

SEQUENCE LISTING

<110> The Provost Fellows and Scholars of the College of the Holy
and Undivided Trinity Of Queen Elizabeth Near Dublin

<120> Treatment of Microbial Infections

<130> 31546WO

<160> 14

<170> PatentIn version 3.3

<210> 1

<211> 933

<212> PRT

<213> Artificial

<220>

<223> recombinant ClfA (wild type) full length protein sequence

<400> 1

Met	Asn	Met	Lys	Lys	Lys	Glu	Lys	His	Ala	Ile	Arg	Lys	Lys	Ser	Ile
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Ser	Ser	Lys	Glu	Ala	Asp	Ala	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp
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Ser	Ala	Ser	Asn	Glu	Ser	Lys	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala
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Ala	Pro	Lys	Thr	Asp	Asp	Thr	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser
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Asn	Thr	Asn	Asn	Gly	Glu	Thr	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln
				85					90					95	

Glu	Thr	Thr	Gln	Ser	Ser	Ser	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro
			100					105					110		

Val	Thr	Gly	Glu	Ala	Thr	Thr	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro
		115					120					125			

Ala	Thr	Thr	Gln	Ser	Ser	Asn	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln
	130					135					140				

Thr	Ser	Asn	Glu	Thr	Thr	Phe	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val
145					150					155					160

Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
165 170 175

Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
180 185 190

Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
195 200 205

Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
210 215 220

Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr
225 230 235 240

Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr
245 250 255

Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly
260 265 270

Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val
275 280 285

Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu
290 295 300

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

Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro
325 330 335

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

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

Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr Ile
370 375 380

Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val
385 390 395 400

Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu
405 410 415

Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser
420 425 430

Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr
435 440 445

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

Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp
465 470 475 480

Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp
485 490 495

Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr
500 505 510

Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala
515 520 525

Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val
530 535 540

Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Asp
545 550 555 560

Ser Asp Ser Asp Pro Gly Ser Asp Ser Gly Ser Asp Ser Asn Ser Asp
565 570 575

Ser Gly Ser Asp Ser Gly Ser Asp Ser Thr Ser Asp Ser Gly Ser Asp
580 585 590

Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp
595 600 605

Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp
610 615 620

Asn Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
625 630 635 640

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
645 650 655

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
660 665 670

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675 680 685

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
690 695 700

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705 710 715 720

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
725 730 735

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
740 745 750

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala
755 760 765

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
770 775 780

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
785 790 795 800

Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Glu Ser Asp
805 810 815

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
820 825 830

Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp
835 840 845

Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser Asp Ser Glu
850 855 860

Ser Gly Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro Lys Asn Gly
865 870 875 880

Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys Glu Pro Leu

885

890

895

Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu Ile Trp Gly
 900 905 910

Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg Lys Lys Glu
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Asn Lys Asp Lys Lys
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<210> 2
 <211> 1560
 <212> DNA
 <213> Artificial

<220>
 <223> recombinant ClfA A domain (wild type) Regions N1 N2 N3

<220>
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 agt aat gat tca agt agc gtt agt gct gca cct aaa aca gac gac aca 96
 Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
 20 25 30
 aac gtg agt gat act aaa aca tcg tca aac act aat aat ggc gaa acg 144
 Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
 35 40 45
 agt gtg gcg caa aat cca gca caa cag gaa acg aca caa tca tca tca 192
 Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
 50 55 60
 aca aat gca act acg gaa gaa acg ccg gta act ggt gaa gct act act 240
 Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
 65 70 75 80
 acg aca acg aat caa gct aat aca ccg gca aca act caa tca agc aat 288
 Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
 85 90 95
 aca aat gcg gag gaa tta gtg aat caa aca agt aat gaa acg act ttt 336
 Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Phe
 100 105 110
 aat gat act aat aca gta tca tct gta aat tca cct caa aat tct aca 384
 Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
 115 120 125

aat gcg gaa aat gtt tca aca acg caa gat act tca act gaa gca aca Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr 130 135 140	432
cct tca aac aat gaa tca gct cca cag agt aca gat gca agt aat aaa Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys 145 150 155 160	480
gat gta gtt aat caa gcg gtt aat aca agt gcg cct aga atg aga gca Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala 165 170 175	528
ttt agt tta gcg gca gta gct gca gat gca ccg gca gct ggc aca gat Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp 180 185 190	576
att acg aat cag ttg acg aat gtg aca gtt ggt att gac tct ggt acg Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr 195 200 205	624
act gtg tat ccg cac caa gca ggt tat gtc aaa ctg aat tat ggt ttt Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe 210 215 220	672
tca gtg cct aat tct gct gtt aaa ggt gac aca ttc aaa ata act gta Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val 225 230 235 240	720
cct aaa gaa tta aac tta aat ggt gta act tca act gct aaa gtg cca Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro 245 250 255	768
cca att atg gct gga gat caa gta ttg gca aat ggt gta atc gat agt Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser 260 265 270	816
gat ggt aat gtt att tat aca ttt aca gac tat gta aat act aaa gat Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp 275 280 285	864
gat gta aaa gca act ttg acc atg ccc gct tat att gac cct gaa aat Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn 290 295 300	912
gtt aaa aag aca ggt aat gtg aca ttg gct act ggc ata ggt agt aca Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr 305 310 315 320	960
aca gca aac aaa aca gta tta gta gat tat gaa aaa tat ggt aag ttt Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe 325 330 335	1008
tat aac tta tct att aaa ggt aca att gac caa atc gat aaa aca aat Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn 340 345 350	1056
aat acg tat cgt cag aca att tat gtc aat cca agt gga gat aac gtt Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val 355 360 365	1104
att gcg ccg gtt tta aca ggt aat tta aaa cca aat acg gat agt aat	1152

Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn		
370						375					380						
gca	tta	ata	gat	cag	caa	aat	aca	agt	att	aaa	gta	tat	aaa	gta	gat	1200	
Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp		
385				390						395					400		
aat	gca	gct	gat	tta	tct	gaa	agt	tac	ttt	gtg	aat	cca	gaa	aac	ttt	1248	
Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe		
				405					410					415			
gag	gat	gtc	act	aat	agt	gtg	aat	att	aca	ttc	cca	aat	cca	aat	caa	1296	
Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln		
			420					425					430				
tat	aaa	gta	gag	ttt	aat	acg	cct	gat	gat	caa	att	aca	aca	cgc	tat	1344	
Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr		
	435						440					445					
ata	gta	gtt	gtt	aat	ggg	cat	att	gat	ccg	aat	agc	aaa	ggg	gat	tta	1392	
Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu		
	450				455					460							
gct	tta	cgt	tca	act	tta	tat	ggg	tat	aac	tcg	aat	ata	att	tgg	cgc	1440	
Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg		
465					470				475					480			
tct	atg	tca	tgg	gac	aac	gaa	gta	gca	ttt	aat	aac	gga	tca	ggg	tct	1488	
Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser		
				485				490					495				
ggg	gac	ggg	atc	gat	aaa	cca	gtt	gtt	cct	gaa	caa	cct	gat	gag	cct	1536	
Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro		
			500					505					510				
ggg	gaa	att	gaa	cca	att	cca	gag									1560	
Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu										
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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 3

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Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr
			20					25					30		

Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr
		35					40					45			

Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
50 55 60

Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
65 70 75 80

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
85 90 95

Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Phe
100 105 110

Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
115 120 125

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
130 135 140

Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
145 150 155 160

Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
165 170 175

Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp
180 185 190

Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
195 200 205

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
210 215 220

Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
225 230 235 240

Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
245 250 255

Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
260 265 270

Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
275 280 285

Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn
290 295 300

Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
305 310 315 320

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

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

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
355 360 365

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

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
385 390 395 400

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
405 410 415

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
420 425 430

Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
435 440 445

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
450 455 460

Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
465 470 475 480

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
485 490 495

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
500 505 510

Gly Glu Ile Glu Pro Ile Pro Glu
515 520

<211> 520
<212> PRT
<213> Artificial

<220>

<223> ClfA A domain Regions N1 N2 N3 with alterations (ClfA P336S
Y338A)

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Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
20 25 30

Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
35 40 45

Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
50 55 60

Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
65 70 75 80

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
85 90 95

Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Phe
100 105 110

Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
115 120 125

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
130 135 140

Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
145 150 155 160

Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
165 170 175

Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp
180 185 190

Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
195 200 205

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
210 215 220

Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
225 230 235 240

Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
245 250 255

Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
260 265 270

Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
275 280 285

Asp Val Lys Ala Thr Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn
290 295 300

Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
305 310 315 320

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

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

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
355 360 365

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

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
385 390 395 400

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
405 410 415

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
420 425 430

Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
435 440 445

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
450 455 460

Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
465 470 475 480

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
485 490 495

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
500 505 510

Gly Glu Ile Glu Pro Ile Pro Glu
515 520

<210> 5

<211> 520

<212> PRT

<213> Artificial

<220>

<223> ClfA A domain Regions N1 N2 N3 with alterations (ClfA P336A
Y338S)

<400> 5

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Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
20 25 30

Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
35 40 45

Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
50 55 60

Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
65 70 75 80

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
85 90 95

Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Phe
100 105 110

Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
115 120 125

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
130 135 140

Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
145 150 155 160

Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
165 170 175

Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp
180 185 190

Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
195 200 205

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
210 215 220

Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
225 230 235 240

Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
245 250 255

Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
260 265 270

Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
275 280 285

Asp Val Lys Ala Thr Leu Thr Met Ala Ala Ser Ile Asp Pro Glu Asn
290 295 300

Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
305 310 315 320

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

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

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
355 360 365

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

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
385 390 395 400

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
405 410 415

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
420 425 430

Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
435 440 445

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
450 455 460

Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
465 470 475 480

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
485 490 495

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
500 505 510

Gly Glu Ile Glu Pro Ile Pro Glu
515 520

<210> 6
<211> 530
<212> PRT
<213> ARTIFICIAL

<220>
<223> wt rClfA A region with additional N and C terminal residues
<400> 6

His His His His His His Gly Ser Ser Glu Asn Ser Val Thr Gln Ser
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Asp Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser
20 25 30

Ala Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser
35 40 45

Ser Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln
50 55 60

Gln Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr
65 70 75 80

Pro Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr
85 90 95

Pro Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn
100 105 110

Gln Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser
115 120 125

Val Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr
130 135 140

Gln Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro
145 150 155 160

Gln Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn
165 170 175

Thr Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala
180 185 190

Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val
195 200 205

Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly
210 215 220

Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys
225 230 235 240

Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly
245 250 255

Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val
260 265 270

Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe
275 280 285

Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met
290 295 300

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

Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val
325 330 335

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

Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr
355 360 365

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

Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr
385 390 395 400

Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser
405 410 415

Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn
420 425 430

Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro
435 440 445

Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile
450 455 460

Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly
465 470 475 480

Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val
485 490 495

Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val
500 505 510

Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu
515 520 525

Lys Leu
530

<210> 7
<211> 530
<212> PRT
<213> ARTIFICIAL

<220>
<223> wt rClfAPYI A region with additional N and C terminal residues

<400> 7

His His His His His His Gly Ser Ser Glu Asn Ser Val Thr Gln Ser
1 5 10 15

Asp Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser
20 25 30

Ala Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser
35 40 45

Ser Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln
50 55 60

Gln Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr
65 70 75 80

Pro Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr
85 90 95

Pro Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn
100 105 110

Gln Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser
115 120 125

Val Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr
130 135 140

Gln Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro
145 150 155 160

Gln Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn
165 170 175

Thr Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala
180 185 190

Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val
195 200 205

Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly
210 215 220

Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys
225 230 235 240

Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly
245 250 255

Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val
260 265 270

Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe
275 280 285

Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met
290 295 300

Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr
305 310 315 320

Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val
325 330 335

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

Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr
355 360 365

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

Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr
385 390 395 400

Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser
405 410 415

Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn
420 425 430

Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro
435 440 445

Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile
450 455 460

Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly
465 470 475 480

Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val
485 490 495

Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val
500 505 510

Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu
515 520 525

Lys Leu
530

<210> 8
<211> 530
<212> PRT
<213> ARTIFICIAL

<220>
<223> wt rClfAPYIII A region with additional N and C terminal residues

<400> 8

His His His His His His Gly Ser Ser Glu Asn Ser Val Thr Gln Ser
1 5 10 15

Asp Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser
20 25 30

Ala Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser
35 40 45

Ser Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln
50 55 60

Gln Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr
65 70 75 80

Pro Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr
85 90 95

Pro Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn
100 105 110

Gln Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser
115 120 125

Val Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr
130 135 140

Gln Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro
145 150 155 160

Gln Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn
165 170 175

Thr Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala
180 185 190

Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val
195 200 205

Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly
210 215 220

Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys
225 230 235 240

Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly
245 250 255

Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val
260 265 270

Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe
275 280 285

Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met
290 295 300

Ala Ala Ser Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr
305 310 315 320

Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val
325 330 335

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

Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr
355 360 365

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

Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr
385 390 395 400

Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser
405 410 415

Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn
420 425 430

Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro
435 440 445

Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile
450 455 460

Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly
465 470 475 480

Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val
485 490 495

Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val
500 505 510

Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu
515 520 525

Lys Leu
530

<210> 9
<211> 339
<212> PRT
<213> ARTIFICIAL

<220>
<223> rClfA residues 221-559

<400> 9

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

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr
275 280 285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
290 295 300

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

Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro
325 330 335

Ile Pro Glu

<210> 10

<211> 349

<212> PRT

<213> ARTIFICIAL

<220>

<223> rClfA residues 221 to 559 with additional N and C terminal
residues

<400> 10

His His His His His His Gly Ser Val Ala Ala Asp Ala Pro Ala Ala
1 5 10 15

Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp
20 25 30

Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn
35 40 45

Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys
50 55 60

Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala
65 70 75 80

Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val
85 90 95

Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn
100 105 110

Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp
115 120 125

Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile
130 135 140

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

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

Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly
180 185 190

Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr
195 200 205

Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr
210 215 220

Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro
225 230 235 240

Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn
245 250 255

Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr
260 265 270

Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys
275 280 285

Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile
290 295 300

Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly
305 310 315 320

Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro
325 330 335

Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Lys Leu
340 345

<210> 11
<211> 339
<212> PRT
<213> ARTIFICIAL

<220>
<223> rClfA PY 221 to 559

<400> 11

Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu
1 5 10 15

Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His
20 25 30

Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser
35 40 45

Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn
50 55 60

Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly
65 70 75 80

Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile
85 90 95

Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr
100 105 110

Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr Gly
115 120 125

Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr
130 135 140

Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile
145 150 155 160

Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln
165 170 175

Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu
180 185 190

Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln
195 200 205

Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu
210 215 220

Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn
225 230 235 240

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr
275 280 285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
290 295 300

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

Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro
325 330 335

Ile Pro Glu

<210> 12
<211> 349
<212> PRT
<213> ARTIFICIAL

<220>
<223> rClfA PY 221 to 559 with additional N and C terminal residues

<400> 12

His His His His His His Gly Ser Val Ala Ala Asp Ala Pro Ala Ala
1 5 10 15

Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp
20 25 30

Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn

35

40

45

Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys
50 55 60

Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala
65 70 75 80

Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val
85 90 95

Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn
100 105 110

Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Ser Ala Ala Ile Asp
115 120 125

Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile
130 135 140

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

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

Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly
180 185 190

Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr
195 200 205

Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr
210 215 220

Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro
225 230 235 240

Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn
245 250 255

Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr
260 265 270

Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys
275 280 285

Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile
290 295 300

Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly
305 310 315 320

Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro
325 330 335

Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Lys Leu
340 345

<210> 13

<211> 321

<212> PRT

<213> ARTIFICIAL

<220>

<223> rClfA residues 221 to 531 with additional N and C terminal
residues (delta latch truncate)

<400> 13

His His His His His His Gly Ser Val Ala Ala Asp Ala Pro Ala Ala
1 5 10 15

Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp
20 25 30

Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn
35 40 45

Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys
50 55 60

Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala
65 70 75 80

Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val
85 90 95

Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn
100 105 110

Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp
115 120 125

Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile
130 135 140

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

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

Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly
180 185 190

Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr
195 200 205

Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr
210 215 220

Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro
225 230 235 240

Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn
245 250 255

Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr
260 265 270

Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys
275 280 285

Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile
290 295 300

Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Arg
305 310 315 320

Ser

<210> 14
<211> 311
<212> PRT
<213> ARTIFICIAL

<220>
<223> rClfA residues 221 to 531 (delta latch truncate)

<400> 14

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

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr
275 280 285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
290 295 300

Asn Glu Val Ala Phe Asn Asn
305 310