

SEQUENCE LISTING

<110> University of Basel

<120> Virulence attenuated bacteria for treatment of malignant solid tumors

<130> P5061PC00

<160> 224

<170> PatentIn version 3.5

<210> 1

<211> 219

<212> PRT

<213> Yersinia enterocolitica

<400> 1

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Gly Ser Gly Pro Leu Arg
130 135 140

Gly Ser Ile Thr Gln Cys Gln Gly Leu Met Gln Phe Cys Gly Gly Glu
 145 150 155 160

Leu Gln Ala Glu Ala Ser Ala Ile Leu Asn Thr Pro Val Cys Gly Ile
 165 170 175

Pro Phe Ser Gln Trp Gly Thr Val Gly Gly Ala Ala Ser Ala Tyr Val
 180 185 190

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

Gly Gln Gln Met Gln Gln Leu Leu Ser Leu Met
 210 215

<210> 2
 <211> 138
 <212> PRT
 <213> *Yersinia enterocolitica*

<400> 2

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
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Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu

100

105

110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr
 130 135

<210> 3

<211> 169

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138-MycHis

<400> 3

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
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Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu

130

135

140

Lys Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser
 145 150 155 160

Ala Val Asp His His His His His His
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<210> 4

<211> 348

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - IpgB1

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Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Leu

130

135

140

Asn Lys Ile Leu Pro Gln Val Glu Phe Ala Ile Pro Arg Pro Ser Phe
 145 150 155 160

Asp Ser Leu Ser Arg Asn Lys Leu Val Lys Lys Ile Leu Ser Val Phe
 165 170 175

Asn Leu Lys Gln Arg Phe Pro Gln Lys Asn Phe Gly Cys Pro Val Asn
 180 185 190

Ile Asn Lys Ile Arg Asp Ser Val Ile Asp Lys Ile Lys Asp Ser Asn
 195 200 205

Ser Gly Asn Gln Leu Phe Cys Trp Met Ser Gln Glu Arg Thr Thr Tyr
 210 215 220

Val Ser Ser Met Ile Asn Arg Ser Ile Asp Glu Met Ala Ile His Asn
 225 230 235 240

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

Glu Lys Lys Phe Pro Asp Ile Lys Leu Asp Glu Lys Ser Ala Gln Thr
 260 265 270

Ser Ile Ser His Thr Ala Leu Asn Glu Ile Ala Ser Ser Gly Leu Arg
 275 280 285

Ala Lys Ile Leu Lys Arg Tyr Ser Ser Asp Met Asp Leu Phe Asn Thr
 290 295 300

Gln Met Lys Asp Leu Thr Asn Leu Val Ser Ser Ser Val Tyr Asp Lys
 305 310 315 320

Ile Phe Asn Glu Ser Thr Lys Val Leu Gln Ile Glu Ile Ser Ala Glu
 325 330 335

Val Leu Lys Ala Val Tyr Arg Gln Ser Asn Thr Asn
 340 345

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 <212> PRT
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<220>
 <223> YopE1-138 - SopE

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Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
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Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Val Thr Asn Ile
 130 135 140

Thr Leu Ser Thr Gln His Tyr Arg Ile His Arg Ser Asp Val Glu Pro
 145 150 155 160

Val Lys Glu Lys Thr Thr Glu Lys Asp Ile Phe Ala Lys Ser Ile Thr
 165 170 175

Ala Val Arg Asn Ser Phe Ile Ser Leu Ser Thr Ser Leu Ser Asp Arg
180 185 190

Phe Ser Leu His Gln Gln Thr Asp Ile Pro Thr Thr His Phe His Arg
195 200 205

Gly Asn Ala Ser Glu Gly Arg Ala Val Leu Thr Ser Lys Thr Val Lys
210 215 220

Asp Phe Met Leu Gln Lys Leu Asn Ser Leu Asp Ile Lys Gly Asn Ala
225 230 235 240

Ser Lys Asp Pro Ala Tyr Ala Arg Gln Thr Cys Glu Ala Ile Leu Ser
245 250 255

Ala Val Tyr Ser Asn Asn Lys Asp Gln Cys Cys Lys Leu Leu Ile Ser
260 265 270

Lys Gly Val Ser Ile Thr Pro Phe Leu Lys Glu Ile Gly Glu Ala Ala
275 280 285

Gln Asn Ala Gly Leu Pro Gly Glu Ile Lys Asn Gly Val Phe Thr Pro
290 295 300

Gly Gly Ala Gly Ala Asn Pro Phe Val Val Pro Leu Ile Ala Ser Ala
305 310 315 320

Ser Ile Lys Tyr Pro His Met Phe Ile Asn His Asn Gln Gln Val Ser
325 330 335

Phe Lys Ala Tyr Ala Glu Lys Ile Val Met Lys Glu Val Thr Pro Leu
340 345 350

Phe Asn Lys Gly Thr Met Pro Thr Pro Gln Gln Phe Gln Leu Thr Ile
355 360 365

Glu Asn Ile Ala Asn Lys Tyr Leu Gln Asn Ala Ser
370 375 380

<210> 6

<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - SopB

<400> 6

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Gln
130 135 140

Ser Phe Tyr His Ser Ala Ser Leu Lys Thr Gln Glu Ala Phe Lys Ser
145 150 155 160

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

Lys Ala Pro Ala Lys Ala Pro Asp Ala Arg Pro Glu Ile Ile Val Leu

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

Leu Arg His Val Gly Ala Glu Asn Lys Ala Lys Glu Val Leu Thr Ala
405 410 415

Ala Leu Phe Ser Lys Pro Glu Leu Leu Asn Lys Ala Leu Ala Gly Glu
420 425 430

Ala Val Ser Leu Lys Leu Val Ser Val Gly Leu Leu Thr Ala Ser Asn
435 440 445

Ile Phe Gly Lys Glu Gly Thr Met Val Glu Asp Gln Met Arg Ala Trp
450 455 460

Gln Ser Leu Thr Gln Pro Gly Lys Met Ile His Leu Lys Ile Arg Asn
465 470 475 480

Lys Asp Gly Asp Leu Gln Thr Val Lys Ile Lys Pro Asp Val Ala Ala
485 490 495

Phe Asn Val Gly Val Asn Glu Leu Ala Leu Lys Leu Gly Phe Gly Leu
500 505 510

Lys Ala Ser Asp Ser Tyr Asn Ala Glu Ala Leu His Gln Leu Leu Gly
515 520 525

Asn Asp Leu Arg Pro Glu Ala Arg Pro Gly Gly Trp Val Gly Glu Trp
530 535 540

Leu Ala Gln Tyr Pro Asp Asn Tyr Glu Val Val Asn Thr Leu Ala Arg
545 550 555 560

Gln Ile Lys Asp Ile Trp Lys Asn Asn Gln His His Lys Asp Gly Gly
565 570 575

Glu Pro Tyr Lys Leu Ala Gln Arg Leu Ala Met Leu Ala His Glu Ile
580 585 590

Asp Ala Val Pro Ala Trp Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly
595 600 605

Met Met Asp Ser Glu Ile Lys Arg Glu Ile Ile Ser Leu His Gln Thr

610

615

620

His Met Leu Ser Ala Pro Gly Ser Leu Pro Asp Ser Gly Gly Gln Lys
 625 630 635 640

Ile Phe Gln Lys Val Leu Leu Asn Ser Gly Asn Leu Glu Ile Gln Lys
 645 650 655

Gln Asn Thr Gly Gly Ala Gly Asn Lys Val Met Lys Asn Leu Ser Pro
 660 665 670

Glu Val Leu Asn Leu Ser Tyr Gln Lys Arg Val Gly Asp Glu Asn Ile
 675 680 685

Trp Gln Ser Val Lys Gly Ile Ser Ser Leu Ile Thr Ser
 690 695 700

<210> 7

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - OspF

<400> 7

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met

85

90

95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
 130 135 140

Met Pro Ile Lys Lys Pro Cys Leu Lys Leu Asn Leu Asp Ser Leu Asn
 145 150 155 160

Val Val Arg Ser Glu Ile Pro Gln Met Leu Ser Ala Asn Glu Arg Leu
 165 170 175

Lys Asn Asn Phe Asn Ile Leu Tyr Asn Gln Ile Arg Gln Tyr Pro Ala
 180 185 190

Tyr Tyr Phe Lys Val Ala Ser Asn Val Pro Thr Tyr Ser Asp Ile Cys
 195 200 205

Gln Ser Phe Ser Val Met Tyr Gln Gly Phe Gln Ile Val Asn His Ser
 210 215 220

Gly Asp Val Phe Ile His Ala Cys Arg Glu Asn Pro Gln Ser Lys Gly
 225 230 235 240

Asp Phe Val Gly Asp Lys Phe His Ile Ser Ile Ala Arg Glu Gln Val
 245 250 255

Pro Leu Ala Phe Gln Ile Leu Ser Gly Leu Leu Phe Ser Glu Asp Ser
 260 265 270

Pro Ile Asp Lys Trp Lys Ile Thr Asp Met Asn Arg Val Ser Gln Gln
 275 280 285

Ser Arg Val Gly Ile Gly Ala Gln Phe Thr Leu Tyr Val Lys Ser Asp
 290 295 300

Gln Glu Cys Ser Gln Tyr Ser Ala Leu Leu Leu His Lys Ile Arg Gln
305 310 315 320

Phe Ile Met Cys Leu Glu Ser Asn Leu Leu Arg Ser Lys Ile Ala Pro
325 330 335

Gly Glu Tyr Pro Ala Ser Asp Val Arg Pro Glu Asp Trp Lys Tyr Val
340 345 350

Ser Tyr Arg Asn Glu Leu Arg Ser Asp Arg Asp Gly Ser Glu Arg Gln
355 360 365

Glu Gln Met Leu Arg Glu Glu Pro Phe Tyr Arg Leu Met Ile Glu
370 375 380

<210> 8
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - SptP

<400> 8

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Leu
130 135 140

Lys Tyr Glu Glu Arg Lys Leu Asn Asn Leu Thr Leu Ser Ser Phe Ser
145 150 155 160

Lys Val Gly Val Ser Asn Asp Ala Arg Leu Tyr Ile Ala Lys Glu Asn
165 170 175

Thr Asp Lys Ala Tyr Val Ala Pro Glu Lys Phe Ser Ser Lys Val Leu
180 185 190

Thr Trp Leu Gly Lys Met Pro Leu Phe Lys Asn Thr Glu Val Val Gln
195 200 205

Lys His Thr Glu Asn Ile Arg Val Gln Asp Gln Lys Ile Leu Gln Thr
210 215 220

Phe Leu His Ala Leu Thr Glu Lys Tyr Gly Glu Thr Ala Val Asn Asp
225 230 235 240

Ala Leu Leu Met Ser Arg Ile Asn Met Asn Lys Pro Leu Thr Gln Arg
245 250 255

Leu Ala Val Gln Ile Thr Glu Cys Val Lys Ala Ala Asp Glu Gly Phe
260 265 270

Ile Asn Leu Ile Lys Ser Lys Asp Asn Val Gly Val Arg Asn Ala Ala
275 280 285

Leu Val Ile Lys Gly Gly Asp Thr Lys Val Ala Glu Lys Asn Asn Asp
290 295 300

Val Gly Ala Glu Ser Lys Gln Pro Leu Leu Asp Ile Ala Leu Lys Gly

305		310		315		320									
Leu	Lys	Arg	Thr	Leu	Pro	Gln	Leu	Glu	Gln	Met	Asp	Gly	Asn	Ser	Leu
				325					330					335	
Arg	Glu	Asn	Phe	Gln	Glu	Met	Ala	Ser	Gly	Asn	Gly	Pro	Leu	Arg	Ser
			340					345					350		
Leu	Met	Thr	Asn	Leu	Gln	Asn	Leu	Asn	Lys	Ile	Pro	Glu	Ala	Lys	Gln
		355					360					365			
Leu	Asn	Asp	Tyr	Val	Thr	Thr	Leu	Thr	Asn	Ile	Gln	Val	Gly	Val	Ala
	370					375					380				
Arg	Phe	Ser	Gln	Trp	Gly	Thr	Cys	Gly	Gly	Glu	Val	Glu	Arg	Trp	Val
385					390					395					400
Asp	Lys	Ala	Ser	Thr	His	Glu	Leu	Thr	Gln	Ala	Val	Lys	Lys	Ile	His
				405					410					415	
Val	Ile	Ala	Lys	Glu	Leu	Lys	Asn	Val	Thr	Ala	Glu	Leu	Glu	Lys	Ile
			420					425					430		
Glu	Ala	Gly	Ala	Pro	Met	Pro	Gln	Thr	Met	Ser	Gly	Pro	Thr	Leu	Gly
		435					440					445			
Leu	Ala	Arg	Phe	Ala	Val	Ser	Ser	Ile	Pro	Ile	Asn	Gln	Gln	Thr	Gln
	450					455					460				
Val	Lys	Leu	Ser	Asp	Gly	Met	Pro	Val	Pro	Val	Asn	Thr	Leu	Thr	Phe
465					470					475					480
Asp	Gly	Lys	Pro	Val	Ala	Leu	Ala	Gly	Ser	Tyr	Pro	Lys	Asn	Thr	Pro
				485				490						495	
Asp	Ala	Leu	Glu	Ala	His	Met	Lys	Met	Leu	Leu	Glu	Lys	Glu	Cys	Ser
			500					505					510		
Cys	Leu	Val	Val	Leu	Thr	Ser	Glu	Asp	Gln	Met	Gln	Ala	Lys	Gln	Leu
		515					520					525			

Pro Pro Tyr Phe Arg Gly Ser Tyr Thr Phe Gly Glu Val His Thr Asn
530 535 540

Ser Gln Lys Val Ser Ser Ala Ser Gln Gly Glu Ala Ile Asp Gln Tyr
545 550 555 560

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

His Val Lys Asn Trp Pro Asp His Gln Pro Leu Pro Ser Thr Asp Gln
580 585 590

Leu Glu Tyr Leu Ala Asp Arg Val Lys Asn Ser Asn Gln Asn Gly Ala
595 600 605

Pro Gly Arg Ser Ser Ser Asp Lys His Leu Pro Met Ile His Cys Leu
610 615 620

Gly Gly Val Gly Arg Thr Gly Thr Met Ala Ala Ala Leu Val Leu Lys
625 630 635 640

Asp Asn Pro His Ser Asn Leu Glu Gln Val Arg Ala Asp Phe Arg Asp
645 650 655

Ser Arg Asn Asn Arg Met Leu Glu Asp Ala Ser Gln Phe Val Gln Leu
660 665 670

Lys Ala Met Gln Ala Gln Leu Leu Met Thr Thr Ala Ser
675 680 685

<210> 9

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - IpgD

<400> 9

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met His Ile Thr
130 135 140

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

Gly Ala Glu Glu Thr Gly Lys His Lys Gly Val Ser Val Ile Ser Tyr
165 170 175

Gln Arg Val Lys Asn Gly Glu Arg Asn Lys Gly Ile Glu Ala Leu Asn
180 185 190

Arg Leu Tyr Leu Gln Asn Gln Thr Ser Leu Thr Gly Lys Ser Leu Leu
195 200 205

Phe Ala Arg Asp Lys Ala Glu Val Phe Cys Glu Ala Ile Lys Leu Ala
210 215 220

Gly Gly Asp Thr Ser Lys Ile Lys Ala Met Met Glu Arg Leu Asp Thr

225		230		235		240									
Tyr	Lys	Leu	Gly	Glu	Val	Asn	Lys	Arg	His	Ile	Asn	Glu	Leu	Asn	Lys
				245					250					255	
Val	Ile	Ser	Glu	Glu	Ile	Arg	Ala	Gln	Leu	Gly	Ile	Lys	Asn	Lys	Lys
			260					265					270		
Glu	Leu	Gln	Thr	Lys	Ile	Lys	Gln	Ile	Phe	Thr	Asp	Tyr	Leu	Asn	Asn
		275					280					285			
Lys	Asn	Trp	Gly	Pro	Val	Asn	Lys	Asn	Ile	Ser	His	His	Gly	Lys	Asn
	290					295					300				
Tyr	Ser	Phe	Gln	Leu	Thr	Pro	Ala	Ser	His	Met	Lys	Ile	Gly	Asn	Lys
305					310					315					320
Asn	Ile	Phe	Val	Lys	Glu	Tyr	Asn	Gly	Lys	Gly	Ile	Cys	Cys	Ala	Ser
			325					330						335	
Thr	Arg	Glu	Arg	Asp	His	Ile	Ala	Asn	Met	Trp	Leu	Ser	Lys	Val	Val
		340						345					350		
Asp	Asp	Glu	Gly	Lys	Glu	Ile	Phe	Ser	Gly	Ile	Arg	His	Gly	Val	Ile
	355						360					365			
Ser	Ala	Tyr	Gly	Leu	Lys	Lys	Asn	Ser	Ser	Glu	Arg	Ala	Val	Ala	Ala
	370					375					380				
Arg	Asn	Lys	Ala	Glu	Glu	Leu	Val	Ser	Ala	Ala	Leu	Tyr	Ser	Arg	Pro
385					390					395					400
Glu	Leu	Leu	Ser	Gln	Ala	Leu	Ser	Gly	Lys	Thr	Val	Asp	Leu	Lys	Ile
			405					410						415	
Val	Ser	Thr	Ser	Leu	Leu	Thr	Pro	Thr	Ser	Leu	Thr	Gly	Gly	Glu	Glu
		420						425					430		
Ser	Met	Leu	Lys	Asp	Gln	Val	Ser	Ala	Leu	Lys	Gly	Leu	Asn	Ser	Lys
	435						440					445			

Arg Gly Gly Pro Thr Lys Leu Leu Ile Arg Asn Ser Asp Gly Leu Leu
 450 455 460

Lys Glu Val Ser Val Asn Leu Lys Val Val Thr Phe Asn Phe Gly Val
 465 470 475 480

Asn Glu Leu Ala Leu Lys Met Gly Leu Gly Trp Arg Asn Val Asp Lys
 485 490 495

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

Asn Gly Val Ile Gly Gly Trp Ala Ala Glu Ala Ile Glu Lys Asn Pro
 515 520 525

Pro Cys Lys Asn Asp Val Ile Tyr Leu Ala Asn Gln Ile Lys Glu Ile
 530 535 540

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

Ser Gln Arg Val Thr Leu Leu Ala Tyr Thr Ile Gly Ala Val Pro Cys
 565 570 575

Trp Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met Gln Asp Ala Glu
 580 585 590

Ile Lys Arg Glu Ile Ile Arg Lys His Glu Thr Gly Gln Phe Ser Gln
 595 600 605

Leu Asn Ser Lys Leu Ser Ser Glu Glu Lys Arg Leu Phe Ser Thr Ile
 610 615 620

Leu Met Asn Ser Gly Asn Met Glu Ile Gln Glu Met Asn Thr Gly Val
 625 630 635 640

Pro Gly Asn Lys Val Met Lys Lys Leu Pro Leu Ser Ser Leu Glu Leu
 645 650 655

Ser Tyr Ser Glu Arg Ile Gly Asp Pro Lys Ile Trp Asn Met Val Lys

660

665

670

Gly Tyr Ser Ser Phe Val
675

<210> 10
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<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - BepA

<400> 10

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Pro
130 135 140

Lys Ala Lys Ala Lys Thr Lys Asn Thr Glu Ile Ile Ser Pro His His

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

Lys Glu Phe Met His Thr Met Lys Asn Thr Gly Arg Asn Val Asn Asp
 370 375 380

Arg Pro Val Met Val Ala Lys Glu Gly Glu Thr Tyr Thr Gly Thr Tyr
 385 390 395 400

Arg Gly Ala Gly Leu Glu Gly Phe Ala Leu Asn Val Lys Gly Ala Tyr
 405 410 415

Ile Ile Gly Asn Ile Asp His Leu Pro Pro Glu Gln Leu Lys Ile Leu
 420 425 430

Lys Pro Gly Asp Lys Ile Thr Phe Thr Ala Pro Lys Ala Glu
 435 440 445

<210> 11
 <211> 284
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - BepA E305-end

<400> 11

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Gly
130 135 140

Asn Gly Arg Thr Gln Arg Leu Phe Phe Glu Asn Leu Ala Lys Ala Ala
145 150 155 160

Gly His Gln Leu Asn Phe Ser Leu Ile Thr Lys Glu Arg Met Met Val
165 170 175

Ala Ser Val Ala Val Ala Glu Asn Gly Asp Leu Glu Pro Met Gln His
180 185 190

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

Phe Met His Thr Met Lys Asn Thr Gly Arg Asn Val Asn Asp Arg Pro
210 215 220

Val Met Val Ala Lys Glu Gly Glu Thr Tyr Thr Gly Thr Tyr Arg Gly
225 230 235 240

Ala Gly Leu Glu Gly Phe Ala Leu Asn Val Lys Gly Ala Tyr Ile Ile
245 250 255

Gly Asn Ile Asp His Leu Pro Pro Glu Gln Leu Lys Ile Leu Lys Pro
260 265 270

Gly Asp Lys Ile Thr Phe Thr Ala Pro Lys Ala Glu
275 280

<210> 12
<211> 672
<212> PRT
<213> Artificial Sequence

<220>

<223> YopE1-138 - murine Traf6

<400> 12

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
130 135 140

Leu Leu Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Ser Ser Asp
145 150 155 160

Cys Cys Ala Ala Met Ala Ala Ser Cys Ser Ala Ala Val Lys Asp Asp
165 170 175

Ser Val Ser Gly Ser Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met
180 185 190

Glu Glu Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser

195	200	205
Lys Tyr Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln 210 215 220		
Thr Pro Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile 225 230 235 240		
Arg Asp Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu 245 250 255		
Asn Gln Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu 260 265 270		
Thr Val Lys Cys Pro Asn Lys Gly Cys Leu Gln Lys Met Glu Leu Arg 275 280 285		
His Leu Glu Asp His Gln Val His Cys Glu Phe Ala Leu Val Asn Cys 290 295 300		
Pro Gln Cys Gln Arg Pro Phe Gln Lys Cys Gln Val Asn Thr His Ile 305 310 315 320		
Ile Glu Asp Cys Pro Arg Arg Gln Val Ser Cys Val Asn Cys Ala Val 325 330 335		
Ser Met Ala Tyr Glu Glu Lys Glu Ile His Asp Gln Ser Cys Pro Leu 340 345 350		
Ala Asn Ile Ile Cys Glu Tyr Cys Gly Thr Ile Leu Ile Arg Glu Gln 355 360 365		
Met Pro Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys 370 375 380		
Thr Phe Ser Val Phe Gly Cys His Gln Lys Met Gln Arg Asn His Leu 385 390 395 400		
Ala Arg His Leu Gln Glu Asn Thr Gln Leu His Met Arg Leu Leu Ala 405 410 415		

Gln Ala Val His Asn Val Asn Leu Ala Leu Arg Pro Cys Asp Ala Ala
420 425 430

Ser Pro Ser Arg Gly Cys Arg Pro Glu Asp Pro Asn Tyr Glu Glu Thr
435 440 445

Ile Lys Gln Leu Glu Ser Arg Leu Val Arg Gln Asp His Gln Ile Arg
450 455 460

Glu Leu Thr Ala Lys Met Glu Thr Gln Ser Met Tyr Val Gly Glu Leu
465 470 475 480

Lys Arg Thr Ile Arg Thr Leu Glu Asp Lys Val Ala Glu Met Glu Ala
485 490 495

Gln Gln Cys Asn Gly Ile Tyr Ile Trp Lys Ile Gly Lys Phe Gly Met
500 505 510

His Leu Lys Ser Gln Glu Glu Glu Arg Pro Val Val Ile His Ser Pro
515 520 525

Gly Phe Tyr Thr Gly Arg Pro Gly Tyr Lys Leu Cys Met Arg Leu His
530 535 540

Leu Gln Leu Pro Thr Ala Gln Arg Cys Ala Asn Tyr Ile Ser Leu Phe
545 550 555 560

Val His Thr Met Gln Gly Glu Tyr Asp Ser His Leu Pro Trp Pro Phe
565 570 575

Gln Gly Thr Ile Arg Leu Thr Ile Leu Asp Gln Ser Glu Ala Leu Ile
580 585 590

Arg Gln Asn His Glu Glu Val Met Asp Ala Lys Pro Glu Leu Leu Ala
595 600 605

Phe Gln Arg Pro Thr Ile Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val
610 615 620

Thr Phe Met His Leu Glu Ala Leu Arg Gln Gly Thr Phe Ile Lys Asp

625						630						635						640
Asp	Thr	Leu	Leu	Val	Arg	Cys	Glu	Val	Ser	Thr	Arg	Phe	Asp	Met	Gly			
				645					650				655					
Gly	Leu	Arg	Lys	Glu	Gly	Phe	Gln	Pro	Arg	Ser	Thr	Asp	Ala	Gly	Val			
				660					665				670					
<210>	13																	
<211>	326																	
<212>	PRT																	
<213>	Artificial Sequence																	
<220>																		
<223>	YopE1-138 - TIFA																	
<400>	13																	
Met	Lys	Ile	Ser	Ser	Phe	Ile	Ser	Thr	Ser	Leu	Pro	Leu	Pro	Ala	Ser			
1				5				10						15				
Val	Ser	Gly	Ser	Ser	Ser	Val	Gly	Glu	Met	Ser	Gly	Arg	Ser	Val	Ser			
			20				25						30					
Gln	Gln	Lys	Ser	Asp	Gln	Tyr	Ala	Asn	Asn	Leu	Ala	Gly	Arg	Thr	Glu			
		35				40					45							
Ser	Pro	Gln	Gly	Ser	Ser	Leu	Ala	Ser	Arg	Ile	Ile	Glu	Arg	Leu	Ser			
50						55					60							
Ser	Met	Ala	His	Ser	Val	Ile	Gly	Phe	Ile	Gln	Arg	Met	Phe	Ser	Glu			
65					70					75					80			
Gly	Ser	His	Lys	Pro	Val	Val	Thr	Pro	Ala	Leu	Thr	Pro	Ala	Gln	Met			
				85				90					95					
Pro	Ser	Pro	Thr	Ser	Phe	Ser	Asp	Ser	Ile	Lys	Gln	Leu	Ala	Ala	Glu			
			100				105					110						
Thr	Leu	Pro	Lys	Tyr	Met	Gln	Gln	Leu	Ser	Ser	Leu	Asp	Ala	Glu	Thr			
			115				120					125						
Leu	Gln	Lys	Asn	His	Asp	Gln	Phe	Ala	Thr	Leu	Glu	Ser	Arg	Met	Thr			

130

135

140

Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met
 145 150 155 160

Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile
 165 170 175

Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly
 180 185 190

Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser
 195 200 205

Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val
 210 215 220

Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val
 225 230 235 240

Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg
 245 250 255

Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp
 260 265 270

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

Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu
 290 295 300

Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu
 305 310 315 320

Met Asp Glu Asn Glu Ser
 325

<210> 14
 <211> 437
 <212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Cdk1

<400> 14

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Glu Asp Tyr
130 135 140

Thr Lys Ile Glu Lys Ile Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys
145 150 155 160

Gly Arg His Lys Thr Thr Gly Gln Val Val Ala Met Lys Lys Ile Arg
165 170 175

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

Ser Leu Leu Lys Glu Leu Arg His Pro Asn Ile Val Ser Leu Gln Asp
195 200 205

Val Leu Met Gln Asp Ser Arg Leu Tyr Leu Ile Phe Glu Phe Leu Ser
210 215 220

Met Asp Leu Lys Lys Tyr Leu Asp Ser Ile Pro Pro Gly Gln Tyr Met
225 230 235 240

Asp Ser Ser Leu Val Lys Ser Tyr Leu Tyr Gln Ile Leu Gln Gly Ile
245 250 255

Val Phe Cys His Ser Arg Arg Val Leu His Arg Asp Leu Lys Pro Gln
260 265 270

Asn Leu Leu Ile Asp Asp Lys Gly Thr Ile Lys Leu Ala Asp Phe Gly
275 280 285

Leu Ala Arg Ala Phe Gly Ile Pro Ile Arg Val Tyr Thr His Glu Val
290 295 300

Val Thr Leu Trp Tyr Arg Ser Pro Glu Val Leu Leu Gly Ser Ala Arg
305 310 315 320

Tyr Ser Thr Pro Val Asp Ile Trp Ser Ile Gly Thr Ile Phe Ala Glu
325 330 335

Leu Ala Thr Lys Lys Pro Leu Phe His Gly Asp Ser Glu Ile Asp Gln
340 345 350

Leu Phe Arg Ile Phe Arg Ala Leu Gly Thr Pro Asn Asn Glu Val Trp
355 360 365

Pro Glu Val Glu Ser Leu Gln Asp Tyr Lys Asn Thr Phe Pro Lys Trp
370 375 380

Lys Pro Gly Ser Leu Ala Ser His Val Lys Asn Leu Asp Glu Asn Gly
385 390 395 400

Leu Asp Leu Leu Ser Lys Met Leu Ile Tyr Asp Pro Ala Lys Arg Ile

405

410

415

Ser Gly Lys Met Ala Leu Asn His Pro Tyr Phe Asn Asp Leu Asp Asn
 420 425 430

Gln Ile Lys Lys Met
 435

<210> 15
 <211> 347
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - Mad2

<400> 15

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ala

130

135

140

Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu
 145 150 155 160

Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln
 165 170 175

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

Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn
 195 200 205

Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln
 210 215 220

Lys Leu Val Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu
 225 230 235 240

Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser
 245 250 255

Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser
 260 265 270

Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu
 275 280 285

Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val
 290 295 300

Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser
 305 310 315 320

Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn
 325 330 335

Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp
 340 345

<210> 16
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - Ink4A

<400> 16

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Glu
 130 135 140

Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr
 145 150 155 160

Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala
 165 170 175

Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln
180 185 190

Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His
195 200 205

Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
210 215 220

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
225 230 235 240

Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
245 250 255

Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu
260 265 270

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

Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
290 295

<210> 17
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Ink4B

<400> 17

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Arg
130 135 140

Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu
145 150 155 160

Ala Ser Ala Ala Ala Arg Gly Leu Val Glu Lys Val Arg Gln Leu Leu
165 170 175

Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg Ala
180 185 190

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
195 200 205

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
210 215 220

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
225 230 235 240

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
245 250 255

Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly

260

265

270

Tyr Leu Arg Thr Ala Thr Gly Asp
275 280

<210> 18

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Ink4C

<400> 18

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ala
130 135 140

Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly Asp Leu

145		150		155		160									
Glu	Gln	Leu	Thr	Ser	Leu	Leu	Gln	Asn	Asn	Val	Asn	Val	Asn	Ala	Gln
				165					170					175	
Asn	Gly	Phe	Gly	Arg	Thr	Ala	Leu	Gln	Val	Met	Lys	Leu	Gly	Asn	Pro
			180					185					190		
Glu	Ile	Ala	Arg	Arg	Leu	Leu	Leu	Arg	Gly	Ala	Asn	Pro	Asp	Leu	Lys
		195					200					205			
Asp	Arg	Thr	Gly	Phe	Ala	Val	Ile	His	Asp	Ala	Ala	Arg	Ala	Gly	Phe
	210					215					220				
Leu	Asp	Thr	Leu	Gln	Ala	Leu	Pro	Glu	Phe	Gln	Ala	Asp	Val	Asn	Ile
225					230					235					240
Glu	Asp	Asn	Glu	Gly	Asn	Leu	Pro	Leu	His	Leu	Ala	Ala	Lys	Glu	Gly
				245					250					255	
His	Leu	Arg	Val	Val	Glu	Phe	Leu	Val	Lys	His	Thr	Ala	Ser	Asn	Val
			260					265					270		
Gly	His	Arg	Asn	His	Lys	Gly	Asp	Thr	Ala	Cys	Asp	Leu	Ala	Arg	Leu
		275					280					285			
Tyr	Gly	Arg	Asn	Glu	Val	Val	Ser	Leu	Met	Gln	Ala	Asn	Gly	Ala	Gly
	290					295					300				
Gly	Ala	Thr	Asn	Leu	Gln										
305					310										

<210> 19
 <211> 329
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - z-Bid

<400> 19

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser

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

Ala Glu Glu Ala Arg Ala Ala Arg Glu Met Ala Ala Glu Leu Ile Arg
 225 230 235 240

Ile Ala Asp Leu Leu Glu Gln Ser Val Leu Ser Gln Ala Ala Glu Ser
 245 250 255

Leu Thr Lys Lys Leu Arg Ser Phe Gln Glu Gln Val Trp Ala Ser His
 260 265 270

Leu Ser Lys Gly Val Gln Thr Leu Leu Gln His Val Ala Ala Ala Lys
 275 280 285

Glu Phe Lys Lys Glu Leu Val Glu Met Ala Phe Thr Phe Met Leu Met
 290 295 300

Lys Thr Val Cys Glu Arg Thr Pro Asp Phe Leu Phe Gly Leu Tyr Gly
 305 310 315 320

Thr Val Val Gln Phe Phe Gly Ser Asn
 325

<210> 20
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - z-t-Bid

<400> 20

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Gly His
130 135 140

Ser Pro Pro Ala Thr Tyr Arg Asp Leu Leu His Glu Leu Gln His Glu
145 150 155 160

Val Gln Pro Gly Leu Ser Val Asn Ala Glu Glu Ala Arg Ala Ala Arg
165 170 175

Glu Met Ala Ala Glu Leu Ile Arg Ile Ala Asp Leu Leu Glu Gln Ser
180 185 190

Val Leu Ser Gln Ala Ala Glu Ser Leu Thr Lys Lys Leu Arg Ser Phe
195 200 205

Gln Glu Gln Val Trp Ala Ser His Leu Ser Lys Gly Val Gln Thr Leu
210 215 220

Leu Gln His Val Ala Ala Ala Lys Glu Phe Lys Lys Glu Leu Val Glu
225 230 235 240

Met Ala Phe Thr Phe Met Leu Met Lys Thr Val Cys Glu Arg Thr Pro
245 250 255

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

Asn

<210> 21
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - z-BIM

<400> 21

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Ser
130 135 140

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

Ser Gly Glu Ser Thr Gly Gly Gly Val Val Leu Pro Ala Gly His Phe

165

170

175

Asp Phe Pro Gln Pro Gly Glu Gly Asp Pro Leu Arg Gly Gly Ile Ser
 180 185 190

Met Ser Asn Asn Gln Ser Arg Ser Pro Met Asn Arg Thr Phe Ser Arg
 195 200 205

Ser Ser Ser Gly Tyr Phe Ser Val Asp Ser Asp Ser Val Pro Gly Ser
 210 215 220

Pro Leu Met Pro Asn Ile Ser Glu Ala Gln Asp Gly Gln Asn Asp Glu
 225 230 235 240

Val Trp Leu Ser Glu His Ser His Gln His Leu Gln Met Ala Ala Pro
 245 250 255

Val Ala Ala Leu Pro Pro Glu Met Val Val Ala Arg Glu Leu Arg Arg
 260 265 270

Ile Gly Asp Glu Phe Asn Arg Leu Tyr Cys Glu Ala Gly Ala Gly Val
 275 280 285

Asn Gln Leu Arg Ala Pro Asn Glu His Ala Ile Val Leu Trp Met Asn
 290 295 300

Val Ile Ile Gly Arg Leu Val His Phe Phe Leu Arg Arg Arg
 305 310 315

<210> 22

<211> 289

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Caspase3 p17

<400> 22

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser

30

Arg Ser Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile
225 230 235 240

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

Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe
260 265 270

Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr
275 280 285

Asp

<210> 23

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Caspase3 p10/12

<400> 23

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Gly Val Asp
130 135 140

Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp Phe Leu Tyr
145 150 155 160

Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp
165 170 175

Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys Gln Tyr Ala
180 185 190

Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn Arg Lys Val
195 200 205

Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe His Ala Lys
210 215 220

Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu Leu Tyr Phe
225 230 235 240

Tyr His

<210> 24
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - human Bid

<400> 24

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Asp
130 135 140

Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile Thr Asn
145 150 155 160

Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser Phe Arg
165 170 175

Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala Pro Gln
180 185 190

Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser Ser His
195 200 205

Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu Asp Ile
210 215 220

Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp
225 230 235 240

Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln Leu Arg

245

250

255

Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala Thr Ala
 260 265 270

Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys Glu Lys
 275 280 285

Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala Ser His
 290 295 300

Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn Phe Ile
 305 310 315 320

Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn Gly Met
 325 330 335

Asp

<210> 25

<211> 277

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - human t-Bid

<400> 25

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu

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

<210> 26
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - Rac1 Q61E

<400> 26

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gln Ala Ile Lys
 130 135 140

Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile
 145 150 155 160

Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe
 165 170 175

Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly Lys Pro Val Asn Leu
180 185 190

Gly Leu Trp Asp Thr Ala Gly Glu Glu Asp Tyr Asp Arg Leu Arg Pro
195 200 205

Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile Cys Phe Ser Leu Val
210 215 220

Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys Trp Tyr Pro Glu Val
225 230 235 240

Arg His His Cys Pro Asn Thr Pro Ile Ile Leu Val Gly Thr Lys Leu
245 250 255

Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys Leu Lys Glu Lys Lys
260 265 270

Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala Met Ala Lys Glu Ile
275 280 285

Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Arg Gly Leu
290 295 300

Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val Leu Cys Pro Pro Pro
305 310 315 320

Val Lys Lys Arg Lys Arg Lys
325

<210> 27
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - RhoA Q63L

<400> 27

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Ala Ala Ile
130 135 140

Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys
145 150 155 160

Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu Val Tyr Val Pro
165 170 175

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

Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Leu Glu Asp Tyr Asp Arg
195 200 205

Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe
210 215 220

Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr

225 230 235 240
 Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly
 245 250 255
 Asn Lys Lys Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala
 260 265 270
 Lys Met Lys Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala
 275 280 285
 Asn Arg Ile Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys
 290 295 300
 Asp Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln
 305 310 315 320
 Ala Arg Arg Gly Lys Lys Lys Ser Gly Cys Leu Val Leu
 325 330

 <210> 28
 <211> 350
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> YopE1-138 - FADD

 <400> 28
 Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

 Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

 Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

 Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

 Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu

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

Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His Leu Val
 290 295 300

Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu Val Gln
 305 310 315 320

Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala Met Ser
 325 330 335

Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
 340 345 350

<210> 29
 <211> 308
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - Bad

<400> 29

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Phe Gln Ile
130 135 140

Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser Ser Ala Glu Arg
145 150 155 160

Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser Gly Ser Gly Lys
165 170 175

His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala Ser His Gln Gln
180 185 190

Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala Gly Ala Val Glu
195 200 205

Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr Glu Asp Asp Glu
210 215 220

Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg Ser Arg Ser Ala
225 230 235 240

Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg
245 250 255

Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly Leu Pro Arg Pro
260 265 270

Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser Ser Ser Trp Thr
275 280 285

Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly Arg Gly Ser Thr
290 295 300

Ala Pro Ser Gln
305

<210> 30

<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - GPCR GNA12

<400> 30

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Ser Gly Val
130 135 140

Val Gly Pro Met Gln Glu Pro Gly Ala Leu Asp Val Gly Gly Leu Arg
145 150 155 160

Ser Gln Arg Gln Lys Trp Phe Gln Cys Phe Asp Gly Ile Thr Ser Ile
165 170 175

Leu Phe Met Val Ser Ser Ser Glu Tyr Asp Gln Val Leu Met Glu Asp

180

185

190

Arg Arg Thr Asn Arg Leu Val Glu Ser Met Asn Ile Phe Glu Thr Ile
 195 200 205

Val Asn Asn Lys Leu Phe Phe Asn Val Ser Ile Ile Leu Phe Leu Asn
 210 215 220

Lys Met Asp Leu Leu Val Glu Lys Val Lys Thr Val Ser Ile Lys Lys
 225 230 235 240

His Phe Pro Asp Phe Arg Gly Asp Pro His Arg Leu Glu Asp Val Gln
 245 250 255

Arg Tyr Leu Val Gln Cys Phe Asp Arg Lys Arg Arg Asn Arg Ser Lys
 260 265 270

Pro Leu Phe His His Phe Thr Thr Ala Ile Asp Thr Glu Asn Val Arg
 275 280 285

Phe Val Phe His Ala Val Lys Asp Thr Ile Leu Gln Glu Asn Leu Lys
 290 295 300

Asp Ile Met Leu Gln
 305

<210> 31
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - VhH4 nanobody recognizing EGFP

<400> 31

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu

35

40

45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Asp
 130 135 140

Gln Val Gln Leu Val Glu Ser Gly Gly Ala Leu Val Gln Pro Gly Gly
 145 150 155 160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Val Asn Arg Tyr
 165 170 175

Ser Met Arg Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Trp Val
 180 185 190

Ala Gly Met Ser Ser Ala Gly Asp Arg Ser Ser Tyr Glu Asp Ser Val
 195 200 205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Arg Asn Thr Val Tyr
 210 215 220

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 225 230 235 240

Asn Val Asn Val Gly Phe Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr
 245 250 255

Val Ser Ser

<210> 32
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Slmb1-VhH4

<400> 32

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Lys Met
130 135 140

Met Lys Met Glu Thr Asp Lys Ile Met Asp Glu Thr Asn Ser Asn Ala
145 150 155 160

Gln Ala Phe Thr Thr Thr Met Leu Tyr Asp Pro Val Arg Lys Lys Asp
165 170 175

Ser Ser Pro Thr Tyr Gln Thr Glu Arg Glu Leu Cys Phe Gln Tyr Phe
180 185 190

Thr Gln Trp Ser Glu Ser Gly Gln Val Asp Phe Val Glu His Leu Leu
195 200 205

Ser Arg Met Cys His Tyr Gln His Gly Gln Ile Asn Ala Tyr Leu Lys
210 215 220

Pro Met Leu Gln Arg Asp Phe Ile Thr Leu Leu Pro Ile Lys Gly Leu
225 230 235 240

Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu Asp Ala Glu Ser Leu
245 250 255

Lys Ser Ser Glu Leu Val Cys Lys Glu Trp Leu Arg Val Ile Ser Glu
260 265 270

Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Lys Val Arg Thr Asp Ser
275 280 285

Leu Trp Arg Gly Leu Ala Glu Arg Arg Asn Trp Met Gln Tyr Leu Phe
290 295 300

Lys Pro Arg Pro Gly Gln Thr Gln Arg Pro His Ser Phe His Arg Glu
305 310 315 320

Leu Phe Pro Lys Ile Met Asn Asp Ile Asp Ser Ile Glu Asn Asn Trp
325 330 335

Arg Thr Gly Arg His Met Asp Gln Val Gln Leu Val Glu Ser Gly Gly
340 345 350

Ala Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
355 360 365

Gly Phe Pro Val Asn Arg Tyr Ser Met Arg Trp Tyr Arg Gln Ala Pro

370

375

380

Gly Lys Glu Arg Glu Trp Val Ala Gly Met Ser Ser Ala Gly Asp Arg
 385 390 395 400

Ser Ser Tyr Glu Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 405 410 415

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

Asp Thr Ala Val Tyr Tyr Cys Asn Val Asn Val Gly Phe Glu Tyr Trp
 435 440 445

Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 450 455

<210> 33

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - NLS-Slmb1-VhH4

<400> 33

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met

85

90

95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Pro Pro
 130 135 140

Lys Lys Lys Arg Lys Val Gln Phe Lys Met Met Lys Met Glu Thr Asp
 145 150 155 160

Lys Ile Met Asp Glu Thr Asn Ser Asn Ala Gln Ala Phe Thr Thr Thr
 165 170 175

Met Leu Tyr Asp Pro Val Arg Lys Lys Asp Ser Ser Pro Thr Tyr Gln
 180 185 190

Thr Glu Arg Glu Leu Cys Phe Gln Tyr Phe Thr Gln Trp Ser Glu Ser
 195 200 205

Gly Gln Val Asp Phe Val Glu His Leu Leu Ser Arg Met Cys His Tyr
 210 215 220

Gln His Gly Gln Ile Asn Ala Tyr Leu Lys Pro Met Leu Gln Arg Asp
 225 230 235 240

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

Ile Leu Ser Tyr Leu Asp Ala Glu Ser Leu Lys Ser Ser Glu Leu Val
 260 265 270

Cys Lys Glu Trp Leu Arg Val Ile Ser Glu Gly Met Leu Trp Lys Lys
 275 280 285

Leu Ile Glu Arg Lys Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala
 290 295 300

Glu Arg Arg Asn Trp Met Gln Tyr Leu Phe Lys Pro Arg Pro Gly Gln
 305 310 315 320

Thr Gln Arg Pro His Ser Phe His Arg Glu Leu Phe Pro Lys Ile Met
 325 330 335

Asn Asp Ile Asp Ser Ile Glu Asn Asn Trp Arg Thr Gly Arg His Leu
 340 345 350

Glu Met Asp Gln Val Gln Leu Val Glu Ser Gly Gly Ala Leu Val Gln
 355 360 365

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Val
 370 375 380

Asn Arg Tyr Ser Met Arg Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg
 385 390 395 400

Glu Trp Val Ala Gly Met Ser Ser Ala Gly Asp Arg Ser Ser Tyr Glu
 405 410 415

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Arg Asn
 420 425 430

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 435 440 445

Tyr Tyr Cys Asn Val Asn Val Gly Phe Glu Tyr Trp Gly Gln Gly Thr
 450 455 460

Gln Val Thr Val Ser Ser
 465 470

<210> 34
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - Slmb1-VhH4-NLS

<400> 34

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Lys Met
130 135 140

Met Lys Met Glu Thr Asp Lys Ile Met Asp Glu Thr Asn Ser Asn Ala
145 150 155 160

Gln Ala Phe Thr Thr Thr Met Leu Tyr Asp Pro Val Arg Lys Lys Asp
165 170 175

Ser Ser Pro Thr Tyr Gln Thr Glu Arg Glu Leu Cys Phe Gln Tyr Phe
180 185 190

Thr Gln Trp Ser Glu Ser Gly Gln Val Asp Phe Val Glu His Leu Leu
195 200 205

Ser Arg Met Cys His Tyr Gln His Gly Gln Ile Asn Ala Tyr Leu Lys

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

Asp Thr Ala Val Tyr Tyr Cys Asn Val Asn Val Gly Phe Glu Tyr Trp
435 440 445

Gly Gln Gly Thr Gln Val Thr Val Ser Ser Pro Pro Lys Lys Lys Arg
450 455 460

Lys Val
465

<210> 35
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Akt PH-domain

<400> 35

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Ala Ile
130 135 140

Val Lys Glu Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp
145 150 155 160

Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr
165 170 175

Lys Glu Arg Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn
180 185 190

Phe Ser Val Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro
195 200 205

Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg
210 215 220

Thr Phe His Val Glu Thr Pro Glu Glu Arg Glu Glu Trp Thr Thr Ala
225 230 235 240

Ile Gln Thr Val Ala Asp
245

<210> 36
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - ET1

<400> 36

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Pro
130 135 140

Arg Pro Lys Leu Lys Ser Asp Asp Glu Val Leu Glu Ala Ala Thr Val
145 150 155 160

Val Leu Lys Arg Cys Gly Pro Ile Glu Phe Thr Leu Ser Gly Val Ala
165 170 175

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

Arg Asp Thr Leu Leu Val Arg Met Met Glu Arg Gly Val Glu Gln Val
195 200 205

Arg His Tyr Leu Asn Ala Ile Pro Ile Gly Ala Gly Pro Gln Gly Leu
210 215 220

Trp Glu Phe Leu Gln Val Leu Val Arg Ser Met Asn Thr Arg Asn Asp
225 230 235 240

Phe Ser Val Asn Tyr Leu Ile Ser Trp Tyr Glu Leu Gln Val Pro Glu
245 250 255

Leu Arg Thr Leu Ala Ile Gln Arg Asn Arg Ala Val Val Glu Gly Ile

260		265		270
Arg	Lys	Arg	Leu	Pro
	275			
		Pro	Gly	Ala
			280	
		Pro	Ala	Ala
				Ala
				Glu
				285
				Leu
				Leu
				Leu
His	Ser	Val	Ile	Ala
	290			
		Gly	Ala	Thr
		295		
		Met	Gln	Trp
				Ala
				300
				Val
				Asp
				Pro
				Asp
Gly	Glu	Leu	Ala	Asp
305				
		His	Val	Leu
		310		
			Ala	Gln
				Ile
				315
				Ala
				Ala
				Ile
				Leu
				Cys
				320
Leu	Met	Phe	Pro	Glu
				325
				His
				Asp
				Asp
				Phe
				Gln
				330
				Leu
				Leu
				Gln
				Ala
				His
				335
				Ala
Ser	Ala	Tyr	Ser	Arg
				340
				Ala
				Arg
				Thr
				Lys
				345
				Asn
				Asn
				Tyr
				Gly
				350
				Ser
				Thr
				Ile
Glu	Gly	Leu	Leu	Asp
				355
				Leu
				Pro
				Asp
				360
				Asp
				Asp
				Ala
				Pro
				365
				Glu
				Glu
				Ala
				Gly
Leu	Ala	Ala	Pro	Arg
				370
				Leu
				Ser
				375
				Phe
				Leu
				Pro
				Ala
				Gly
				380
				His
				Thr
				Arg
				Arg
Leu	Ser	Thr	Ala	Pro
385				
				Pro
				390
				Thr
				Asp
				Val
				Ser
				395
				Leu
				Gly
				Asp
				Glu
				Leu
				His
				400
Leu	Asp	Gly	Glu	Asp
				405
				Val
				Ala
				Met
				Ala
				His
				410
				Ala
				Asp
				Ala
				Leu
				Asp
				415
Phe	Asp	Leu	Asp	Met
				420
				Leu
				Gly
				Asp
				Gly
				425
				Asp
				Ser
				Pro
				Gly
				430
				Pro
				Gly
				Phe
Thr	Pro	His	Asp	Ser
				435
				Ala
				Pro
				Tyr
				440
				Gly
				Ala
				Leu
				Asp
				Met
				445
				Ala
				Asp
				Phe
Glu	Phe	Glu	Gln	Met
				450
				Phe
				Thr
				455
				Asp
				Ala
				Leu
				Gly
				Ile
				460
				Asp
				Glu
				Tyr
				Gly
Gly				
465				

<210> 37
 <211> 381
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - EGFP

<400> 37

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Met Val
 130 135 140

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 145 150 155 160

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 165 170 175

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
180 185 190

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr
195 200 205

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
210 215 220

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
225 230 235 240

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

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
260 265 270

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
275 280 285

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
290 295 300

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
305 310 315 320

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
325 330 335

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
340 345 350

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
355 360 365

Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
370 375 380

<210> 38

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

<220>
<223> YopE1-138 - 2xTEVsite - NLS - EGFP

<400> 38

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
130 135 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Pro Pro Lys Lys
145 150 155 160

Lys Arg Lys Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
165 170 175

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser

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

Tyr Lys

<210> 39
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - 2xTEVsite - EGFP - NLS

<400> 39

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
130 135 140

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

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
165 170 175

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
180 185 190

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
195 200 205

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val
210 215 220

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
225 230 235 240

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
245 250 255

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
260 265 270

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

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
290 295 300

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
305 310 315 320

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
325 330 335

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
340 345 350

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
355 360 365

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly

370

375

380

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Pro Pro Lys Lys Lys Arg
 385 390 395 400

Lys Val

<210> 40

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - 2x TEVsite - INK4C

<400> 40

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn

130

135

140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Met Ala Glu Pro
 145 150 155 160

Trp Gly Asn Glu Leu Ala Ser Ala Ala Arg Gly Asp Leu Glu Gln
 165 170 175

Leu Thr Ser Leu Leu Gln Asn Asn Val Asn Val Asn Ala Gln Asn Gly
 180 185 190

Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly Asn Pro Glu Ile
 195 200 205

Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp Leu Lys Asp Arg
 210 215 220

Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala Gly Phe Leu Asp
 225 230 235 240

Thr Leu Gln Ala Leu Pro Glu Phe Gln Ala Asp Val Asn Ile Glu Asp
 245 250 255

Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys Glu Gly His Leu
 260 265 270

Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser Asn Val Gly His
 275 280 285

Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala Arg Leu Tyr Gly
 290 295 300

Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly Ala Gly Gly Ala
 305 310 315 320

Thr Asn Leu Gln

<210> 41

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - 2x TEVsite - ET1

<400> 41

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
130 135 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Met Pro Arg Pro
145 150 155 160

Lys Leu Lys Ser Asp Asp Glu Val Leu Glu Ala Ala Thr Val Val Leu
165 170 175

Lys Arg Cys Gly Pro Ile Glu Phe Thr Leu Ser Gly Val Ala Lys Glu
180 185 190

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

Thr Leu Leu Val Arg Met Met Glu Arg Gly Val Glu Gln Val Arg His
210 215 220

Tyr Leu Asn Ala Ile Pro Ile Gly Ala Gly Pro Gln Gly Leu Trp Glu
225 230 235 240

Phe Leu Gln Val Leu Val Arg Ser Met Asn Thr Arg Asn Asp Phe Ser
245 250 255

Val Asn Tyr Leu Ile Ser Trp Tyr Glu Leu Gln Val Pro Glu Leu Arg
260 265 270

Thr Leu Ala Ile Gln Arg Asn Arg Ala Val Val Glu Gly Ile Arg Lys
275 280 285

Arg Leu Pro Pro Gly Ala Pro Ala Ala Ala Glu Leu Leu Leu His Ser
290 295 300

Val Ile Ala Gly Ala Thr Met Gln Trp Ala Val Asp Pro Asp Gly Glu
305 310 315 320

Leu Ala Asp His Val Leu Ala Gln Ile Ala Ala Ile Leu Cys Leu Met
325 330 335

Phe Pro Glu His Asp Asp Phe Gln Leu Leu Gln Ala His Ala Ser Ala
340 345 350

Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
355 360 365

Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
370 375 380

Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
385 390 395 400

Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp

405

410

415

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 420 425 430

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 435 440 445

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 450 455 460

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
 465 470 475

<210> 42

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - TEV protease S219V

<400> 42

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu

100	105	110
Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr		
115	120	125
Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Glu Ser Leu Phe		
130	135	140
Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu		
145	150	155
Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe		
	165	170
Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly		
	180	185
Thr Leu Leu Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr		
	195	200
Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile		
	210	215
Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg		
225	230	235
Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln		
	245	250
Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro		
	260	265
Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly		
	275	280
Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly		
	290	295
Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser		
305	310	315
		320

Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln
325 330 335

Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly
340 345 350

His Lys Val Phe Met Val Lys Pro Glu Glu Pro Phe Gln Pro Val Lys
355 360 365

Glu Ala Thr Gln Leu Met Asn Arg Arg Arg Arg Arg
370 375 380

<210> 43
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - 2x TEVsite - Flag - INK4C

<400> 43

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Glu Asn
130 135 140

Leu Tyr Phe Gln Ser Glu Asn Leu Tyr Phe Gln Ser Asp Tyr Lys Asp
145 150 155 160

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

Ala Ala Arg Gly Asp Leu Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn
180 185 190

Val Asn Val Asn Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val
195 200 205

Met Lys Leu Gly Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly
210 215 220

Ala Asn Pro Asp Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp
225 230 235 240

Ala Ala Arg Ala Gly Phe Leu Asp Thr Leu Gln Ala Leu Pro Glu Phe
245 250 255

Gln Ala Asp Val Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His
260 265 270

Leu Ala Ala Lys Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys
275 280 285

His Thr Ala Ser Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala
290 295 300

Cys Asp Leu Ala Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met
305 310 315 320

Gln Ala Asn Gly Ala Gly Gly Ala Thr Asn Leu Gln

<210> 44
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_285

<400> 44
 cataccatgg gagtgagcaa gggcgag 27

<210> 45
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_286

<400> 45
 ggaagatctt tacttgtaca gctcgtccat 30

<210> 46
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_287

<400> 46
 cggggtacct caactaaatg accgtggtg 29

<210> 47
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_288

<400> 47
 gttaaagctt ttcgaatcta gactcgagcg tggcgaactg gtc 43

<210> 48
 <211> 35
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<213> Artificial Sequence
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 <223> Primer No. : Si_292
 <400> 48
 cagtctcgag caaattctaa acaaaatact tccac 35

<210> 49
 <211> 32
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_293
 <400> 49
 cagtttcgaa ttaatttgta ttgctttgac gg 32

<210> 50
 <211> 34
 <212> DNA
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 <223> Primer No. : Si_296
 <400> 50
 cagtctcgag actaacataa cactatccac ccag 34

<210> 51
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_297
 <400> 51
 gttaaagctt tcaggaggca ttctgaag 28

<210> 52
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_299
 <400> 52

cagtctcgag caggccatca agtgtgtg	28
<210> 53	
<211> 33	
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<220>	
<223> Primer No. : Si_300	
<400> 53	
cagtttcgaa tcattttctc ttcctcttct tca	33
<210> 54	
<211> 24	
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<223> Primer No. : Si_301	
<400> 54	
cagtctcgag gctgccatcc ggaa	24
<210> 55	
<211> 28	
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<220>	
<223> Primer No. : Si_302	
<400> 55	
cagtttcgaa tcacaagaca aggcaccc	28
<210> 56	
<211> 34	
<212> DNA	
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<220>	
<223> Primer No. : Si_306	
<400> 56	
gttaaagctt ggaggcattc tgaagatact tatt	34
<210> 57	
<211> 35	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Primer No. : Si_307

<400> 57

cagtctcgag caaatacaga gcttctatca ctcag

35

<210> 58

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer No. : Si_308

<400> 58

gttaaagctt tcaagatgtg attaatagaag aaatg

35

<210> 59

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer No. : Si_317

<400> 59

cagtttcgaa cccataaaaa agccctgtc

29

<210> 60

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer No. : Si_318

<400> 60

gttaaagctt ctactctatc atcaaacgat aaaatgg

37

<210> 61

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer No. : Si_324

<400> 61

cagtctcgag ttcactcaag aaacgcaaa	29
<210> 62	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_339	
<400> 62	
cagtttcgaa ttttctcttc ctcttcttca cg	32
<210> 63	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_341	
<400> 63	
cgtatctaga aaaatgatga aaatggagac tg	32
<210> 64	
<211> 28	
<212> DNA	
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<220>	
<223> Primer No. : Si_342	
<400> 64	
gttaaagctt ttagctggag acggtgac	28
<210> 65	
<211> 29	
<212> DNA	
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<220>	
<223> Primer No. : Si_346	
<400> 65	
cagtctcgag ttccagatcc cagagtttg	29
<210> 66	
<211> 24	
<212> DNA	

<213> Artificial Sequence

 <220>
 <223> Primer No. : Si_347

 <400> 66
 gttaaagctt tcactgggag gggg 24

 <210> 67
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_351

 <400> 67
 cagtctcgag ctcgagttat ctactcatag aaactacttt tgcag 45

 <210> 68
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_352

 <400> 68
 cgcggatcct cagtgtctct gcggcatta 29

 <210> 69
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_353

 <400> 69
 catttatcc tcctagttag tcacagcaac tgctgctcct ttc 43

 <210> 70
 <211> 43
 <212> DNA
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 <220>
 <223> Primer No. : Si_354

 <400> 70

gaaaggagca gcagttgctg tgactaacta ggaggaataa atg 43

<210> 71
 <211> 41
 <212> DNA
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<220>
 <223> Primer No. : Si_355

<400> 71
 cgattcacgg attgctttct cattattccc tccaggtact a 41

<210> 72
 <211> 41
 <212> DNA
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<220>
 <223> Primer No. : Si_356

<400> 72
 tagtacctgg aggggaataat gagaaagcaa tccgtgaatc g 41

<210> 73
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_357

<400> 73
 cgtatctaga cggctttaag tgcgacattc 30

<210> 74
 <211> 36
 <212> DNA
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<220>
 <223> Primer No. : Si_364

<400> 74
 cgtatctaga ctaaagtatg aggagagaaa attgaa 36

<210> 75
 <211> 25
 <212> DNA

<213> Artificial Sequence
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 <223> Primer No. : Si_365
 <400> 75
 gttaaagctt tcagcttgcc gtcgt 25

<210> 76
 <211> 26
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 <213> Artificial Sequence
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 <223> Primer No. : Si_367
 <400> 76
 cgtatctaga gacccgttcc tgggtgc 26

<210> 77
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 <212> DNA
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 <223> Primer No. : Si_369
 <400> 77
 cgtatctaga ccccccaaga agaagc 26

<210> 78
 <211> 26
 <212> DNA
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 <223> Primer No. : Si_373
 <400> 78
 gttaaagctt gctggagacg gtgacc 26

<210> 79
 <211> 30
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 <223> Primer No. : Si_386
 <400> 79

cgatatctaga tcaggacgct tcggaggtag 30

<210> 80
<211> 30
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<220>
<223> Primer No. : Si_387

<400> 80
cgatatctaga atggactgtg aggtcaacaa 30

<210> 81
<211> 23
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<220>
<223> Primer No. : Si_389

<400> 81
cgatatctaga ggcaaccgca gca 23

<210> 82
<211> 29
<212> DNA
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<220>
<223> Primer No. : Si_391

<400> 82
gttaaagctt tcagtccatc ccatttctg 29

<210> 83
<211> 29
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<220>
<223> Primer No. : Si_403

<400> 83
cgatatctaga tctggaatat ccctggaca 29

<210> 84
<211> 30
<212> DNA

<213> Artificial Sequence
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 <223> Primer No. : Si_406
 <400> 84
 gttaaagctt gtctgtctca atgccacagt 30

<210> 85
 <211> 25
 <212> DNA
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 <223> Primer No. : Si_410
 <400> 85
 cagtctcgag atgtccgggg tgggtg 25

<210> 86
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer No. : Si_413
 <400> 86
 cagtttcgaa tcactgcagc atgatgtc 28

<210> 87
 <211> 31
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_417
 <400> 87
 cagtctcgag agtgggtgtg atgatgacat g 31

<210> 88
 <211> 40
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_420
 <400> 88

cagtttcgaa ttagtgataa aaatagagtt cttttgtgag 40

<210> 89
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_423

<400> 89
cagtctcgag atgcacataa ctaatttggg att 33

<210> 90
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_424

<400> 90
cagtttcgaa ttatacaaat gacgaatacc cttt 34

<210> 91
<211> 52
<212> DNA
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<220>
<223> Primer No. : Si_425

<400> 91
gttaaagctt ttacaccttg cgcttcttct tgggcgggct ggagacggtg ac 52

<210> 92
<211> 31
<212> DNA
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<220>
<223> Primer No. : Si_428

<400> 92
cgtatctaga atggacttca acaggaactt t 31

<210> 93
<211> 28
<212> DNA

<213> Artificial Sequence
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 <223> Primer No. : Si_429
 <400> 93
 cgtatctaga ggacatagtc caccagcg 28

<210> 94
 <211> 29
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_430
 <400> 94
 gttaaagctt tcagttggat ccgaaaaac 29

<210> 95
 <211> 34
 <212> DNA
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 <223> Primer No. : Si_433
 <400> 95
 cgtatctaga gaattaaaaa aaacactcat ccca 34

<210> 96
 <211> 29
 <212> DNA
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 <223> Primer No. : Si_434
 <400> 96
 cgtatctaga ccaaaggcaa aagcaaaaa 29

<210> 97
 <211> 29
 <212> DNA
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 <223> Primer No. : Si_435
 <400> 97

gttaaagctt ttagctagcc atggcaagc 29

<210> 98
 <211> 22
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<220>
 <223> Primer No. : Si_436

<400> 98
 cgtatctaga atgccccgcc cc 22

<210> 99
 <211> 31
 <212> DNA
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<220>
 <223> Primer No. : Si_437

<400> 99
 gttaaagctt ctaccaccg tactcgtcaa t 31

<210> 100
 <211> 31
 <212> DNA
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<220>
 <223> Primer No. : Si_438

<400> 100
 cgtatctaga atgtctgaca cgtccagaga g 31

<210> 101
 <211> 32
 <212> DNA
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<220>
 <223> Primer No. : Si_439

<400> 101
 gttaaagctt tcattcttctt cgcaggaaaa ag 32

<210> 102
 <211> 30
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<213> Artificial Sequence
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 <223> Primer No. : Si_445
 <400> 102
 cgcggtatcct tatgggttct cacagcaaaa 30

<210> 103
 <211> 43
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 <223> Primer No. : Si_446
 <400> 103
 catttattcc tcctagttag tcaaggcaac agccaatcaa gag 43

<210> 104
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 <223> Primer No. : Si_447
 <400> 104
 ctcttgattg gctgttgctt tgactaacta ggaggaataa atg 43

<210> 105
 <211> 41
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 <400> 105
 ttgattgcag tgacatggtg cattattccc tccaggtact a 41

<210> 106
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 <400> 106

tagtacctgg agggaataat gcaccatgtc actgcaatca a	41
<210> 107	
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cgtatctaga tagccgcaga tgttggtatg	30
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<400> 108	
cgtatctaga gatcaagtcc aactggtgg	29
<210> 109	
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<400> 109	
cagtctcgag gaaagcttgt ttaaggggc	29
<210> 110	
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<400> 110	
cagtttcgaa ttagcgacgg cgacg	25
<210> 111	
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 <223> Primer No. : Si_476
 <400> 111
 gttaaagctt ttacttgtac agctcgtcca t 31

<210> 112
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 <223> Primer No. : Si_477
 <400> 112
 cgtatctaga gtgagcaagg gcgag 25

<210> 113
 <211> 37
 <212> DNA
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 <223> Primer No. : Si_478
 <400> 113
 cagtctcgag atggaagatt ataccaaaat agagaaa 37

<210> 114
 <211> 36
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer No. : Si_479
 <400> 114
 gttaaagctt ctacatcttc ttaatctgat tgtcca 36

<210> 115
 <211> 24
 <212> DNA
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 <223> Primer No. : Si_482
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cgtatctaga atggcgctgc agct	24
<210> 116	
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gttaaagctt tcagtcattg acaggaattt tg	32
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cgtatctaga atggagccgg cggcg	25
<210> 118	
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<223> Primer No. : Si_487	
<400> 118	
gttaaagctt tcaatcgggg atgtctg	27
<210> 119	
<211> 30	
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<223> Primer No. : Si_492	
<400> 119	
cgtatctaga atgcgcgagg agaacaaggg	30
<210> 120	
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<220>

<223> Primer No. : Si_493

<400> 120
gttaaagctt tcagtcccct gtggctgtgc 30

<210> 121
<211> 24
<212> DNA
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<220>

<223> Primer No. : Si_494

<400> 121
cgtatctaga atggccgagc cttg 24

<210> 122
<211> 31
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<220>

<223> Primer No. : Si_495

<400> 122
gttaaagctt ttattgaaga tttgtggctc c 31

<210> 123
<211> 64
<212> DNA
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<220>

<223> Primer No. : Si_504

<400> 123
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtatgccccg 60
cccc 64

<210> 124
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<220>

<223> Primer No. : Si_505

<400> 124
gttaaagctt cccaccgtac tcgtcaattc 30

<210> 125
<211> 66
<212> DNA
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<220>
<223> Primer No. : Si_508

<400> 125
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtatggccga 60
gccttg 66

<210> 126
<211> 29
<212> DNA
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<220>
<223> Primer No. : Si_509

<400> 126
gttaaagctt ttgaagattt gtggctccc 29

<210> 127
<211> 67
<212> DNA
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<220>
<223> Primer No. : Si_511

<400> 127
cgtatctaga gaaaatctgt attttcaaag tgaaaatctg tattttcaaa gtgtgagcaa 60
gggcgag 67

<210> 128
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_512

<400> 128

cgtatctaga gaaaatctgt attttcaaag tgaaaatctg ttttttcaaa gtccgccgaa 60
 aaaaaaacgt aaagttgtga gcaagggcga g 91

<210> 129
 <211> 55
 <212> DNA
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<220>
 <223> Primer No. : Si_513

<400> 129
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<210> 130
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<220>
 <223> Primer No. : Si_515

<400> 130
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 agatgatgat gataaaatgg ccgagccttg 90

<210> 131
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 <212> DNA
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<220>
 <223> Primer No. : Si_558

<400> 131
 cgtatctaga atgaccagtt ttgaagatgc 30

<210> 132
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_559

<400> 132
 gttaaagctt tcatgactca ttttcatcca t 31

<210> 133
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_561

 <400> 133
 cgtatctaga atgagtctct taaactgtga gaacag 36

<210> 134
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_562

 <400> 134
 gttaaagctt ctacaccccc gcatca 26

<210> 135
 <211> 405
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> YopE1-138 - SopE - MycHis

 <400> 135

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Val Thr Asn Ile
130 135 140

Thr Leu Ser Thr Gln His Tyr Arg Ile His Arg Ser Asp Val Glu Pro
145 150 155 160

Val Lys Glu Lys Thr Thr Glu Lys Asp Ile Phe Ala Lys Ser Ile Thr
165 170 175

Ala Val Arg Asn Ser Phe Ile Ser Leu Ser Thr Ser Leu Ser Asp Arg
180 185 190

Phe Ser Leu His Gln Gln Thr Asp Ile Pro Thr Thr His Phe His Arg
195 200 205

Gly Asn Ala Ser Glu Gly Arg Ala Val Leu Thr Ser Lys Thr Val Lys
210 215 220

Asp Phe Met Leu Gln Lys Leu Asn Ser Leu Asp Ile Lys Gly Asn Ala
225 230 235 240

Ser Lys Asp Pro Ala Tyr Ala Arg Gln Thr Cys Glu Ala Ile Leu Ser
245 250 255

Ala Val Tyr Ser Asn Asn Lys Asp Gln Cys Cys Lys Leu Leu Ile Ser
260 265 270

Lys Gly Val Ser Ile Thr Pro Phe Leu Lys Glu Ile Gly Glu Ala Ala
275 280 285

Gln Asn Ala Gly Leu Pro Gly Glu Ile Lys Asn Gly Val Phe Thr Pro

290

295

300

Gly Gly Ala Gly Ala Asn Pro Phe Val Val Pro Leu Ile Ala Ser Ala
 305 310 315 320

Ser Ile Lys Tyr Pro His Met Phe Ile Asn His Asn Gln Gln Val Ser
 325 330 335

Phe Lys Ala Tyr Ala Glu Lys Ile Val Met Lys Glu Val Thr Pro Leu
 340 345 350

Phe Asn Lys Gly Thr Met Pro Thr Pro Gln Gln Phe Gln Leu Thr Ile
 355 360 365

Glu Asn Ile Ala Asn Lys Tyr Leu Gln Asn Ala Ser Lys Leu Gly Pro
 370 375 380

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
 385 390 395 400

His His His His His
 405

<210> 136
 <211> 435
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138 - BepG 715-end

<400> 136

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser

50

55

60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Phe Thr Gln Glu
130 135 140

Thr Gln Lys Met Leu Ile Glu Lys Glu Ile Ile Pro Pro Leu Ser Tyr
145 150 155 160

Val Asp Val Ala Ser Lys Ile Arg Glu Ser Glu Val Val Lys Ser Ser
165 170 175

Met Gln Lys Ile Lys Thr Leu Cys Gly Val Val Tyr Gly Asn Pro Asp
180 185 190

Ile Leu Glu Gly Lys Met Pro Lys Met Gly Ile Pro Val Thr Asn Lys
195 200 205

Asn Val Glu Glu Leu Glu Lys Phe Ala Arg Gln Val Gly Asn Phe Pro
210 215 220

Ser Ser Cys Gly Lys Ile Val Gly Phe Ser Phe Leu Gly Ile Lys Ser
225 230 235 240

Glu Ala Arg Ala His Ala Glu Glu Asn Phe Leu Pro Leu Ser His Ala
245 250 255

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

Glu Ala Tyr Phe Lys Glu Gln Glu Arg Cys Ala Gln Ser Val Glu Thr
275 280 285

Pro Ser Glu Glu Ile Thr Asn Leu Leu Ser Phe Thr Gln Glu Gln Gln
290 295 300

Lys Glu Ile Leu Ser Asn Ser Pro Lys Leu Arg Thr Gln Val Lys Ala
305 310 315 320

Tyr Ser Gln Lys Leu His Asn Arg Leu Ser Pro Asn Asp Leu Gln Ala
325 330 335

Ile Ser Glu Arg Ser His Thr Lys Leu Ala Glu Ser Leu Gly Thr Ser
340 345 350

Val Asn Gln Ala Glu Lys Ile Ala Gln Ile Leu Thr Gln Thr Lys Asp
355 360 365

Val Val Gln Ile Leu Gln Gln Gln Glu Lys Leu Gly Leu Tyr Gln Ser
370 375 380

Ile Met Lys Gly Asp Gly Arg Glu Thr Ala Lys Val Asn Met Ser Ala
385 390 395 400

Ile Lys Ala Thr Gln Met Thr Thr Lys Val Thr Ser Leu Lys Ala Val
405 410 415

Glu Gln Ile Val Arg Pro Pro Lys Val Glu Thr Ala Lys Val Val Ser
420 425 430

Met Ser Arg
435

<210> 137
<211> 354
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Rac1 Q61E - MycHis

<400> 137

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gln Ala Ile Lys
130 135 140

Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile
145 150 155 160

Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe
165 170 175

Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly Lys Pro Val Asn Leu
180 185 190

Gly Leu Trp Asp Thr Ala Gly Glu Glu Asp Tyr Asp Arg Leu Arg Pro
195 200 205

Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile Cys Phe Ser Leu Val

210

215

220

Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys Trp Tyr Pro Glu Val
 225 230 235 240

Arg His His Cys Pro Asn Thr Pro Ile Ile Leu Val Gly Thr Lys Leu
 245 250 255

Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys Leu Lys Glu Lys Lys
 260 265 270

Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala Met Ala Lys Glu Ile
 275 280 285

Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Arg Gly Leu
 290 295 300

Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val Leu Cys Pro Pro Pro
 305 310 315 320

Val Lys Lys Arg Lys Arg Lys Phe Glu Lys Leu Gly Pro Glu Gln Lys
 325 330 335

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 340 345 350

His His

<210> 138

<211> 163

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Y. enterocolitica codon optimized murine BID BH3 part

<400> 138

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
130 135 140

Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu
145 150 155 160

Met Asp His

<210> 139

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138 - Y. enterocolitica codon optimized murine Bax BH3 part

<400> 139

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Lys Lys Leu Ser
130 135 140

Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
145 150 155

<210> 140
<211> 20
<212> PRT
<213> Salmonella enterica

<220>
<223> SteA1-20

<400> 140

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
1 5 10 15

Lys Leu Pro His
20

<210> 141
<211> 210

<212> PRT
<213> Salmonella enterica

<220>
<223> SteA

<400> 141

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
1 5 10 15

Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
20 25 30

Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
35 40 45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
50 55 60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
65 70 75 80

Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly
85 90 95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
195 200 205

Asn Tyr
210

<210> 142
<211> 81
<212> PRT
<213> Salmonella enterica

<220>
<223> SopE1-81

<400> 142

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65 70 75 80

Lys

<210> 143
<211> 105
<212> PRT
<213> Salmonella enterica

<220>
<223> SopE1-105

<400> 143

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln

1	5	10	15
Glu Thr Thr	Leu Leu Lys	Glu Lys Ser Thr	Glu Lys Asn Ser Leu Ala
	20	25	30
Lys Ser Ile	Leu Ala Val	Lys Asn His Phe Ile	Glu Leu Arg Ser Lys
	35	40	45
Leu Ser Glu	Arg Phe Ile	Ser His Lys Asn Thr	Glu Ser Ser Ala Thr
	50	55	60
His Phe His	Arg Gly Ser	Ala Ser Glu Gly	Arg Ala Val Leu Thr Asn
65	70	75	80
Lys Val Val	Lys Asp Phe Met	Leu Gln Thr	Leu Asn Asp Ile Asp Ile
	85	90	95
Arg Gly Ser	Ala Ser Lys	Asp Pro Ala	
	100	105	

<210> 144
 <211> 158
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SteA1-20 - *S. enterica* codon optimized murine t-BID

<400> 144

Met Pro Tyr	Thr Ser Val	Ser Thr Tyr	Ala Arg Ala	Leu Ser Gly	Asn
1	5	10	15		
Lys Leu Pro	His Gly Thr	Gly Ser Gln	Ala Ser Arg	Ser Phe Asn	Gln
	20	25	30		
Gly Arg Ile	Glu Pro Asp	Ser Glu Ser	Gln Glu Glu	Ile Ile His	Asn
	35	40	45		
Ile Ala Arg	His Leu Ala	Gln Ile Gly	Asp Glu Met	Asp His Asn	Ile
	50	55	60		
Gln Pro Thr	Leu Val Arg	Gln Leu Ala	Ala Gln Phe	Met Asn Gly	Ser

65		70		75		80
Leu Ser Glu Glu Asp Lys Arg Asn Cys Leu Ala Lys Ala Leu Asp Glu	85		90		95	
Val Lys Thr Ala Phe Pro Arg Asp Met Glu Asn Asp Lys Ala Met Leu	100		105		110	
Ile Met Thr Met Leu Leu Ala Lys Lys Val Ala Ser His Ala Pro Ser	115		120		125	
Leu Leu Arg Asp Val Phe His Thr Thr Val Asn Phe Ile Asn Gln Asn	130		135		140	
Leu Phe Ser Tyr Val Arg Asn Leu Val Arg Asn Glu Met Asp	145		150		155	
<210> 145						
<211> 348						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> SteA - S. enterica codon optimized murine t-BID						
<400> 145						
Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn	1	5	10		15	
Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr	20		25		30	
Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr	35		40		45	
Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val	50		55		60	
Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp	65		70		75	80
Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly						

85

90

95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
 100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
 115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
 130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
 145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
 165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
 180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
 195 200 205

Asn Tyr Gly Thr Gly Ser Gln Ala Ser Arg Ser Phe Asn Gln Gly Arg
 210 215 220

Ile Glu Pro Asp Ser Glu Ser Gln Glu Glu Ile Ile His Asn Ile Ala
 225 230 235 240

Arg His Leu Ala Gln Ile Gly Asp Glu Met Asp His Asn Ile Gln Pro
 245 250 255

Thr Leu Val Arg Gln Leu Ala Ala Gln Phe Met Asn Gly Ser Leu Ser
 260 265 270

Glu Glu Asp Lys Arg Asn Cys Leu Ala Lys Ala Leu Asp Glu Val Lys
 275 280 285

Thr Ala Phe Pro Arg Asp Met Glu Asn Asp Lys Ala Met Leu Ile Met
 290 295 300

Thr Met Leu Leu Ala Lys Lys Val Ala Ser His Ala Pro Ser Leu Leu
 305 310 315 320

Arg Asp Val Phe His Thr Thr Val Asn Phe Ile Asn Gln Asn Leu Phe
 325 330 335

Ser Tyr Val Arg Asn Leu Val Arg Asn Glu Met Asp
 340 345

<210> 146
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SopE1-81 - S. enterica codon optimized murine t-BID

<400> 146

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
 1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
 20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
 35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
 50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
 65 70 75 80

Lys Gly Thr Gly Ser Gln Ala Ser Arg Ser Phe Asn Gln Gly Arg Ile
 85 90 95

Glu Pro Asp Ser Glu Ser Gln Glu Glu Ile Ile His Asn Ile Ala Arg
 100 105 110

His Leu Ala Gln Ile Gly Asp Glu Met Asp His Asn Ile Gln Pro Thr
 115 120 125

Leu Val Arg Gln Leu Ala Ala Gln Phe Met Asn Gly Ser Leu Ser Glu
 130 135 140

Glu Asp Lys Arg Asn Cys Leu Ala Lys Ala Leu Asp Glu Val Lys Thr
 145 150 155 160

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

Met Leu Leu Ala Lys Lys Val Ala Ser His Ala Pro Ser Leu Leu Arg
 180 185 190

Asp Val Phe His Thr Thr Val Asn Phe Ile Asn Gln Asn Leu Phe Ser
 195 200 205

Tyr Val Arg Asn Leu Val Arg Asn Glu Met Asp
 210 215

<210> 147
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SopE1-105 - S. enterica codon optimized murine t-BID

<400> 147

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
 1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
 20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
 35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
 50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
 65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Gly Thr Gly Ser Gln Ala Ser
100 105 110

Arg Ser Phe Asn Gln Gly Arg Ile Glu Pro Asp Ser Glu Ser Gln Glu
115 120 125

Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu
130 135 140

Met Asp His Asn Ile Gln Pro Thr Leu Val Arg Gln Leu Ala Ala Gln
145 150 155 160

Phe Met Asn Gly Ser Leu Ser Glu Glu Asp Lys Arg Asn Cys Leu Ala
165 170 175

Lys Ala Leu Asp Glu Val Lys Thr Ala Phe Pro Arg Asp Met Glu Asn
180 185 190

Asp Lys Ala Met Leu Ile Met Thr Met Leu Leu Ala Lys Lys Val Ala
195 200 205

Ser His Ala Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
210 215 220

Phe Ile Asn Gln Asn Leu Phe Ser Tyr Val Arg Asn Leu Val Arg Asn
225 230 235 240

Glu Met Asp

<210> 148
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_677

<400> 148

ttactattcg aagaaattat tcataatatt gcccgccatc tggcccaaat tggatgatgaa	60
atggatcatt aagcttggag ta	82
<210> 149	
<211> 82	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_678	
<400> 149	
tactccaagc ttaatgatcc atttcatcac caatttgggc cagatggcgg gcaatattat	60
gaataatttc ttcgaatagt aa	82
<210> 150	
<211> 73	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_682	
<400> 150	
ttactactcg agaaaaaact gagcgaatgt ctgcgccgca ttggtgatga actggatagc	60
taagcttgga gta	73
<210> 151	
<211> 73	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_683	
<400> 151	
tactccaagc ttagctatcc agttcatcac caatgcggcg cagacattcg ctgagttttt	60
tctcgagtag taa	73
<210> 152	
<211> 34	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer No. : Si_580	

<400> 152
 catgccatgg atttatggtc atagatatga cctc 34

<210> 153
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_612

<400> 153
 cggggtacca tgaggtagct tatttcctga taaag 35

<210> 154
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_613

<400> 154
 cggggtacca taattgtcca aatagttatg gtagc 35

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_614

<400> 155
 catgccatggc ggcaaggctc ctc 24

<210> 156
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer No. : Si_615

<400> 156
 cggggtacct ttatttgtca acactgccc 29

<210> 157

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_616

<400> 157
cggggtacct gcggggtctt tactcg

26

<210> 158
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Y. enterocolitica codon optimized Ink4A 84-103

<400> 158

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp

130

135

140

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 145 150 155 160

Ala Gly Ala Arg

<210> 159

<211> 164

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138-Y. enterocolitica codon optimized p107/RBL1 657-662
 (AAA02489.1)

<400> 159

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

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

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Pro Val Lys Arg
145 150 155 160

Arg Leu Phe Gly

<210> 160
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Y. enterocolitica codon optimized p21 141-160
(AAH13967.1)

<400> 160

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Lys Arg Arg Gln Thr Ser Met Thr Ala Phe Tyr His Ser Lys Arg Arg
 145 150 155 160

Leu Ile Phe Ser

<210> 161
 <211> 160
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138-Y. enterocolitica codon optimized p21 145-160
 (AAH13967.1)

<400> 161

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

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

Thr Ser Met Thr Ala Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
145 150 155 160

<210> 162
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Y. enterocolitica codon optimized p21 17-33
(AAH13967.1)

<400> 162

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Gly Ala Ile Asp

130

135

140

Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
 145 150 155 160

Asp

<210> 163

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138-Y. enterocolitica codon optimized cyclin D2 139-147 (
 CAA48493.1)

<400> 163

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
 115 120 125

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

Trp Glu Leu Val Val Leu Gly Lys Leu
 145 150

<210> 164
 <211> 397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SteA-Ink4a-MycHis

<400> 164

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
 1 5 10 15

Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
 20 25 30

Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
 35 40 45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
 50 55 60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
 65 70 75 80

Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly
 85 90 95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
 100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
 115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
 130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
195 200 205

Asn Tyr Gly Thr Ile Trp Glu Phe Met Glu Pro Ala Ala Gly Ser Ser
210 215 220

Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala Arg Gly Arg
225 230 235 240

Val Glu Glu Val Arg Ala Leu Leu Glu Ala Gly Ala Leu Pro Asn Ala
245 250 255

Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met Met Gly Ser
260 265 270

Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys
275 280 285

Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu
290 295 300

Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg Leu
305 310 315 320

Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu
325 330 335

Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala Ala Gly Gly
340 345 350

Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu Gly Pro Ser
355 360 365

Asp Ile Pro Asp Lys Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu
 370 375 380

Asp Leu Asn Ser Ala Val Asp His His His His His His
 385 390 395

<210> 165
 <211> 292
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SopE1-105-Ink4a-MycHis

<400> 165

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
 1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
 20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
 35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
 50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
 65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
 85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Gly Thr Ile Trp Glu Phe Met
 100 105 110

Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala
 115 120 125

Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu
 130 135 140

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

Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu
 165 170 175

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro
 180 185 190

Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu
 195 200 205

His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu
 210 215 220

Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr
 225 230 235 240

Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile
 245 250 255

Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp Lys Leu Gly Pro Glu
 260 265 270

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

His His His His
 290

<210> 166
 <211> 409
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SteA-Ink4c-MycHis

<400> 166

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
 1 5 10 15

Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
20 25 30

Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
35 40 45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
50 55 60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
65 70 75 80

Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly
85 90 95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
195 200 205

Asn Tyr Gly Thr Ile Trp Glu Phe Met Ala Glu Pro Trp Gly Asn Glu
210 215 220

Leu Ala Ser Ala Ala Ala Arg Gly Asp Leu Glu Gln Leu Thr Ser Leu
225 230 235 240

Leu Gln Asn Asn Val Asn Val Asn Ala Gln Asn Gly Phe Gly Arg Thr
245 250 255

Ala Leu Gln Val Met Lys Leu Gly Asn Pro Glu Ile Ala Arg Arg Leu
260 265 270

Leu Leu Arg Gly Ala Asn Pro Asp Leu Lys Asp Arg Thr Gly Phe Ala
275 280 285

Val Ile His Asp Ala Ala Arg Ala Gly Phe Leu Asp Thr Leu Gln Thr
290 295 300

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

Leu Pro Leu His Leu Ala Ala Lys Glu Gly His Leu Arg Val Val Glu
325 330 335

Phe Leu Val Lys His Thr Ala Ser Asn Val Gly His Arg Asn His Lys
340 345 350

Gly Asp Thr Ala Cys Asp Leu Ala Arg Leu Tyr Gly Arg Asn Glu Val
355 360 365

Val Ser Leu Met Gln Ala Asn Gly Ala Gly Gly Ala Thr Asn Leu Gln
370 375 380

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

Ala Val Asp His His His His His His
405

<210> 167
<211> 304
<212> PRT
<213> Artificial Sequence

<220>

<223> SopE1-105-Ink4c-MycHis

<400> 167

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Gly Thr Ile Trp Glu Phe Met
100 105 110

Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly Asp
115 120 125

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

Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly Asn
145 150 155 160

Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp Leu
165 170 175

Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala Gly
180 185 190

Phe Leu Asp Thr Leu Gln Thr Leu Leu Glu Phe Gln Ala Asp Val Asn
195 200 205

Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys Glu
 210 215 220

Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser Asn
 225 230 235 240

Val Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala Arg
 245 250 255

Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly Ala
 260 265 270

Gly Gly Ala Thr Asn Leu Gln Lys Leu Gly Pro Glu Gln Lys Leu Ile
 275 280 285

Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His His
 290 295 300

<210> 168
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SteA-Mad2-MycHis

<400> 168

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
 1 5 10 15

Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
 20 25 30

Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
 35 40 45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
 50 55 60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
 65 70 75 80

Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly
85 90 95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
195 200 205

Asn Tyr Gly Thr Ile Trp Glu Phe Met Ala Leu Gln Leu Ser Arg Glu
210 215 220

Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu Phe Phe
225 230 235 240

Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr Pro Ser
245 250 255

Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu Val Thr
260 265 270

Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Glu Gln Leu
275 280 285

Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val Val Ile
290 295 300

Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe Asp Ile
305 310 315 320

Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu Lys Ser
325 330 335

Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln Ile Thr
340 345 350

Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser Phe Asp
355 360 365

Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys Trp Glu
370 375 380

Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg Leu Arg
385 390 395 400

Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala Tyr Lys
405 410 415

Ile Pro Val Asn Asp Lys Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu
420 425 430

Glu Asp Leu Asn Ser Ala Val Asp His His His His His His
435 440 445

<210> 169

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> SopE1-105-Mad2-MycHis

<400> 169

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Gly Thr Ile Trp Glu Phe Met
100 105 110

Ala Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala
115 120 125

Glu Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr
130 135 140

Gln Arg Gly Ile Tyr Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr
145 150 155 160

Gly Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu
165 170 175

Asn Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val
180 185 190

Gln Lys Leu Val Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu
195 200 205

Glu Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp
210 215 220

Ser Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg
225 230 235 240

Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu
245 250 255

Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu
260 265 270

Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn
275 280 285

Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val
290 295 300

Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp Lys Leu Gly Pro
305 310 315 320

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
325 330 335

His His His His His
340

<210> 170
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> SteA-Cdk1-MycHis

<400> 170

Met Pro Tyr Thr Ser Val Ser Thr Tyr Ala Arg Ala Leu Ser Gly Asn
1 5 10 15

Lys Leu Pro His Val Ala Ala Gly Asp Tyr Glu Asn Lys Leu Ser Thr
20 25 30

Lys Ile Met Lys Gly Ile Leu Tyr Val Leu Thr Ala Gly Leu Ala Tyr
35 40 45

Gly Phe Thr Arg Val Ile Glu His Tyr Cys Asn Val Thr Pro Lys Val
50 55 60

Ala Glu Phe Cys Ala Asn Ala Gly Asn Ile His Asn His Leu Ala Asp
65 70 75 80

Ala Val Arg Asp Gly Leu Phe Thr Ile Asp Val Glu Leu Ser Asp Gly
85 90 95

Arg Met Leu Thr Phe Glu Gln Leu Ser Leu Ile Ala Glu Gly Lys Pro
100 105 110

Ile Val Arg Ile Ser Asp Gly Glu His Thr Val Glu Val Glu Gly Thr
115 120 125

Phe Glu Glu Ile Cys Met Arg Leu Glu Glu Gly Phe Phe Glu Ala Pro
130 135 140

Ala Tyr Tyr Asp Tyr Asp Ile Asp Glu Lys Tyr Lys Thr Val Arg Glu
145 150 155 160

Arg Met Ala Ala Tyr Asn Ala Leu Pro Gln Ala Leu Gly Ala Ile Pro
165 170 175

Cys Leu Glu Tyr Tyr Ile Ala Arg Ala Ser Asn Met Gln Glu Ala Lys
180 185 190

Ala Gln Trp Ala Ala Asp Ile Lys Ala Arg Tyr His Asn Tyr Leu Asp
195 200 205

Asn Tyr Gly Thr Ile Trp Glu Phe Met Glu Asp Tyr Thr Lys Ile Glu
210 215 220

Lys Ile Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Gly Arg His Lys
225 230 235 240

Thr Thr Gly Gln Val Val Ala Met Lys Lys Ile Arg Leu Glu Ser Glu
245 250 255

Glu Glu Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys
260 265 270

Glu Leu Arg His Pro Asn Ile Val Ser Leu Gln Asp Val Leu Met Gln
275 280 285

Asp Ser Arg Leu Tyr Leu Ile Phe Glu Phe Leu Ser Met Asp Leu Lys
290 295 300

Lys Tyr Leu Asp Ser Ile Pro Pro Gly Gln Tyr Met Asp Ser Ser Leu
305 310 315 320

Val Lys Ser Tyr Leu Tyr Gln Ile Leu Gln Gly Ile Val Phe Cys His
325 330 335

Ser Arg Arg Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile
340 345 350

Asp Asp Lys Gly Thr Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala
355 360 365

Phe Gly Ile Pro Ile Arg Val Tyr Thr His Glu Val Val Thr Leu Trp
370 375 380

Tyr Arg Ser Pro Glu Val Leu Leu Gly Ser Ala Arg Tyr Ser Thr Pro
385 390 395 400

Val Asp Ile Trp Ser Ile Gly Thr Ile Phe Ala Glu Leu Ala Thr Lys
405 410 415

Lys Pro Leu Phe His Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile
420 425 430

Phe Arg Ala Leu Gly Thr Pro Asn Asn Glu Val Trp Pro Glu Val Glu
435 440 445

Ser Leu Gln Asp Tyr Lys Asn Thr Phe Pro Lys Trp Lys Pro Gly Ser
450 455 460

Leu Ala Ser His Val Lys Asn Leu Asp Glu Asn Gly Leu Asp Leu Leu
465 470 475 480

Ser Lys Met Leu Ile Tyr Asp Pro Ala Lys Arg Ile Ser Gly Lys Met
485 490 495

Ala Leu Asn His Pro Tyr Phe Asn Asp Leu Asp Asn Gln Ile Lys Lys
500 505 510

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

Ser Ala Val Asp His His His His His His
530 535

<210> 171
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> SopE1-105-Cdk1-MycHis

<400> 171

Val Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile
85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Gly Thr Ile Trp Glu Phe Met
100 105 110

Glu Asp Tyr Thr Lys Ile Glu Lys Ile Gly Glu Gly Thr Tyr Gly Val
115 120 125

Val Tyr Lys Gly Arg His Lys Thr Thr Gly Gln Val Val Ala Met Lys
130 135 140

Lys Ile Arg Leu Glu Ser Glu Glu Glu Gly Val Pro Ser Thr Ala Ile
145 150 155 160

Arg Glu Ile Ser Leu Leu Lys Glu Leu Arg His Pro Asn Ile Val Ser
165 170 175

Leu Gln Asp Val Leu Met Gln Asp Ser Arg Leu Tyr Leu Ile Phe Glu
180 185 190

Phe Leu Ser Met Asp Leu Lys Lys Tyr Leu Asp Ser Ile Pro Pro Gly
195 200 205

Gln Tyr Met Asp Ser Ser Leu Val Lys Ser Tyr Leu Tyr Gln Ile Leu
210 215 220

Gln Gly Ile Val Phe Cys His Ser Arg Arg Val Leu His Arg Asp Leu
225 230 235 240

Lys Pro Gln Asn Leu Leu Ile Asp Asp Lys Gly Thr Ile Lys Leu Ala
245 250 255

Asp Phe Gly Leu Ala Arg Ala Phe Gly Ile Pro Ile Arg Val Tyr Thr
260 265 270

His Glu Val Val Thr Leu Trp Tyr Arg Ser Pro Glu Val Leu Leu Gly
275 280 285

Ser Ala Arg Tyr Ser Thr Pro Val Asp Ile Trp Ser Ile Gly Thr Ile
290 295 300

Phe Ala Glu Leu Ala Thr Lys Lys Pro Leu Phe His Gly Asp Ser Glu
305 310 315 320

Ile Asp Gln Leu Phe Arg Ile Phe Arg Ala Leu Gly Thr Pro Asn Asn
325 330 335

Glu Val Trp Pro Glu Val Glu Ser Leu Gln Asp Tyr Lys Asn Thr Phe
340 345 350

Pro Lys Trp Lys Pro Gly Ser Leu Ala Ser His Val Lys Asn Leu Asp
355 360 365

Glu Asn Gly Leu Asp Leu Leu Ser Lys Met Leu Ile Tyr Asp Pro Ala
370 375 380

Lys Arg Ile Ser Gly Lys Met Ala Leu Asn His Pro Tyr Phe Asn Asp
385 390 395 400

Leu Asp Asn Gln Ile Lys Lys Met Lys Leu Gly Pro Glu Gln Lys Leu
405 410 415

Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His
420 425 430

His

<210> 172
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_745

<400> 172
catgctcgag ggtgccatcg atgatgccgc ccgcgaaggt tttctggata ccctggtggt 60
gctgcatcgc gccggtgccc gctaattcga acatg 95

<210> 173
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_746

<400> 173
catgttcgaa ttagcgggca ccggcgcgat gcagcaccac cagggtatcc agaaaacctt 60
cgcgggcggc atcatcgatg gcaccctcga gcatg 95

<210> 174
 <211> 95
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_747

 <400> 174
 catgctcgag ggtgccatcg attatggctg caaaaaacgc cgccaacgcc gccgcggtcc 60

 ggtgaaacgc cgcctgtttg gttaattcga acatg 95

 <210> 175
 <211> 95
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_748

 <400> 175
 catgttcgaa ttaaccaaac aggcggcggtt tcaccggacc gcggcggcgt tggcggcgtt 60

 ttttgcgacc ataatcgatg gcaccctcga gcatg 95

 <210> 176
 <211> 95
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_749

 <400> 176
 catgctcgag ggtgccatcg ataaacgccg ccaaaccagc atgaccgcct tttatcatag 60

 caaacgccgc ctgattttta gctaattcga acatg 95

 <210> 177
 <211> 95
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_750

 <400> 177
 catgttcgaa ttagctaaaa atcaggcggc gtttgctatg ataaaaggcg gtcatgctgg 60

tttggcggcg tttatcgatg gcaccctcga gcatg 95

<210> 178
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_753

<400> 178
catgctcgag ggtgccatcg ataccagcat gaccgccttt tatcatagca aacgccgcct 60
gatttttagc taattcgaac atg 83

<210> 179
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_754

<400> 179
catgttcgaa ttagctaaaa atcaggcggc gtttgctatg ataaaaggcg gtcatgctgg 60
tatcgatggc accctcgagc atg 83

<210> 180
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_755

<400> 180
catgctcgag ggtgccatcg atgcctgtcg ccgcctgttt ggtccggtgg atagcgaaca 60
actgagccgc gattaattcg aacatg 86

<210> 181
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_756

<400> 181
catgttcgaa ttaatcgcg ctcagttggt cgctatccac cggaccaaac aggcggcgac 60
aggcatcgat ggcaccctcg agcatg 86

<210> 182
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_757

<400> 182
catgctcgag ggtgcatcg attgggaact ggtggtgctg ggtaaactgt aattcgaaca 60
tg 62

<210> 183
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_758

<400> 183
catgttcgaa ttacagttta cccagcacca ccagttccca atcgatggca ccctcgagca 60
tg 62

<210> 184
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_703

<400> 184
gacatggaat tcatggagcc ggcggcg 27

<210> 185
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_704

<400> 185
catgaagctt atcggggatg tctgaggg 28

<210> 186
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_705

<400> 186
gacatggaat tcatggccga gccttgggg 29

<210> 187
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_706

<400> 187
gttaacatca gcttgaaact ccagcaaagt ctgtaaagtg tccaggaaac c 51

<210> 188
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_707

<400> 188
ggtttcctgg acactttaca gactttgctg gagtttcaag ctgatgttaa c 51

<210> 189
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer No. : Si_708

<400> 189
catgaagctt ttgaagattt gtggctcccc 30

<210> 190
<211> 30

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_709

 <400> 190
 gacatggaat tcatggcgct gcagctctcc 30

 <210> 191
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_710

 <400> 191
 catgaagctt gtcattgaca ggaattttgt agg 33

 <210> 192
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_711

 <400> 192
 gacatggaat tcatggaaga ttatacaaaa atagagaa 38

 <210> 193
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_712

 <400> 193
 catgaagctt catcttctta atctgattgt ccaa 34

 <210> 194
 <211> 276
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> YopE1-138-Y. enterocolitica codon optimized murine tBid

<400> 194

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ser Arg Ser Phe Asn Gln Gly Arg Ile Glu Pro Asp Ser Glu Ser Gln
145 150 155 160

Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp
165 170 175

Glu Met Asp His Asn Ile Gln Pro Thr Leu Val Arg Gln Leu Ala Ala
180 185 190

Gln Phe Met Asn Gly Ser Leu Ser Glu Glu Asp Lys Arg Asn Cys Leu
195 200 205

Ala Lys Ala Leu Asp Glu Val Lys Thr Ala Phe Pro Arg Asp Met Glu
 210 215 220

Asn Asp Lys Ala Met Leu Ile Met Thr Met Leu Leu Ala Lys Lys Val
 225 230 235 240

Ala Ser His Ala Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val
 245 250 255

Asn Phe Ile Asn Gln Asn Leu Phe Ser Tyr Val Arg Asn Leu Val Arg
 260 265 270

Asn Glu Met Asp
 275

<210> 195
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YopE1-138-Ubiquitin

<400> 195

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Phe
130 135 140

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
145 150 155 160

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
165 170 175

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
180 185 190

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

Leu Val Leu Arg Leu Arg Gly Gly Phe Glu Ala Ser Lys Leu Gly Pro
210 215 220

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
225 230 235 240

His His His His His
245

<210> 196
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138-Ubiquitin-Flag-INK4C-MycHis

<400> 196

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Met Gln Ile Phe
130 135 140

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
145 150 155 160

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
165 170 175

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
180 185 190

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

Leu Val Leu Arg Leu Arg Gly Gly Phe Glu Asp Tyr Lys Asp Asp Asp
210 215 220

Asp Lys Met Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala
225 230 235 240

Arg Gly Asp Leu Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn Val Asn
245 250 255

Val Asn Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys
260 265 270

Leu Gly Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn
275 280 285

Pro Asp Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala
290 295 300

Arg Ala Gly Phe Leu Asp Thr Leu Gln Ala Leu Pro Glu Phe Gln Ala
305 310 315 320

Asp Val Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala
325 330 335

Ala Lys Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr
340 345 350

Ala Ser Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp
355 360 365

Leu Ala Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala
370 375 380

Asn Gly Ala Gly Gly Ala Thr Asn Leu Gln Lys Leu Gly Pro Glu Gln
385 390 395 400

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

His His His

<210> 197
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer No. : Si_585

 <400> 197
 cagtctcgag atgcagatct tcgtcaagac 30

 <210> 198
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_586

 <400> 198
 gttaaagctt gctagcttcg aaaccaccac gtagacgtaa gac 43

 <210> 199
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer No. : Si_588

 <400> 199
 cagtttcgaa gattataaag atgatgatga taaaatggcc gaggccttg 48

 <210> 200
 <211> 165
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> YopE1-138 - Y. enterocolitica codon optimized murine BID BH3 part

 <400> 200

 Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
 1 5 10 15

 Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30

 Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145 150 155 160

Asp Glu Met Asp His
165

<210> 201
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - Y. enterocolitica codon optimized murine Bax BH3 part

<400> 201

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ala Lys Lys Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp
145 150 155 160

Ser

<210> 202
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - (Y. enterocolitica codon optimized murine BID BH3
part) 2

<400> 202

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145 150 155 160

Asp Glu Met Asp His Gly Ala Phe Asp Ala Glu Glu Ile Ile His Asn
165 170 175

Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu Met Asp His
180 185 190

<210> 203
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> YopE1-138 - (Y. enterocolitica codon optimized murine BID BH3
part)(Y. enterocolitica codon optimized murine Bax BH3 part)

<400> 203

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly
145 150 155 160

Asp Glu Met Asp His Gly Ala Phe Asp Ala Lys Lys Leu Ser Glu Cys
165 170 175

Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
180 185

<210> 204
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer No. 733

<400> 204
ttactactcg aggggtgcat cgatgccgaa gaaattattc ataattattgc ccg

53

<210> 205
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 735

 <400> 205
 tactccttcg aattaatgat ccatttcatc accaatttg 39

<210> 206
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 736

 <400> 206
 ttactactcg agggtgccat cgatgccaaa aaactgagcg aatgtctgcg 50

<210> 207
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 738

 <400> 207
 tactccttcg aattagctat ccagttcatc accaatg 37

<210> 208
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 734

 <400> 208
 tactccttcg aaggcaccat gatccatttc atcaccaatt tgg 43

<210> 209
 <211> 167
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> YopE1-138- codon optimized murine tBid BH3 extended part

<400> 209

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
130 135 140

Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu
145 150 155 160

Met Asp His Asn Ile Gln Pro
165

<210> 210

<211> 168

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-138-10 Aa linker - Y. enterocolitica codon optimized murine
tBid BH3 part

<400> 210

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Leu Glu Ser Arg Phe Glu
130 135 140

Ala Gly Gly Ala Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala
145 150 155 160

Gln Ile Gly Asp Glu Met Asp His
165

<210> 211

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> YopE1-(138-Y. enterocolitica codon optimized murine Bax BH3 part-
Y. enterocolitica codon optimized murine tBid BH3 part

<400> 211

Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Ala Ser
1 5 10 15

Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
20 25 30

Gln Gln Lys Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
35 40 45

Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
50 55 60

Ser Met Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Leu Thr Pro Ala Gln Met
85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Ser Ser Leu Asp Ala Glu Thr
115 120 125

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

Ala Lys Lys Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp
145 150 155 160

Ser Gly Ala Phe Asp Ala Glu Glu Ile Ile His Asn Ile Ala Arg His
165 170 175

Leu Ala Gln Ile Gly Asp Glu Met Asp His
180 185

<210> 212
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 725

 <400> 212
 ttactattcg aagaaattat tcataatatt gcc 33

<210> 213
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 726

 <400> 213
 tactccaagc ttacggttga atattatgat ccatttcac accaatttgg 50

<210> 214
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 727

 <400> 214
 ttactattcg aagccggtgg tgccgaagaa attattcata atattgccc 49

<210> 215
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer No. 728

 <400> 215
 tactccaagc ttaatgatcc atttcatca 29

<210> 216
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> primer No. 737

<400> 216
tactccttcg aaggcaccgc tatccagttc atcaccaatg

40

<210> 217
<211> 20
<212> PRT
<213> Mus musculus

<400> 217

Glu Glu Ile Ile His Asn Ile Ala Arg His Leu Ala Gln Ile Gly Asp
1 5 10 15

Glu Met Asp His
20

<210> 218
<211> 14
<212> PRT
<213> Mus musculus

<400> 218

Ile Ala Arg His Leu Ala Gln Ile Gly Asp Glu Met Asp His
1 5 10

<210> 219
<211> 20
<212> PRT
<213> Homo sapiens

<400> 219

Glu Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp
1 5 10 15

Ser Met Asp Arg
20

<210> 220
<211> 15
<212> PRT
<213> Homo sapiens

<400> 220

Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp Arg Ser

1 5 10 15

<210> 221
<211> 17
<212> PRT
<213> Mus musculus

<400> 221

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

Asn

<210> 222
<211> 14
<212> PRT
<213> Mus musculus

<400> 222

Leu Ser Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10

<210> 223
<211> 17
<212> PRT
<213> Homo sapiens

<400> 223

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

Asn

<210> 224
<211> 14
<212> PRT
<213> Homo sapiens

<400> 224

Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser
1 5 10