211> 2505
 <212> DNA
 <213> Clostridium difficile

<220>
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 <222> (1763)..(1763)
 <223> n is a, c, g, or t

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gaggaaaaga aggtcgataa gctgctcgac aaggataaga gcgacgttaa gtcaatcagg	180
tggaccggca gaatcatccc atccaaggat ggagagtaca ctctctctac agaccgtgac	240
gatgtcttga tgcaggtgaa caccgaatcg actatctcca acactctgaa ggtgaacatg	300

aagaagggaa aggagtacaa ggtgcgcatc gaactgcaag ataagaacct cggttctatc	360
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ctgagatcat acttcactgg tggcgagaac atcatgacat acaagaagct gcgtatctac	2460
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 <211> 1608
 <212> DNA
 <213> Clostridium difficile

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gggtggcgctg cctccatcgg cgagaccatc atcgacgata agaactacta cttcaaccag	180
agcggagttc tccaaactgg tgtgttctca acagaggacg gtttcaagta cttcgctccg	240
gccaacacct tggacgaaaa cctggagggt gaagccatcg acttcactgg caagttgatc	300
atcgatgaga acatctacta cttcgacgat aactaccgcg gtgctgtgga gtggaaggaa	360
ctcgacggcg agatgcacta cttctctcca gaaaccggca aggccttcaa gggattgaac	420
cagatcgggtg actacaagta ctacttcaac tcggatggcg tgatgcaaaa gggattcgtc	480
tccatcaacg acaacaagca ctacttcgac gattccggtg ttatgaaagt gggctacaca	540
gagatcgacg gcaagcactt ctacttcgct gagaacggag aaatgcagat cggtgtcttc	600
aacactgaag atggtttcaa gtacttcgcc caccacaacg aagatttggg caacgaggaa	660
ggagaggaaa tcagctactc aggcattcctg aacttcaaca acaagatcta ctacttcgat	720
gactctttca ccgctgtggt cggatggaag gacctggagg atggtagcaa gtactacttc	780
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aagaggctact acttcaccga cgaatacatc gctgccactg gtcctgcat catcgacgga	1560
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<210> 8
 <211> 1317
 <212> DNA
 <213> Clostridium difficile

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ggcaagaagt attattttga caacgattct aaggccgtta ctggctggca aacaatcgac	180
ggaaagaagt attatttcaa tctgaacact gccgaggctg ccaccggttg gcagactatc	240
gatggcaaga agtactactt taacctcaac actgccgaag ctgccacagg atggcaaacc	300
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agcatcaacg gaaagcattt ttatttcaac accgatggaa tcatgcagat cgggtgtgttc	420
aaggggaccaa acggttttga atacttcgct ccggctaaca cagacgctaa caacatcgag	480
ggccaggcta tcttgtacca aaacaagttc ctcactttga acggcaagaa gtactatttt	540
ggctctgaca gcaaggccgt cactggactg aggacaatcg atggcaagaa gtactacttt	600
aatactaaca cagccgttgc tgtgaccggc tggcagacta tcaacggaaa gaagtattat	660
ttcaatacca acacttcaat cgcttcgacc ggttacacta tcattctctgg caagcatttt	720
tatttttaaca ccgacggcat catgcaaatc ggtgtcttca agggccccga tggcttcgaa	780
tacttcgccc ccgctaacac tgatgctaac aacatcgagg gacaggctat ccgttaccaa	840
aaccgcttcc tgtacctcca cgacaacatc tactacttcg gcaacaactc aaaggctgcc	900
acaggatggg tgaccatcga tggtaacctg tactacttcg agcccaacac tgccatgggt	960

gctaacggct acaagacaat cgacaacaag aacttctact tccgcaacgg tctcccacag 1020
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aacaacatcg agggccaagc tatcaggtac caaaacagat tcctgcacct gctcggcaag 1140
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gtgtactact tcatgccaga caccgctatg gctgccgctg gtggcctctt cgaaatcgac 1260
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<210> 9
<211> 1820
<212> PRT
<213> Artificial Sequence

<220>
<223> Triple toxin vaccine BV1420

<220>
<221> misc_feature
<222> (595)..(595)
<223> Xaa can be any naturally occurring amino acid

<400> 9

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Tyr	Tyr	Phe	Thr	Asp	Glu	His	Phe	Lys	Asp	Leu	Lys	Leu	Met	Ala	Pro
			20					25					30		

Ile	Lys	Asp	Gly	Asn	Leu	Lys	Phe	Glu	Glu	Lys	Lys	Val	Asp	Lys	Leu
		35					40					45			

Leu	Asp	Lys	Asp	Lys	Ser	Asp	Val	Lys	Ser	Ile	Arg	Trp	Thr	Gly	Arg
	50					55					60				

Ile	Ile	Pro	Ser	Lys	Asp	Gly	Glu	Tyr	Thr	Leu	Ser	Thr	Asp	Arg	Asp
65					70					75				80	

Asp	Val	Leu	Met	Gln	Val	Asn	Thr	Glu	Ser	Thr	Ile	Ser	Asn	Thr	Leu
				85					90					95	

Lys	Val	Asn	Met	Lys	Lys	Gly	Lys	Glu	Tyr	Lys	Val	Arg	Ile	Glu	Leu
			100					105					110		

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
 115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
 130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
 145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Arg Ala Arg Arg Arg Lys Lys
 165 170 175

Arg Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn Asp Asn
 180 185 190

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

Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys Lys Tyr
 210 215 220

Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr Asp Tyr
 225 230 235 240

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

Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly Met Glu Lys
 260 265 270

Leu Ile Ile Ser Thr Asn Glu His Ala Ser Thr Asp Gln Gly Lys Thr
 275 280 285

Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn Thr Ala Gly
 290 295 300

Val Ser Val Asn Val Gly Tyr Gln Asn Gly Phe Thr Ala Asn Val Thr
 305 310 315 320

Thr Asn Tyr Ser His Thr Thr Asp Asn Ser Thr Ala Val Gln Asp Ser
 325 330 335

Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys Gly Glu Ser
 340 345 350

Ala	Tyr	Ile	Asn	Ala	Asn	Val	Arg	Tyr	Tyr	Asn	Thr	Gly	Thr	Ala	Pro	355	360	365	
Met	Tyr	Lys	Val	Thr	Pro	Thr	Thr	Asn	Leu	Val	Leu	Asp	Gly	Asp	Thr	370	375	380	
Leu	Ser	Thr	Ile	Lys	Ala	Gln	Glu	Asn	Gln	Ile	Gly	Asn	Asn	Leu	Ser	385	390	395	400
Pro	Gly	Asp	Thr	Tyr	Pro	Lys	Lys	Gly	Leu	Ser	Pro	Leu	Ala	Leu	Asn	405	410	415	
Thr	Met	Asp	Gln	Phe	Ser	Ser	Arg	Leu	Ile	Pro	Ile	Asn	Tyr	Asp	Gln	420	425	430	
Leu	Lys	Lys	Leu	Asp	Ala	Gly	Lys	Gln	Ile	Lys	Leu	Glu	Thr	Thr	Gln	435	440	445	
Val	Ser	Gly	Asn	Phe	Gly	Thr	Lys	Asn	Ser	Ser	Gly	Gln	Ile	Val	Thr	450	455	460	
Glu	Gly	Asn	Ser	Trp	Ser	Asp	Tyr	Ile	Ser	Gln	Ile	Asp	Ser	Ile	Ser	465	470	475	480
Ala	Ser	Ile	Ile	Leu	Asp	Thr	Glu	Asn	Glu	Ser	Tyr	Glu	Arg	Arg	Val	485	490	495	
Thr	Ala	Lys	Asn	Leu	Gln	Asp	Pro	Glu	Asp	Lys	Thr	Pro	Glu	Leu	Thr	500	505	510	
Ile	Gly	Glu	Ala	Ile	Glu	Lys	Ala	Phe	Gly	Ala	Thr	Lys	Lys	Asp	Gly	515	520	525	
Leu	Leu	Tyr	Phe	Asn	Asp	Ile	Pro	Ile	Asp	Glu	Ser	Cys	Val	Glu	Leu	530	535	540	
Ile	Phe	Asp	Asp	Asn	Thr	Ala	Asn	Lys	Ile	Lys	Asp	Ser	Leu	Lys	Thr	545	550	555	560
Leu	Ser	Asp	Lys	Lys	Ile	Tyr	Asn	Val	Lys	Leu	Glu	Arg	Gly	Met	Asn	565	570	575	

Ile	Leu	Ile	Lys	Thr	Pro	Thr	Tyr	Phe	Thr	Asn	Phe	Asp	Asp	Tyr	Asn	
			580					585					590			
Asn	Tyr	Xaa	Ser	Thr	Trp	Ser	Asn	Val	Asn	Thr	Thr	Asn	Gln	Asp	Gly	
		595					600					605				
Leu	Gln	Gly	Ser	Ala	Asn	Lys	Leu	Asn	Gly	Glu	Thr	Lys	Ile	Lys	Ile	
	610					615					620					
Pro	Met	Ser	Glu	Leu	Lys	Pro	Tyr	Lys	Arg	Tyr	Val	Phe	Ser	Gly	Tyr	
625					630					635					640	
Ser	Lys	Asp	Pro	Leu	Thr	Ser	Asn	Ser	Ile	Ile	Val	Lys	Ile	Lys	Ala	
				645					650					655		
Lys	Glu	Glu	Lys	Thr	Asp	Tyr	Leu	Val	Pro	Glu	Gln	Gly	Tyr	Thr	Lys	
			660					665					670			
Phe	Ser	Tyr	Glu	Phe	Glu	Thr	Thr	Glu	Lys	Asp	Ser	Ser	Asn	Ile	Glu	
		675					680					685				
Ile	Thr	Leu	Ile	Gly	Ser	Gly	Thr	Thr	Tyr	Leu	Asp	Asn	Leu	Ser	Ile	
	690					695					700					
Thr	Glu	Leu	Asn	Ser	Thr	Pro	Glu	Ile	Leu	Asp	Glu	Pro	Glu	Val	Lys	
705					710					715					720	
Ile	Pro	Thr	Asp	Gln	Glu	Ile	Met	Asp	Ala	His	Lys	Ile	Tyr	Phe	Ala	
				725					730					735		
Asp	Leu	Asn	Phe	Asn	Pro	Ser	Thr	Gly	Asn	Thr	Tyr	Ile	Asn	Gly	Met	
			740					745					750			
Tyr	Phe	Ala	Pro	Thr	Gln	Thr	Asn	Lys	Glu	Ala	Leu	Asp	Tyr	Ile	Gln	
		755					760					765				
Lys	Tyr	Arg	Val	Glu	Ala	Thr	Leu	Gln	Tyr	Ser	Gly	Phe	Lys	Asp	Ile	
	770					775					780					
Gly	Thr	Lys	Asp	Lys	Glu	Met	Arg	Asn	Tyr	Leu	Gly	Asp	Pro	Asn	Gln	
785					790					795					800	
Pro	Lys	Thr	Asn	Tyr	Val	Asn	Leu	Arg	Ser	Tyr	Phe	Thr	Gly	Gly	Glu	
			805						810					815		

Asn Ile Met Thr Tyr Lys Lys Leu Arg Ile Tyr Ala Ile Thr Pro Asp
820 825 830

Asp Arg Glu Leu Leu Val Leu Ser Val Asp Ala Ser Met Val Ser Gly
835 840 845

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

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

Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp
885 890 895

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

Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu
915 920 925

Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile
930 935 940

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

Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser Pro Glu Thr
965 970 975

Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr
980 985 990

Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser Ile Asn Asp
995 1000 1005

Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys Val Gly Tyr
1010 1015 1020

Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn Gly Glu
1025 1030 1035

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

Ile	Met	Arg	Thr	Gly	Leu	Ile	Ser	Phe	Glu	Asn	Asn	Asn	Tyr	Tyr
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Phe	Asn	Glu	Asn	Gly	Glu	Met	Gln	Phe	Gly	Tyr	Ile	Asn	Ile	Glu
	1280					1285					1290			
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	1310					1315					1320			
Thr	Leu	Asp	Glu	Asn	Phe	Glu	Gly	Glu	Ser	Ile	Asn	Tyr	Thr	Gly
	1325					1330					1335			
Trp	Leu	Asp	Leu	Asp	Glu	Lys	Arg	Tyr	Tyr	Phe	Thr	Asp	Glu	Tyr
	1340					1345					1350			
Ile	Ala	Ala	Thr	Gly	Ser	Val	Ile	Ile	Asp	Gly	Glu	Glu	Tyr	Tyr
	1355					1360					1365			
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	1370					1375					1380			
Val	Thr	Gly	Val	Phe	Lys	Gly	Pro	Asn	Gly	Phe	Glu	Tyr	Phe	Ala
	1385					1390					1395			
Pro	Ala	Asn	Thr	His	Asn	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Val
	1400					1405					1410			
Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe
	1415					1420					1425			
Asp	Asn	Asp	Ser	Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly
	1430					1435					1440			
Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly
	1445					1450					1455			
Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr
	1460					1465					1470			

Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr
1475						1480					1485			
Tyr	Phe	Asn	Thr	Asn	Thr	Phe	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ser
1490						1495					1500			
Ile	Asn	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln
1505						1510					1515			
Ile	Gly	Val	Phe	Lys	Gly	Pro	Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro
1520						1525					1530			
Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Leu	Tyr
1535						1540					1545			
Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Gly
1550						1555					1560			
Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly	Leu	Arg	Thr	Ile	Asp	Gly	Lys
1565						1570					1575			
Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ala	Val	Ala	Val	Thr	Gly	Trp
1580						1585					1590			
Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ser
1595						1600					1605			
Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile	Ile	Ser	Gly	Lys	His	Phe	Tyr
1610						1615					1620			
Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro
1625						1630					1635			
Asp	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn
1640						1645					1650			
Ile	Glu	Gly	Gln	Ala	Ile	Arg	Tyr	Gln	Asn	Arg	Phe	Leu	Tyr	Leu
1655						1660					1665			
His	Asp	Asn	Ile	Tyr	Tyr	Phe	Gly	Asn	Asn	Ser	Lys	Ala	Ala	Thr
1670						1675					1680			
Gly	Trp	Val	Thr	Ile	Asp	Gly	Asn	Arg	Tyr	Tyr	Phe	Glu	Pro	Asn
1685						1690					1695			

Thr Ala Met Gly Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn
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Phe Tyr Phe Arg Asn Gly Leu Pro Gln Ile Gly Val Phe Lys Gly
 1715 1720 1725

Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn
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Asn Ile Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu His
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Leu Leu Gly Lys Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Val
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Thr Gly Trp Gln Thr Ile Asn Gly Lys Val Tyr Tyr Phe Met Pro
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Asp Thr Ala Met Ala Ala Ala Gly Gly Leu Phe Glu Ile Asp Gly
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Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys Ala Pro Gly Ile
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Tyr Gly
 1820

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 <213> Clostridium difficile

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Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
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Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
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Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
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Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
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Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
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Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Arg Ala Arg Arg Arg Lys Lys
165 170 175

Arg Met Ser Asp Trp Glu Asp Glu Asp Leu Asp Thr Asp Asn Asp Asn
180 185 190

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

Ala Val Lys Trp Glu Asp Ser Phe Ala Glu Gln Gly Tyr Lys Lys Tyr
210 215 220

Val Ser Asn Tyr Leu Glu Ser Asn Thr Ala Gly Asp Pro Tyr Asp Tyr
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Glu Lys Ala Ser Gly Ser Phe Asp Lys Ala Ile Lys Thr Glu Ala Arg
245 250 255

Asp Pro Leu Val Ala Ala Tyr Pro Ile Val Gly Val Gly Met Glu Lys

260	265	270
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Val Ser Arg Ala Thr Thr Asn Ser Lys Thr Glu Ser Asn Thr Ala Gly 290 295 300		
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Asn Gly Glu Ser Trp Asn Thr Gly Leu Ser Ile Asn Lys Gly Glu Ser 340 345 350		
Ala Tyr Ile Asn Ala Asn Val Arg Tyr Tyr Asn Thr Gly Thr Ala Pro 355 360 365		
Met Tyr Lys Val Thr Pro Thr Thr Asn Leu Val Leu Asp Gly Asp Thr 370 375 380		
Leu Ser Thr Ile Lys Ala Gln Glu Asn Gln Ile Gly Asn Asn Leu Ser 385 390 395 400		
Pro Gly Asp Thr Tyr Pro Lys Lys Gly Leu Ser Pro Leu Ala Leu Asn 405 410 415		
Thr Met Asp Gln Phe Ser Ser Arg Leu Ile Pro Ile Asn Tyr Asp Gln 420 425 430		
Leu Lys Lys Leu Asp Ala Gly Lys Gln Ile Lys Leu Glu Thr Thr Gln 435 440 445		
Val Ser Gly Asn Phe Gly Thr Lys Asn Ser Ser Gly Gln Ile Val Thr 450 455 460		
Glu Gly Asn Ser Trp Ser Asp Tyr Ile Ser Gln Ile Asp Ser Ile Ser 465 470 475 480		
Ala Ser Ile Ile Leu Asp Thr Glu Asn Glu Ser Tyr Glu Arg Arg Val 485 490 495		

Thr Ala Lys Asn Leu Gln Asp Pro Glu Asp Lys Thr Pro Glu Leu Thr
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Ile Gly Glu Ala Ile Glu Lys Ala Phe Gly Ala Thr Lys Lys Asp Gly
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Leu Leu Tyr Phe Asn Asp Ile Pro Ile Asp Glu Ser Cys Val Glu Leu
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Ile Phe Asp Asp Asn Thr Ala Asn Lys Ile Lys Asp Ser Leu Lys Thr
545 550 555 560

Leu Ser Asp Lys Lys Ile Tyr Asn Val Lys Leu Glu Arg Gly Met Asn
565 570 575

Ile Leu Ile Lys Thr Pro Thr Tyr Phe Thr Asn Phe Asp Asp Tyr Asn
580 585 590

Asn Tyr Xaa Ser Thr Trp Ser Asn Val Asn Thr Thr Asn Gln Asp Gly
595 600 605

Leu Gln Gly Ser Ala Asn Lys Leu Asn Gly Glu Thr Lys Ile Lys Ile
610 615 620

Pro Met Ser Glu Leu Lys Pro Tyr Lys Arg Tyr Val Phe Ser Gly Tyr
625 630 635 640

Ser Lys Asp Pro Leu Thr Ser Asn Ser Ile Ile Val Lys Ile Lys Ala
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Lys Glu Glu Lys Thr Asp Tyr Leu Val Pro Glu Gln Gly Tyr Thr Lys
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Phe Ser Tyr Glu Phe Glu Thr Thr Glu Lys Asp Ser Ser Asn Ile Glu
675 680 685

Ile Thr Leu Ile Gly Ser Gly Thr Thr Tyr Leu Asp Asn Leu Ser Ile
690 695 700

Thr Glu Leu Asn Ser Thr Pro Glu Ile Leu Asp Glu Pro Glu Val Lys
705 710 715 720

Ile Pro Thr Asp Gln Glu Ile Met Asp Ala His Lys Ile Tyr Phe Ala

Ala	Asn	Thr	Leu	Asp	Glu	Asn	Leu	Glu	Gly	Glu	Ala	Ile	Asp	Phe	Thr		
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Gly	Lys	Leu	Ile	Ile	Asp	Glu	Asn	Ile	Tyr	Tyr	Phe	Asp	Asp	Asn	Tyr		
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Arg	Gly	Ala	Val	Glu	Trp	Lys	Glu	Leu	Asp	Gly	Glu	Met	His	Tyr	Phe		
		115					120					125					
Ser	Pro	Glu	Thr	Gly	Lys	Ala	Phe	Lys	Gly	Leu	Asn	Gln	Ile	Gly	Asp		
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Tyr	Lys	Tyr	Tyr	Phe	Asn	Ser	Asp	Gly	Val	Met	Gln	Lys	Gly	Phe	Val		
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Val	Gly	Tyr	Thr	Glu	Ile	Asp	Gly	Lys	His	Phe	Tyr	Phe	Ala	Glu	Asn		
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Phe	Ala	His	His	Asn	Glu	Asp	Leu	Gly	Asn	Glu	Glu	Gly	Glu	Glu	Ile		
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Lys	Tyr	Tyr	Phe	Asp	Glu	Asp	Thr	Ala	Glu	Ala	Tyr	Ile	Gly	Leu	Ser		
			260					265					270				
Leu	Ile	Asn	Asp	Gly	Gln	Tyr	Tyr	Phe	Asn	Asp	Asp	Gly	Ile	Met	Gln		
		275					280					285					
Val	Gly	Phe	Val	Thr	Ile	Asn	Asp	Lys	Val	Phe	Tyr	Phe	Ser	Asp	Ser		
	290					295					300						
Gly	Ile	Ile	Glu	Ser	Gly	Val	Gln	Asn	Ile	Asp	Asp	Asn	Tyr	Phe	Tyr		
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Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
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Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
385 390 395 400

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

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
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Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
465 470 475 480

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

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
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Thr Ala Gln Leu Val Ile Ser Glu
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 <213> Clostridium difficile

<400> 12

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Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
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Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
 35 40 45

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

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
 65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
 85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
 100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
 115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
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Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
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Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
 165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
 180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
 195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
 210 215 220

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe
 225 230 235 240

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
 245 250 255

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile
 260 265 270

Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp
 275 280 285

Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val
 290 295 300

Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly
 305 310 315 320

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

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

Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
 355 360 365

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
 370 375 380

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
 385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
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<210> 14
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 <213> Clostridium difficile

<220>
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gaggaaaaga aggtcgataa gctgctcgac aaggataaga gcgacgttaa gtcaatcagg	180
tggaccggca gaatcatccc atccaaggat ggagagtaca ctctctctac agaccgtgac	240
gatgtcttga tgcaggtgaa caccgaatcg actatctcca acactctgaa ggtgaacatg	300
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gacaacctct cctctccaaa cctctactgg gagttggatg gcatgaagaa gatcatcccg	420
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gccaacacct tggacgaaaa cctggagggg gaagccatcg acttcaactgg caagttgatc	300
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ctcgacggcg agatgcacta cttctctcca gaaaccggca aggccttcaa gggattgaac	420
cagatcggtg actacaagta ctacttcaac tcggatggcg tgatgcaaaa gggattcgtc	480
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gagatcgacg gcaagcactt ctacttcgct gagaacggag aaatgcagat cggtgtcttc	600
aacactgaag atggtttcaa gtacttcgcc caccacaacg aagatttggg caacgaggaa	660
ggagaggaaa tcagctactc aggcattctg aacttcaaca acaagatcta ctacttcgat	720
gactctttca ccgctgtggg cggatggaag gacctggagg atggtagcaa gtactacttc	780
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aagaggtact acttcaccga cgaatacatc gctgccactg gctccgtcat catcgacgga	1560
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<210> 16
 <211> 1317
 <212> DNA
 <213> Clostridium difficile

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ggcaagaagt attattttga caacgattct aaggccgtta ctggctggca aacaatcgac	180
ggaaagaagt attatttcaa tctgaacact gccgaggctg ccaccggttg gcagactatc	240
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aagggaccaa acggtttcga atacttcgct ccggctaaca cagacgctaa caacatcgag	480
ggccaggcta tcttgtacca aaacaagttc ctcactttga acggcaagaa gtactatttt	540
ggctctgaca gcaaggccgt cactggactg aggacaatcg atggcaagaa gtactacttt	600
aatactaaca cagccgttgc tgtgaccggc tggcagacta tcaacggaaa gaagtattat	660
ttcaatacca acacttcaat cgcttcgacc ggttacacta tcatctcttg caagcatttt	720
tattttaaca ccgacggcat catgcaaata ggtgtcttca agggccccga tggcttcgaa	780
tacttcgccc ccgctaacac tgatgctaac aacatcgagg gacaggctat ccgttaccaa	840
aaccgcttcc tgtacctcca cgacaacatc tactacttcg gcaacaactc aaaggctgcc	900
acaggatggg tgaccatcga tggtaacgt tactacttcg agcccaacac tgccatgggt	960
gctaacggct acaagacaat cgacaacaag aacttctact tccgcaacgg tctcccacag	1020
atcggcgtct tcaagggatc aaacggtttc gagtacttcg ctcttgccaa caccgacgcc	1080
aacaacatcg agggccaagc tatcaggtac caaaacagat tcctgcacct gctcggcaag	1140

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<210> 17
 <211> 2307
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Triple toxin vaccine BV1512

<220>
 <221> misc_feature
 <222> (588)..(588)
 <223> Xaa can be any naturally occurring amino acid

<400> 17

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
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Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
 35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
 50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
 65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
 85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
 100 105 110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
 115 120 125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
 130 135 140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
 145 150 155 160

Asn Asn Asn Phe Phe Asp Pro Lys Leu Met Ser Asp Trp Glu Asp Glu
 165 170 175

Asp Leu Asp Thr Asp Asn Asp Asn Ile Pro Asp Ser Tyr Glu Arg Asn
 180 185 190

Gly Tyr Thr Ile Lys Asp Leu Ile Ala Val Lys Trp Glu Asp Ser Phe
 195 200 205

Ala Glu Gln Gly Tyr Lys Lys Tyr Val Ser Asn Tyr Leu Glu Ser Asn
 210 215 220

Thr Ala Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ser Gly Ser Phe
 225 230 235 240

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
 245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
 260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
 275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
 290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
 305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
 325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
 340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
 355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
 370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
 385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
 405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
 420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
 450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
 465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
 485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
 500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
 515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
 530 535 540

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

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
 565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
 580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
 595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

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

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Gln Glu Ile Arg Asn Asn Ser Asn Ser Ser
835 840 845

Asp Ile Glu Leu Glu Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn
850 855 860

Val Ile Ser Asn Ile Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu
865 870 875 880

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

Lys Leu Ile Glu Ser Ile Ser Asp Ala Leu Cys Asp Leu Lys Gln Gln
900 905 910

Asn Glu Leu Glu Asp Ser His Phe Ile Ser Phe Glu Asp Ile Ser Glu
915 920 925

Thr Asp Glu Gly Phe Ser Ile Arg Phe Ile Asn Lys Glu Thr Gly Glu
930 935 940

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

His Ile Thr Glu Glu Ile Ser Lys Ile Lys Gly Thr Ile Phe Asp Thr
965 970 975

Val Asn Gly Lys Leu Val Lys Lys Val Asn Leu Asp Thr Thr His Glu
980 985 990

Val Asn Thr Leu Asn Ala Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr
995 1000 1005

Asn Ser Ser Lys Glu Ser Leu Ser Asn Leu Ser Val Ala Met Lys
1010 1015 1020

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

Thr Asp Ala Ala Lys Val Val Glu Leu Val Ser Thr Ala Leu Asp
1040 1045 1050

Glu Thr Ile Asp Leu Leu Pro Thr Leu Ser Glu Gly Leu Pro Ile
1055 1060 1065

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

Ser	Leu	Glu	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Asp	Arg	Ile	Arg	Asp
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1310						1315					1320			
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1325						1330					1335			
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1340						1345					1350			
Tyr	Gly	Ser	Gly	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ser	Gln	Tyr	Asn
1355						1360					1365			
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1370						1375					1380			
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1385						1390					1395			
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1400						1405					1410			
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1415						1420					1425			
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1430						1435					1440			
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1445						1450					1455			
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1460						1465					1470			
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1475						1480					1485			
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1490						1495					1500			

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Gly	Leu	Phe	Val	Ser	Glu	Leu	Pro	Asp	Val	Val	Leu	Ile	Ser	Lys
1520						1525					1530			
Val	Tyr	Met	Asp	Asp	Ser	Lys	Pro	Ser	Phe	Gly	Tyr	Tyr	Ser	Asn
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1550						1555					1560			
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1580						1585					1590			
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1595						1600					1605			
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1610						1615					1620			
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1655						1660					1665			
Gln	Pro	Tyr	Phe	Ile	Lys	Phe	Asn	Thr	Leu	Glu	Thr	Asn	Tyr	Thr
1670						1675					1680			
Leu	Tyr	Val	Gly	Asn	Arg	Gln	Asn	Met	Ile	Val	Glu	Pro	Asn	Tyr
1685						1690					1695			
Asp	Leu	Asp	Asp	Ser	Gly	Asp	Ile	Ser	Ser	Thr	Val	Ile	Asn	Phe
1700						1705					1710			

Ser	Gln	Lys	Tyr	Leu	Tyr	Gly	Ile	Asp	Ser	Cys	Val	Asn	Lys	Val
1715						1720					1725			
Val	Ile	Ser	Pro	Asn	Ile	Tyr	Thr	Asp	Glu	Ile	Asn	Ile	Thr	Pro
1730						1735					1740			
Val	Tyr	Glu	Thr	Asn	Asn	Thr	Tyr	Pro	Glu	Val	Ile	Val	Leu	Asp
1745						1750					1755			
Ala	Asn	Tyr	Ile	Asn	Glu	Lys	Ile	Asn	Val	Asn	Ile	Asn	Asp	Leu
1760						1765					1770			
Ser	Ile	Arg	Tyr	Val	Trp	Ser	Asn	Asp	Gly	Asn	Asp	Phe	Ile	Leu
1775						1780					1785			
Met	Ser	Thr	Ser	Glu	Glu	Asn	Lys	Val	Ser	Gln	Val	Lys	Ile	Arg
1790						1795					1800			
Phe	Val	Asn	Val	Phe	Lys	Asp	Lys	Thr	Leu	Ala	Asn	Lys	Leu	Ser
1805						1810					1815			
Phe	Asn	Phe	Ser	Asp	Lys	Gln	Asp	Val	Pro	Val	Ser	Glu	Ile	Ile
1820						1825					1830			
Leu	Ser	Phe	Thr	Pro	Ser	Tyr	Tyr	Glu	Asp	Gly	Leu	Ile	Gly	Tyr
1835						1840					1845			
Asp	Leu	Gly	Leu	Val	Ser	Leu	Tyr	Asn	Glu	Lys	Phe	Tyr	Ile	Asn
1850						1855					1860			
Asn	Phe	Gly	Met	Ser	Arg	Met	Val	Thr	Gly	Val	Phe	Lys	Gly	Pro
1865						1870					1875			
Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	His	Asn	Asn	Asn
1880						1885					1890			
Ile	Glu	Gly	Gln	Ala	Ile	Val	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu
1895						1900					1905			
Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asp	Asn	Asp	Ser	Lys	Ala	Val	Thr
1910						1915					1920			
Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu	Asn
1925						1930					1935			

Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys
1940						1945					1950			
Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln
1955						1960					1965			
Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Phe	Ile
1970						1975					1980			
Ala	Ser	Thr	Gly	Tyr	Thr	Ser	Ile	Asn	Gly	Lys	His	Phe	Tyr	Phe
1985						1990					1995			
Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro	Asn
2000						2005					2010			
Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile
2015						2020					2025			
Glu	Gly	Gln	Ala	Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn
2030						2035					2040			
Gly	Lys	Lys	Tyr	Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly
2045						2050					2055			
Leu	Arg	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr
2060						2065					2070			
Ala	Val	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr
2075						2080					2085			
Tyr	Phe	Asn	Thr	Asn	Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile
2090						2095					2100			
Ile	Ser	Gly	Lys	His	Phe	Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln
2105						2110					2115			
Ile	Gly	Val	Phe	Lys	Gly	Pro	Asp	Gly	Phe	Glu	Tyr	Phe	Ala	Pro
2120						2125					2130			
Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile	Arg	Tyr
2135						2140					2145			

Gln Asn Arg Phe Leu Tyr Leu His Asp Asn Ile Tyr Tyr Phe Gly
 2150 2155 2160

Asn Asn Ser Lys Ala Ala Thr Gly Trp Val Thr Ile Asp Gly Asn
 2165 2170 2175

Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala Asn Gly Tyr
 2180 2185 2190

Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu Pro
 2195 2200 2205

Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe Ala
 2210 2215 2220

Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg
 2225 2230 2235

Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
 2240 2245 2250

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly
 2255 2260 2265

Lys Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly
 2270 2275 2280

Gly Leu Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp
 2285 2290 2295

Gly Val Lys Ala Pro Gly Ile Tyr Gly
 2300 2305

<210> 18
 <211> 835
 <212> PRT
 <213> Clostridium difficile

<220>
 <221> misc_feature
 <222> (588)..(588)
 <223> Xaa can be any naturally occurring amino acid

<400> 18

Met Glu Ile Val Asn Glu Asp Ile Leu Pro Asn Asn Gly Leu Met Gly

1		5		10		15										
Tyr	Tyr	Phe	Thr	Asp	Glu	His	Phe	Lys	Asp	Leu	Lys	Leu	Met	Ala	Pro	
			20					25					30			
Ile	Lys	Asp	Gly	Asn	Leu	Lys	Phe	Glu	Glu	Lys	Lys	Val	Asp	Lys	Leu	
		35					40					45				
Leu	Asp	Lys	Asp	Lys	Ser	Asp	Val	Lys	Ser	Ile	Arg	Trp	Thr	Gly	Arg	
	50					55					60					
Ile	Ile	Pro	Ser	Lys	Asp	Gly	Glu	Tyr	Thr	Leu	Ser	Thr	Asp	Arg	Asp	
65					70					75					80	
Asp	Val	Leu	Met	Gln	Val	Asn	Thr	Glu	Ser	Thr	Ile	Ser	Asn	Thr	Leu	
				85					90					95		
Lys	Val	Asn	Met	Lys	Lys	Gly	Lys	Glu	Tyr	Lys	Val	Arg	Ile	Glu	Leu	
			100					105					110			
Gln	Asp	Lys	Asn	Leu	Gly	Ser	Ile	Asp	Asn	Leu	Ser	Ser	Pro	Asn	Leu	
		115					120					125				
Tyr	Trp	Glu	Leu	Asp	Gly	Met	Lys	Lys	Ile	Ile	Pro	Glu	Glu	Asn	Leu	
	130					135					140					
Phe	Leu	Arg	Asp	Tyr	Ser	Asn	Ile	Glu	Lys	Asp	Asp	Pro	Phe	Ile	Pro	
145					150					155					160	
Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu	
				165					170					175		
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn	
			180					185					190			
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe	
		195					200					205				
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn	
	210					215					220					
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe	
225					230					235					240	

Asp Lys Ala Ile Lys Thr Glu Ala Arg Asp Pro Leu Val Ala Ala Tyr
245 250 255

Pro Ile Val Gly Val Gly Met Glu Lys Leu Ile Ile Ser Thr Asn Glu
260 265 270

His Ala Ser Thr Asp Gln Gly Lys Thr Val Ser Arg Ala Thr Thr Asn
275 280 285

Ser Lys Thr Glu Ser Asn Thr Ala Gly Val Ser Val Asn Val Gly Tyr
290 295 300

Gln Asn Gly Phe Thr Ala Asn Val Thr Thr Asn Tyr Ser His Thr Thr
305 310 315 320

Asp Asn Ser Thr Ala Val Gln Asp Ser Asn Gly Glu Ser Trp Asn Thr
325 330 335

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr

465		470		475		480
Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp						
		485		490		495
Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys						
		500		505		510
Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile						
		515		520		525
Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala						
		530		535		540
Asn Lys Ile Lys Asp Ser Leu Lys Thr Leu Ser Asp Lys Lys Ile Tyr						
		545		550		555
Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr						
		565		570		575
Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser						
		580		585		590
Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys						
		595		600		605
Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro						
		610		615		620
Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser						
		625		630		635
Asn Ser Ile Ile Val Lys Ile Lys Ala Lys Glu Glu Lys Thr Asp Tyr						
		645		650		655
Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr						
		660		665		670
Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly						
		675		680		685
Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro						
		690		695		700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp
835

<210> 19
<211> 1030
<212> PRT
<213> Clostridium difficile

<400> 19

Met Gln Glu Ile Arg Asn Asn Ser Asn Ser Ser Asp Ile Glu Leu Glu
1 5 10 15

Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ile Ser Asn Ile
20 25 30

Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu Ala Lys Asn Leu Thr
35 40 45

Ser Asp Ser Ile Asn Tyr Ile Lys Asp Glu Phe Lys Leu Ile Glu Ser
50 55 60

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

Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro
 290 295 300

Ser Leu Val Asn Asn Glu Leu Val Leu Arg Asp Lys Ala Thr Lys Val
 305 310 315 320

Val Asp Tyr Phe Lys His Val Ser Leu Val Glu Thr Glu Gly Val Phe
 325 330 335

Thr Leu Leu Asp Asp Lys Ile Met Met Pro Gln Asp Asp Leu Val Ile
 340 345 350

Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Val Leu Gly Lys Cys Glu
 355 360 365

Ile Trp Arg Met Glu Gly Gly Ser Gly His Thr Val Thr Asp Asp Ile
 370 375 380

Asp His Phe Phe Ser Ala Pro Ser Ile Thr Tyr Arg Glu Pro His Leu
 385 390 395 400

Ser Ile Tyr Asp Val Leu Glu Val Gln Lys Glu Glu Leu Asp Leu Ser
 405 410 415

Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Ala Trp
 420 425 430

Glu Thr Gly Trp Thr Pro Gly Leu Arg Ser Leu Glu Asn Asp Gly Thr
 435 440 445

Lys Leu Leu Asp Arg Ile Arg Asp Asn Tyr Glu Gly Glu Phe Tyr Trp
 450 455 460

Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Thr Leu Lys Pro
 465 470 475 480

Arg Tyr Glu Asp Thr Asn Ile Arg Ile Asn Leu Asp Ser Asn Thr Arg
 485 490 495

Ser Phe Ile Val Pro Ile Ile Thr Thr Glu Tyr Ile Arg Glu Lys Leu
 500 505 510

Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Thr Tyr Ala Leu Ser Leu Ser
 515 520 525

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

Ile Ile Asp Val Asp Asn Val Val Arg Asp Val Thr Ile Glu Ser Asp
545 550 555 560

Lys Ile Lys Lys Gly Asp Leu Ile Glu Gly Ile Leu Ser Thr Leu Ser
565 570 575

Ile Glu Glu Asn Lys Ile Ile Leu Asn Ser His Glu Ile Asn Phe Ser
580 585 590

Gly Glu Val Asn Gly Ser Asn Gly Phe Val Ser Leu Thr Phe Ser Ile
595 600 605

Leu Glu Gly Ile Asn Ala Ile Ile Glu Val Asp Leu Leu Ser Lys Ser
610 615 620

Tyr Lys Leu Leu Ile Ser Gly Glu Leu Lys Ile Leu Met Leu Asn Ser
625 630 635 640

Asn His Ile Gln Gln Lys Ile Asp Tyr Ile Gly Phe Asn Ser Glu Leu
645 650 655

Gln Lys Asn Ile Pro Tyr Ser Phe Val Asp Ser Glu Gly Lys Glu Asn
660 665 670

Gly Phe Ile Asn Gly Ser Thr Lys Glu Gly Leu Phe Val Ser Glu Leu
675 680 685

Pro Asp Val Val Leu Ile Ser Lys Val Tyr Met Asp Asp Ser Lys Pro
690 695 700

Ser Phe Gly Tyr Tyr Ser Asn Asn Leu Lys Asp Val Lys Val Ile Thr
705 710 715 720

Lys Asp Asn Val Asn Ile Leu Thr Gly Tyr Tyr Leu Lys Asp Asp Ile
725 730 735

Lys Ile Ser Leu Ser Leu Thr Leu Gln Asp Glu Lys Thr Ile Lys Leu
740 745 750

Asn	Ser	Val	His	Leu	Asp	Glu	Ser	Gly	Val	Ala	Glu	Ile	Leu	Lys	Phe	755	760	765
Met	Asn	Arg	Lys	Gly	Asn	Thr	Asn	Thr	Ser	Asp	Ser	Leu	Met	Ser	Phe	770	775	780
Leu	Glu	Ser	Met	Asn	Ile	Lys	Ser	Ile	Phe	Val	Asn	Phe	Leu	Gln	Ser	785	790	795
Asn	Ile	Lys	Phe	Ile	Leu	Asp	Ala	Asn	Phe	Ile	Ile	Ser	Gly	Thr	Thr	805	810	815
Ser	Ile	Gly	Gln	Phe	Glu	Phe	Ile	Cys	Asp	Glu	Asn	Asp	Asn	Ile	Gln	820	825	830
Pro	Tyr	Phe	Ile	Lys	Phe	Asn	Thr	Leu	Glu	Thr	Asn	Tyr	Thr	Leu	Tyr	835	840	845
Val	Gly	Asn	Arg	Gln	Asn	Met	Ile	Val	Glu	Pro	Asn	Tyr	Asp	Leu	Asp	850	855	860
Asp	Ser	Gly	Asp	Ile	Ser	Ser	Thr	Val	Ile	Asn	Phe	Ser	Gln	Lys	Tyr	865	870	875
Leu	Tyr	Gly	Ile	Asp	Ser	Cys	Val	Asn	Lys	Val	Val	Ile	Ser	Pro	Asn	885	890	895
Ile	Tyr	Thr	Asp	Glu	Ile	Asn	Ile	Thr	Pro	Val	Tyr	Glu	Thr	Asn	Asn	900	905	910
Thr	Tyr	Pro	Glu	Val	Ile	Val	Leu	Asp	Ala	Asn	Tyr	Ile	Asn	Glu	Lys	915	920	925
Ile	Asn	Val	Asn	Ile	Asn	Asp	Leu	Ser	Ile	Arg	Tyr	Val	Trp	Ser	Asn	930	935	940
Asp	Gly	Asn	Asp	Phe	Ile	Leu	Met	Ser	Thr	Ser	Glu	Glu	Asn	Lys	Val	945	950	955
Ser	Gln	Val	Lys	Ile	Arg	Phe	Val	Asn	Val	Phe	Lys	Asp	Lys	Thr	Leu	965	970	975
Ala	Asn	Lys	Leu	Ser	Phe	Asn	Phe	Ser	Asp	Lys	Gln	Asp	Val	Pro	Val	980	985	990

Ser Glu Ile Ile Leu Ser Phe Thr Pro Ser Tyr Tyr Glu Asp Gly Leu
 995 1000 1005

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

Tyr Ile Asn Asn Phe Gly Met
 1025 1030

<210> 20
 <211> 438
 <212> PRT
 <213> Clostridium difficile

<400> 20

Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala
 1 5 10 15

Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
 20 25 30

Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
 35 40 45

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

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
 65 70 75 80

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
 85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
 100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
 115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
 130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu

145		150		155		160									
Gly	Gln	Ala	Ile	Leu	Tyr	Gln	Asn	Lys	Phe	Leu	Thr	Leu	Asn	Gly	Lys
				165					170					175	
Lys	Tyr	Tyr	Phe	Gly	Ser	Asp	Ser	Lys	Ala	Val	Thr	Gly	Leu	Arg	Thr
			180					185					190		
Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn	Thr	Ala	Val	Ala	Val
		195					200					205			
Thr	Gly	Trp	Gln	Thr	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Thr	Asn
	210					215					220				
Thr	Ser	Ile	Ala	Ser	Thr	Gly	Tyr	Thr	Ile	Ile	Ser	Gly	Lys	His	Phe
225					230					235					240
Tyr	Phe	Asn	Thr	Asp	Gly	Ile	Met	Gln	Ile	Gly	Val	Phe	Lys	Gly	Pro
				245					250					255	
Asp	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile
			260					265					270		
Glu	Gly	Gln	Ala	Ile	Arg	Tyr	Gln	Asn	Arg	Phe	Leu	Tyr	Leu	His	Asp
		275					280					285			
Asn	Ile	Tyr	Tyr	Phe	Gly	Asn	Asn	Ser	Lys	Ala	Ala	Thr	Gly	Trp	Val
	290					295					300				
Thr	Ile	Asp	Gly	Asn	Arg	Tyr	Tyr	Phe	Glu	Pro	Asn	Thr	Ala	Met	Gly
305					310					315					320
Ala	Asn	Gly	Tyr	Lys	Thr	Ile	Asp	Asn	Lys	Asn	Phe	Tyr	Phe	Arg	Asn
				325					330					335	
Gly	Leu	Pro	Gln	Ile	Gly	Val	Phe	Lys	Gly	Ser	Asn	Gly	Phe	Glu	Tyr
			340					345					350		
Phe	Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile
		355					360					365			
Arg	Tyr	Gln	Asn	Arg	Phe	Leu	His	Leu	Leu	Gly	Lys	Ile	Tyr	Tyr	Phe
	370					375					380				

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
 385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
 405 410 415

Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys
 420 425 430

Ala Pro Gly Ile Tyr Gly
 435

<210> 21
 <211> 2351
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Q-Toxin fusion protein

<220>
 <221> misc_feature
 <222> (588)..(588)
 <223> Xaa can be any naturally occurring amino acid

<400> 21

Met Glu Ile Val Asn Glu Asp Ile Leu Pro Asn Asn Gly Leu Met Gly
 1 5 10 15

Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
 20 25 30

Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
 35 40 45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
 50 55 60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
 65 70 75 80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
 85 90 95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu

100					105					110					
Gln	Asp	Lys	Asn	Leu	Gly	Ser	Ile	Asp	Asn	Leu	Ser	Ser	Pro	Asn	Leu
		115					120					125			
Tyr	Trp	Glu	Leu	Asp	Gly	Met	Lys	Lys	Ile	Ile	Pro	Glu	Glu	Asn	Leu
	130					135					140				
Phe	Leu	Arg	Asp	Tyr	Ser	Asn	Ile	Glu	Lys	Asp	Asp	Pro	Phe	Ile	Pro
145						150					155				160
Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu
				165					170					175	
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn
			180					185					190		
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe
		195					200					205			
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn
	210					215					220				
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe
225						230					235				240
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr
				245					250					255	
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu
			260					265					270		
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn
		275					280					285			
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr
	290					295					300				
Gln	Asn	Gly	Phe	Thr	Ala	Asn	Val	Thr	Thr	Asn	Tyr	Ser	His	Thr	Thr
305						310					315				320
Asp	Asn	Ser	Thr	Ala	Val	Gln	Asp	Ser	Asn	Gly	Glu	Ser	Trp	Asn	Thr
				325					330					335	

Gly Leu Ser Ile Asn Lys Gly Glu Ser Ala Tyr Ile Asn Ala Asn Val
340 345 350

Arg Tyr Tyr Asn Thr Gly Thr Ala Pro Met Tyr Lys Val Thr Pro Thr
355 360 365

Thr Asn Leu Val Leu Asp Gly Asp Thr Leu Ser Thr Ile Lys Ala Gln
370 375 380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
530 535 540

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

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr

				565						570						575
Tyr	Phe	Thr	Asn	Phe	Asp	Asp	Tyr	Asn	Asn	Tyr	Xaa	Ser	Thr	Trp	Ser	
			580					585					590			
Asn	Val	Asn	Thr	Thr	Asn	Gln	Asp	Gly	Leu	Gln	Gly	Ser	Ala	Asn	Lys	
		595					600					605				
Leu	Asn	Gly	Glu	Thr	Lys	Ile	Lys	Ile	Pro	Met	Ser	Glu	Leu	Lys	Pro	
	610					615					620					
Tyr	Lys	Arg	Tyr	Val	Phe	Ser	Gly	Tyr	Ser	Lys	Asp	Pro	Leu	Thr	Ser	
625					630					635					640	
Asn	Ser	Ile	Ile	Val	Lys	Ile	Lys	Ala	Lys	Glu	Glu	Lys	Thr	Asp	Tyr	
				645					650					655		
Leu	Val	Pro	Glu	Gln	Gly	Tyr	Thr	Lys	Phe	Ser	Tyr	Glu	Phe	Glu	Thr	
			660					665					670			
Thr	Glu	Lys	Asp	Ser	Ser	Asn	Ile	Glu	Ile	Thr	Leu	Ile	Gly	Ser	Gly	
		675					680					685				
Thr	Thr	Tyr	Leu	Asp	Asn	Leu	Ser	Ile	Thr	Glu	Leu	Asn	Ser	Thr	Pro	
	690					695					700					
Glu	Ile	Leu	Asp	Glu	Pro	Glu	Val	Lys	Ile	Pro	Thr	Asp	Gln	Glu	Ile	
705					710					715					720	
Met	Asp	Ala	His	Lys	Ile	Tyr	Phe	Ala	Asp	Leu	Asn	Phe	Asn	Pro	Ser	
				725					730					735		
Thr	Gly	Asn	Thr	Tyr	Ile	Asn	Gly	Met	Tyr	Phe	Ala	Pro	Thr	Gln	Thr	
			740					745					750			
Asn	Lys	Glu	Ala	Leu	Asp	Tyr	Ile	Gln	Lys	Tyr	Arg	Val	Glu	Ala	Thr	
		755					760					765				
Leu	Gln	Tyr	Ser	Gly	Phe	Lys	Asp	Ile	Gly	Thr	Lys	Asp	Lys	Glu	Met	
	770					775					780					
Arg	Asn	Tyr	Leu	Gly	Asp	Pro	Asn	Gln	Pro	Lys	Thr	Asn	Tyr	Val	Asn	
785					790					795					800	

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp Ala Ser Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser
835 840 845

Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val
850 855 860

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

Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn
885 890 895

Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe
900 905 910

Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu
915 920 925

Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr
930 935 940

Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly
945 950 955 960

Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu
965 970 975

Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met
980 985 990

Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp
995 1000 1005

Ser Gly Val Met Lys Val Gly Tyr Thr Glu Ile Asp Gly Lys His
1010 1015 1020

Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln Ile Gly Val Phe Asn

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

Lys	Tyr	Tyr	Phe	Asp	Glu	Lys	Gly	Ile	Met	Arg	Thr	Gly	Leu	Ile
1250						1255					1260			
Ser	Phe	Glu	Asn	Asn	Asn	Tyr	Tyr	Phe	Asn	Glu	Asn	Gly	Glu	Met
1265						1270					1275			
Gln	Phe	Gly	Tyr	Ile	Asn	Ile	Glu	Asp	Lys	Met	Phe	Tyr	Phe	Gly
1280						1285					1290			
Glu	Asp	Gly	Val	Met	Gln	Ile	Gly	Val	Phe	Asn	Thr	Pro	Asp	Gly
1295						1300					1305			
Phe	Lys	Tyr	Phe	Ala	His	Gln	Asn	Thr	Leu	Asp	Glu	Asn	Phe	Glu
1310						1315					1320			
Gly	Glu	Ser	Ile	Asn	Tyr	Thr	Gly	Trp	Leu	Asp	Leu	Asp	Glu	Lys
1325						1330					1335			
Arg	Tyr	Tyr	Phe	Thr	Asp	Glu	Tyr	Ile	Ala	Ala	Thr	Gly	Ser	Val
1340						1345					1350			
Ile	Ile	Asp	Gly	Glu	Glu	Tyr	Tyr	Phe	Asp	Pro	Asp	Thr	Ala	Gln
1355						1360					1365			
Leu	Val	Ile	Ser	Glu	Ser	Arg	Met	Val	Thr	Gly	Val	Phe	Lys	Gly
1370						1375					1380			
Pro	Asn	Gly	Phe	Glu	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	His	Asn	Asn
1385						1390					1395			
Asn	Ile	Glu	Gly	Gln	Ala	Ile	Val	Tyr	Gln	Asn	Lys	Phe	Leu	Thr
1400						1405					1410			
Leu	Asn	Gly	Lys	Lys	Tyr	Tyr	Phe	Asp	Asn	Asp	Ser	Lys	Ala	Val
1415						1420					1425			
Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys	Lys	Tyr	Tyr	Phe	Asn	Leu
1430						1435					1440			
Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp	Gln	Thr	Ile	Asp	Gly	Lys
1445						1450					1455			
Lys	Tyr	Tyr	Phe	Asn	Leu	Asn	Thr	Ala	Glu	Ala	Ala	Thr	Gly	Trp

1460						1465						1470			
Gln Thr	Ile Asp	Gly Lys	Lys	Tyr Tyr	Phe Asn	Thr	Asn Thr	Phe							
1475						1480						1485			
Ile Ala	Ser Thr	Gly Tyr	Thr	Ser Ile	Asn Gly	Lys	His Phe	Tyr							
1490						1495						1500			
Phe Asn	Thr Asp	Gly Ile	Met	Gln Ile	Gly Val	Phe	Lys Gly	Pro							
1505						1510						1515			
Asn Gly	Phe Glu	Tyr Phe	Ala	Pro Ala	Asn Thr	Asp	Ala Asn	Asn							
1520						1525						1530			
Ile Glu	Gly Gln	Ala Ile	Leu	Tyr Gln	Asn Lys	Phe	Leu Thr	Leu							
1535						1540						1545			
Asn Gly	Lys Lys	Tyr Tyr	Phe	Gly Ser	Asp Ser	Lys	Ala Val	Thr							
1550						1555						1560			
Gly Leu	Arg Thr	Ile Asp	Gly	Lys Lys	Tyr Tyr	Phe	Asn Thr	Asn							
1565						1570						1575			
Thr Ala	Val Ala	Val Thr	Gly	Trp Gln	Thr Ile	Asn	Gly Lys	Lys							
1580						1585						1590			
Tyr Tyr	Phe Asn	Thr Asn	Thr	Ser Ile	Ala Ser	Thr	Gly Tyr	Thr							
1595						1600						1605			
Ile Ile	Ser Gly	Lys His	Phe	Tyr Phe	Asn Thr	Asp	Gly Ile	Met							
1610						1615						1620			
Gln Ile	Gly Val	Phe Lys	Gly	Pro Asp	Gly Phe	Glu	Tyr Phe	Ala							
1625						1630						1635			
Pro Ala	Asn Thr	Asp Ala	Asn	Asn Ile	Glu Gly	Gln	Ala Ile	Arg							
1640						1645						1650			
Tyr Gln	Asn Arg	Phe Leu	Tyr	Leu His	Asp Asn	Ile	Tyr Tyr	Phe							
1655						1660						1665			
Gly Asn	Asn Ser	Lys Ala	Ala	Thr Gly	Trp Val	Thr	Ile Asp	Gly							
1670						1675						1680			

Asn	Arg	Tyr	Tyr	Phe	Glu	Pro	Asn	Thr	Ala	Met	Gly	Ala	Asn	Gly
1685						1690					1695			
Tyr	Lys	Thr	Ile	Asp	Asn	Lys	Asn	Phe	Tyr	Phe	Arg	Asn	Gly	Leu
1700						1705					1710			
Pro	Gln	Ile	Gly	Val	Phe	Lys	Gly	Ser	Asn	Gly	Phe	Glu	Tyr	Phe
1715						1720					1725			
Ala	Pro	Ala	Asn	Thr	Asp	Ala	Asn	Asn	Ile	Glu	Gly	Gln	Ala	Ile
1730						1735					1740			
Arg	Tyr	Gln	Asn	Arg	Phe	Leu	His	Leu	Leu	Gly	Lys	Ile	Tyr	Tyr
1745						1750					1755			
Phe	Gly	Asn	Asn	Ser	Lys	Ala	Val	Thr	Gly	Trp	Gln	Thr	Ile	Asn
1760						1765					1770			
Gly	Lys	Val	Tyr	Tyr	Phe	Met	Pro	Asp	Thr	Ala	Met	Ala	Ala	Ala
1775						1780					1785			
Gly	Gly	Leu	Phe	Glu	Ile	Asp	Gly	Val	Ile	Tyr	Phe	Phe	Gly	Val
1790						1795					1800			
Asp	Gly	Val	Lys	Ala	Pro	Gly	Ile	Tyr	Gly	Thr	Ser	Met	Val	Ser
1805						1810					1815			
Gly	Leu	Ile	Tyr	Ile	Asn	Asp	Ser	Leu	Tyr	Tyr	Phe	Lys	Pro	Pro
1820						1825					1830			
Val	Asn	Asn	Leu	Ile	Thr	Gly	Phe	Val	Thr	Val	Gly	Asp	Asp	Lys
1835						1840					1845			
Tyr	Tyr	Phe	Asn	Pro	Ile	Asn	Gly	Gly	Ala	Ala	Ser	Ile	Gly	Glu
1850						1855					1860			
Thr	Ile	Ile	Asp	Asp	Lys	Asn	Tyr	Tyr	Phe	Asn	Gln	Ser	Gly	Val
1865						1870					1875			
Leu	Gln	Thr	Gly	Val	Phe	Ser	Thr	Glu	Asp	Gly	Phe	Lys	Tyr	Phe
1880						1885					1890			
Ala	Pro	Ala	Asn	Thr	Leu	Asp	Glu	Asn	Leu	Glu	Gly	Glu	Ala	Ile

1895						1900						1905					
Asp Phe Thr Gly Lys Leu Ile 1910						Ile Asp Glu Asn Ile 1915						Tyr Tyr Phe 1920					
Asp Asp Asn Tyr Arg Gly Ala 1925						Val Glu Trp Lys Glu 1930						Leu Asp Gly 1935					
Glu Met His Tyr Phe Ser 1940						Pro Glu Thr Gly Lys Ala 1945						Phe Lys Gly 1950					
Leu Asn Gln Ile Gly Asp 1955						Tyr Lys Tyr Tyr Phe Asn 1960						Ser Asp Gly 1965					
Val Met Gln Lys Gly Phe 1970						Val Ser Ile Asn Asp Asn 1975						Lys His Tyr 1980					
Phe Asp Asp Ser Gly Val 1985						Met Lys Val Gly Tyr Thr 1990						Glu Ile Asp 1995					
Gly Lys His Phe Tyr Phe 2000						Ala Glu Asn Gly Glu Met 2005						Gln Ile Gly 2010					
Val Phe Asn Thr Glu Asp 2015						Gly Phe Lys Tyr Phe Ala 2020						His His Asn 2025					
Glu Asp Leu Gly Asn Glu 2030						Glu Gly Glu Glu Ile Ser 2035						Tyr Ser Gly 2040					
Ile Leu Asn Phe Asn Asn 2045						Lys Ile Tyr Tyr Phe Asp 2050						Asp Ser Phe 2055					
Thr Ala Val Val Gly Trp 2060						Lys Asp Leu Glu Asp Gly 2065						Ser Lys Tyr 2070					
Tyr Phe Asp Glu Asp Thr 2075						Ala Glu Ala Tyr Ile Gly 2080						Leu Ser Leu 2085					
Ile Asn Asp Gly Gln Tyr 2090						Tyr Phe Asn Asp Asp Gly 2095						Ile Met Gln 2100					
Val Gly Phe Val Thr Ile 2105						Asn Asp Lys Val Phe Tyr 2110						Phe Ser Asp 2115					

Ser	Gly	Ile	Ile	Glu	Ser	Gly	Val	Gln	Asn	Ile	Asp	Asp	Asn	Tyr
	2120					2125					2130			
Phe	Tyr	Ile	Asp	Asp	Asn	Gly	Ile	Val	Gln	Ile	Gly	Val	Phe	Asp
	2135					2140					2145			
Thr	Ser	Asp	Gly	Tyr	Lys	Tyr	Phe	Ala	Pro	Ala	Asn	Thr	Val	Asn
	2150					2155					2160			
Asp	Asn	Ile	Tyr	Gly	Gln	Ala	Val	Glu	Tyr	Ser	Gly	Leu	Val	Arg
	2165					2170					2175			
Val	Gly	Glu	Asp	Val	Tyr	Tyr	Phe	Gly	Glu	Thr	Tyr	Thr	Ile	Glu
	2180					2185					2190			
Thr	Gly	Trp	Ile	Tyr	Asp	Met	Glu	Asn	Glu	Ser	Asp	Lys	Tyr	Tyr
	2195					2200					2205			
Phe	Asn	Pro	Glu	Thr	Lys	Lys	Ala	Cys	Lys	Gly	Ile	Asn	Leu	Ile
	2210					2215					2220			
Asp	Asp	Ile	Lys	Tyr	Tyr	Phe	Asp	Glu	Lys	Gly	Ile	Met	Arg	Thr
	2225					2230					2235			
Gly	Leu	Ile	Ser	Phe	Glu	Asn	Asn	Asn	Tyr	Tyr	Phe	Asn	Glu	Asn
	2240					2245					2250			
Gly	Glu	Met	Gln	Phe	Gly	Tyr	Ile	Asn	Ile	Glu	Asp	Lys	Met	Phe
	2255					2260					2265			
Tyr	Phe	Gly	Glu	Asp	Gly	Val	Met	Gln	Ile	Gly	Val	Phe	Asn	Thr
	2270					2275					2280			
Pro	Asp	Gly	Phe	Lys	Tyr	Phe	Ala	His	Gln	Asn	Thr	Leu	Asp	Glu
	2285					2290					2295			
Asn	Phe	Glu	Gly	Glu	Ser	Ile	Asn	Tyr	Thr	Gly	Trp	Leu	Asp	Leu
	2300					2305					2310			
Asp	Glu	Lys	Arg	Tyr	Tyr	Phe	Thr	Asp	Glu	Tyr	Ile	Ala	Ala	Thr
	2315					2320					2325			
Gly	Ser	Val	Ile	Ile	Asp	Gly	Glu	Glu	Tyr	Tyr	Phe	Asp	Pro	Asp

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2330                               2335                               2340

Thr Ala  Gln Leu Val Ile Ser  Glu
2345                               2350

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<220>
<221>  misc_feature
<222>  (588)..(588)
<223>  Xaa can be any naturally occurring amino acid

<400>  22

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Tyr Tyr Phe Thr Asp Glu His Phe Lys Asp Leu Lys Leu Met Ala Pro
                               20                               25                               30

Ile Lys Asp Gly Asn Leu Lys Phe Glu Glu Lys Lys Val Asp Lys Leu
                               35                               40                               45

Leu Asp Lys Asp Lys Ser Asp Val Lys Ser Ile Arg Trp Thr Gly Arg
                               50                               55                               60

Ile Ile Pro Ser Lys Asp Gly Glu Tyr Thr Leu Ser Thr Asp Arg Asp
65                               70                               75                               80

Asp Val Leu Met Gln Val Asn Thr Glu Ser Thr Ile Ser Asn Thr Leu
                               85                               90                               95

Lys Val Asn Met Lys Lys Gly Lys Glu Tyr Lys Val Arg Ile Glu Leu
                               100                              105                              110

Gln Asp Lys Asn Leu Gly Ser Ile Asp Asn Leu Ser Ser Pro Asn Leu
                               115                              120                              125

Tyr Trp Glu Leu Asp Gly Met Lys Lys Ile Ile Pro Glu Glu Asn Leu
                               130                              135                              140

Phe Leu Arg Asp Tyr Ser Asn Ile Glu Lys Asp Asp Pro Phe Ile Pro
145                               150                               155                               160

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Asn	Asn	Asn	Phe	Phe	Asp	Pro	Lys	Leu	Met	Ser	Asp	Trp	Glu	Asp	Glu	165	170	175
Asp	Leu	Asp	Thr	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ser	Tyr	Glu	Arg	Asn	180	185	190
Gly	Tyr	Thr	Ile	Lys	Asp	Leu	Ile	Ala	Val	Lys	Trp	Glu	Asp	Ser	Phe	195	200	205
Ala	Glu	Gln	Gly	Tyr	Lys	Lys	Tyr	Val	Ser	Asn	Tyr	Leu	Glu	Ser	Asn	210	215	220
Thr	Ala	Gly	Asp	Pro	Tyr	Thr	Asp	Tyr	Glu	Lys	Ala	Ser	Gly	Ser	Phe	225	230	235
Asp	Lys	Ala	Ile	Lys	Thr	Glu	Ala	Arg	Asp	Pro	Leu	Val	Ala	Ala	Tyr	245	250	255
Pro	Ile	Val	Gly	Val	Gly	Met	Glu	Lys	Leu	Ile	Ile	Ser	Thr	Asn	Glu	260	265	270
His	Ala	Ser	Thr	Asp	Gln	Gly	Lys	Thr	Val	Ser	Arg	Ala	Thr	Thr	Asn	275	280	285
Ser	Lys	Thr	Glu	Ser	Asn	Thr	Ala	Gly	Val	Ser	Val	Asn	Val	Gly	Tyr	290	295	300
Gln	Asn	Gly	Phe	Thr	Ala	Asn	Val	Thr	Thr	Asn	Tyr	Ser	His	Thr	Thr	305	310	315
Asp	Asn	Ser	Thr	Ala	Val	Gln	Asp	Ser	Asn	Gly	Glu	Ser	Trp	Asn	Thr	325	330	335
Gly	Leu	Ser	Ile	Asn	Lys	Gly	Glu	Ser	Ala	Tyr	Ile	Asn	Ala	Asn	Val	340	345	350
Arg	Tyr	Tyr	Asn	Thr	Gly	Thr	Ala	Pro	Met	Tyr	Lys	Val	Thr	Pro	Thr	355	360	365
Thr	Asn	Leu	Val	Leu	Asp	Gly	Asp	Thr	Leu	Ser	Thr	Ile	Lys	Ala	Gln	370	375	380

Glu Asn Gln Ile Gly Asn Asn Leu Ser Pro Gly Asp Thr Tyr Pro Lys
 385 390 395 400

Lys Gly Leu Ser Pro Leu Ala Leu Asn Thr Met Asp Gln Phe Ser Ser
 405 410 415

Arg Leu Ile Pro Ile Asn Tyr Asp Gln Leu Lys Lys Leu Asp Ala Gly
 420 425 430

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

Lys Asn Ser Ser Gly Gln Ile Val Thr Glu Gly Asn Ser Trp Ser Asp
 450 455 460

Tyr Ile Ser Gln Ile Asp Ser Ile Ser Ala Ser Ile Ile Leu Asp Thr
 465 470 475 480

Glu Asn Glu Ser Tyr Glu Arg Arg Val Thr Ala Lys Asn Leu Gln Asp
 485 490 495

Pro Glu Asp Lys Thr Pro Glu Leu Thr Ile Gly Glu Ala Ile Glu Lys
 500 505 510

Ala Phe Gly Ala Thr Lys Lys Asp Gly Leu Leu Tyr Phe Asn Asp Ile
 515 520 525

Pro Ile Asp Glu Ser Cys Val Glu Leu Ile Phe Asp Asp Asn Thr Ala
 530 535 540

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

Asn Val Lys Leu Glu Arg Gly Met Asn Ile Leu Ile Lys Thr Pro Thr
 565 570 575

Tyr Phe Thr Asn Phe Asp Asp Tyr Asn Asn Tyr Xaa Ser Thr Trp Ser
 580 585 590

Asn Val Asn Thr Thr Asn Gln Asp Gly Leu Gln Gly Ser Ala Asn Lys
 595 600 605

Leu Asn Gly Glu Thr Lys Ile Lys Ile Pro Met Ser Glu Leu Lys Pro
 610 615 620

Tyr Lys Arg Tyr Val Phe Ser Gly Tyr Ser Lys Asp Pro Leu Thr Ser
625 630 635 640

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

Leu Val Pro Glu Gln Gly Tyr Thr Lys Phe Ser Tyr Glu Phe Glu Thr
660 665 670

Thr Glu Lys Asp Ser Ser Asn Ile Glu Ile Thr Leu Ile Gly Ser Gly
675 680 685

Thr Thr Tyr Leu Asp Asn Leu Ser Ile Thr Glu Leu Asn Ser Thr Pro
690 695 700

Glu Ile Leu Asp Glu Pro Glu Val Lys Ile Pro Thr Asp Gln Glu Ile
705 710 715 720

Met Asp Ala His Lys Ile Tyr Phe Ala Asp Leu Asn Phe Asn Pro Ser
725 730 735

Thr Gly Asn Thr Tyr Ile Asn Gly Met Tyr Phe Ala Pro Thr Gln Thr
740 745 750

Asn Lys Glu Ala Leu Asp Tyr Ile Gln Lys Tyr Arg Val Glu Ala Thr
755 760 765

Leu Gln Tyr Ser Gly Phe Lys Asp Ile Gly Thr Lys Asp Lys Glu Met
770 775 780

Arg Asn Tyr Leu Gly Asp Pro Asn Gln Pro Lys Thr Asn Tyr Val Asn
785 790 795 800

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

Leu Arg Ile Tyr Ala Ile Thr Pro Asp Asp Arg Glu Leu Leu Val Leu
820 825 830

Ser Val Asp
835

<210> 23
 <211> 536
 <212> PRT
 <213> Clostridium difficile

<400> 23

Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys
 1 5 10 15

Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
 20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
 35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
 50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
 65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr
 85 90 95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
 100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
 115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
 130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
 145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
 165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
 180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
 195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
210 215 220
Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp
225 230 235 240
Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser
245 250 255
Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser
260 265 270
Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
275 280 285
Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
290 295 300
Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
305 310 315 320
Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
325 330 335
Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
340 345 350
Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
355 360 365
Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
370 375 380
Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
385 390 395 400
Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
405 410 415
Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
420 425 430
Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile

435 440 445
 Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
 450 455 460
 Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
 465 470 475 480
 Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu
 485 490 495
 Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
 500 505 510
 Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
 515 520 525
 Thr Ala Gln Leu Val Ile Ser Glu
 530 535

 <210> 24
 <211> 438
 <212> PRT
 <213> Clostridium difficile

 <400> 24
 Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala
 1 5 10 15
 Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr
 20 25 30
 Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn
 35 40 45
 Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr
 50 55 60
 Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile
 65 70 75 80
 Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr
 85 90 95

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr
100 105 110

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr
115 120 125

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn
130 135 140

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu
145 150 155 160

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys
165 170 175

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr
180 185 190

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val
195 200 205

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn
210 215 220

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe
225 230 235 240

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro
245 250 255

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile
260 265 270

Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp
275 280 285

Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val
290 295 300

Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly
305 310 315 320

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

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

Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile
 355 360 365

Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe
 370 375 380

Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys
 385 390 395 400

Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu
 405 410 415

Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys
 420 425 430

Ala Pro Gly Ile Tyr Gly
 435

<210> 25
 <211> 536
 <212> PRT
 <213> Clostridium difficile

<400> 25

Met Val Ser Gly Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys
 1 5 10 15

Pro Pro Val Asn Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp
 20 25 30

Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu
 35 40 45

Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu
 50 55 60

Gln Thr Gly Val Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro
 65 70 75 80

Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr

85

90

95

Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr
 100 105 110

Arg Gly Ala Val Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe
 115 120 125

Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp
 130 135 140

Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val
 145 150 155 160

Ser Ile Asn Asp Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys
 165 170 175

Val Gly Tyr Thr Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn
 180 185 190

Gly Glu Met Gln Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr
 195 200 205

Phe Ala His His Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile
 210 215 220

Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp
 225 230 235 240

Asp Ser Phe Thr Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser
 245 250 255

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

Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln
 275 280 285

Val Gly Phe Val Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser
 290 295 300

Gly Ile Ile Glu Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr
 305 310 315 320

Ile Asp Asp Asn Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp
325 330 335

Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr
340 345 350

Gly Gln Ala Val Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val
355 360 365

Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp
370 375 380

Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys
385 390 395 400

Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp
405 410 415

Glu Lys Gly Ile Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn
420 425 430

Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile
435 440 445

Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly
450 455 460

Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr
465 470 475 480

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

Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala
500 505 510

Thr Gly Ser Val Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp
515 520 525

Thr Ala Gln Leu Val Ile Ser Glu
530 535

<210> 26

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

<220>
<223> synthetically synthesized peptide linker

<400> 26

Gly Gly Gly Gly
1

<210> 27
<211> 8
<212> PRT
<213> Unknown

<220>
<223> furin cleavage site sequence

<400> 27

Arg Ala Arg Arg Arg Lys Lys Arg
1 5

<210> 28
<211> 24
<212> DNA
<213> Unknown

<220>
<223> furin cleavage site sequence

<400> 28
cgcgctcgcc gccgcaagaa gcgc

24