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eolf-seq1

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eolf-seq1

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eof-seq1

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Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro
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Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val
305 310 315 320

Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly
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Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys
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Val Gly Lys Leu Trp Gly Glu Ile Lys
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eolf-seq1

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Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
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Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

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

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Glu Leu Gly Gly Lys Leu Glu Val Ser Lys
210 215 220

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
225 230 235 240

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp
245 250 255

eof-seq1

Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro
260 265 270

Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
275 280 285

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

Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu
305 310 315 320

Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
325 330 335

Gly Lys Leu Trp Gly Glu Ile Lys
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Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
20 25 30

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

eof-seq1

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

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

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225 230 235 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
245 250 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
275 280 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
290 295 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305 310 315 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
325 330 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
340 345 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
355 360 365

eof-seq1

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380
 Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400
 Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala
 405 410 415
 Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg
 420 425 430
 Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
 435 440 445
 Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val
 450 455 460
 Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
 465 470 475 480
 Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
 485 490 495
 Ile Lys Glu Leu Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
 500 505 510
 Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
 515 520 525
 Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
 530 535 540
 Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
 545 550 555 560
 Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
 565 570 575
 Gly Asn Phe Gly Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp
 580 585 590
 Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
 595 600 605
 Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn

eolf-seq1

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
865 870 875 880

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
885 890 895

Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
900 905 910

Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
915 920 925

Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu
930 935 940

Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
945 950 955 960

Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
965 970 975

Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
980 985

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Leu Thr Lys Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys
20 25 30

Gln Phe Asn Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala
35 40 45

Asn Ala Gly Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly
50 55 60

Ala Lys Asp Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val
65 70 75 80

Tyr Gln Asn Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val

															eolf-seq1															
										90					95															
Phe	Gly	Ser	Asn	Tyr	Gly	Ala	Gly	Tyr	Gly	His	Val	Ala	Trp	Val	Ile															
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Glu	Ala	Thr	Leu	Asp	Tyr	Ile	Ile	Val	Tyr	Glu	Gln	Asn	Trp	Leu	Gly															
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Gly	Gly	Trp	Thr	Asp	Gly	Ile	Glu	Gln	Pro	Gly	Trp	Gly	Trp	Glu	Lys															
		130				135					140																			
Val	Thr	Arg	Arg	Gln	His	Ala	Tyr	Asp	Phe	Pro	Met	Trp	Phe	Ile	Arg															
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Pro	Asn	Phe	Lys	Ser	Glu	Thr	Ala	Pro	Arg	Ser	Val	Gln	Ser	Pro	Thr															
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Gln	Ala	Pro	Lys	Lys	Glu	Thr	Ala	Gly	Ser	Met	Leu	Thr	Ala	Ile	Asp															
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Tyr	Leu	Thr	Lys	Lys	Gly	Trp	Lys	Ile	Ser	Ser	Asp	Pro	Arg	Thr	Tyr															
		195					200					205																		
Asp	Gly	Tyr	Pro	Lys	Asn	Tyr	Gly	Tyr	Arg	Asn	Tyr	His	Glu	Asn	Gly															
		210				215					220																			
Ile	Asn	Tyr	Asp	Glu	Phe	Cys	Gly	Gly	Tyr	His	Arg	Ala	Phe	Asp	Val															
225					230					235					240															
Tyr	Ser	Asn	Glu	Thr	Asn	Asp	Val	Pro	Ala	Val	Thr	Ser	Gly	Thr	Val															
			245					250						255																
Ile	Glu	Ala	Asn	Asp	Tyr	Gly	Asn	Phe	Gly	Gly	Thr	Phe	Val	Ile	Arg															
			260				265					270																		
Asp	Ala	Asn	Asp	Asn	Asp	Trp	Ile	Tyr	Gly	His	Leu	Gln	Arg	Gly	Ser															
		275					280					285																		
Met	Arg	Phe	Val	Val	Gly	Asp	Lys	Val	Asn	Gln	Gly	Asp	Ile	Ile	Gly															
		290				295					300																			
Leu	Gln	Gly	Asn	Ser	Asn	Tyr	Tyr	Asp	Asn	Pro	Met	Ser	Val	His	Leu															
305					310					315					320															
His	Leu	Gln	Leu	Arg	Pro	Lys	Asp	Ala	Lys	Lys	Asp	Glu	Lys	Ser	Gln															
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eolf-seq1

Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn
340 345 350

Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His
355 360 365

Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro
370 375 380

Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro
385 390 395 400

Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His
405 410 415

Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp
420 425 430

Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala
435 440 445

Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg
450 455 460

Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val
465 470 475 480

Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr
485 490 495

Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser
500 505 510

Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile
515 520 525

Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp
530 535 540

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

Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala
565 570 575

Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His
580 585 590

eolf-seq1

Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys
595 600 605

Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln
610 615 620

Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val
625 630 635 640

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

Leu Pro Lys Arg Gly Ser Asn Pro Lys Gly Ile Val Ile His Asn Asp
35 40 45

Ala Gly Ser Lys Gly Ala Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val
50 55 60

Asn Ala Pro Leu Ser Arg Leu Glu Ala Gly Ile Ala His Ser Tyr Val
65 70 75 80

Ser Gly Asn Thr Val Trp Gln Ala Leu Asp Glu Ser Gln Val Gly Trp
85 90 95

His Thr Ala Asn Gln Ile Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val
100 105 110

Cys Gln Ser Met Gly Ala Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln
115 120 125

eolf-seq1

Ala Thr Phe Gln Glu Cys Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro
130 135 140

Ala Asn Arg Asn Thr Ile Arg Leu His Asn Glu Phe Thr Ser Thr Ser
145 150 155 160

Cys Pro His Arg Ser Ser Val Leu His Thr Gly Phe Asp Pro Val Thr
165 170 175

Arg Gly Leu Leu Pro Glu Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe
180 185 190

Ile Lys Gln Ile Arg Ala Tyr Met Asp Gly Lys Ile Pro Val Ala Thr
195 200 205

Val Ser Asn Glu Ser Ser Ala Ser Ser Asn Thr Val Lys Pro Val Ala
210 215 220

Ser Ala Gly Ser Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
225 230 235 240

Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
245 250 255

Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
260 265 270

Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
275 280 285

Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
290 295 300

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

Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
325 330 335

Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn
340 345 350

Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
355 360 365

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
370 375 380

eolf-seq1

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

Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile
405 410 415

Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val
420 425 430

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
435 440 445

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
450 455 460

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
465 470 475 480

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
485 490 495

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
500 505 510

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
515 520 525

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

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
545 550 555 560

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
565 570 575

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
580 585 590

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
595 600 605

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
610 615 620

Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
625 630 635 640

eof-seq1

Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
645 650 655

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

Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
675 680 685

Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
690 695 700

Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
705 710

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

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys Asn
65 70 75 80

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
115 120 125

eo1f-seq1

Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His Asp
130 135 140

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

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

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
210 215 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225 230 235 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
245 250 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
260 265 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
275 280 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
290 295 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305 310 315 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
325 330 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
340 345 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
355 360 365

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

eof-seq1

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385 390 395 400

Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
405 410 415

Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
420 425 430

Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
435 440 445

Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
450 455 460

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
465 470 475 480

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
485 490 495

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
500 505 510

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
515 520 525

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
530 535 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545 550 555 560

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
565 570 575

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
580 585 590

Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
595 600 605

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
610 615 620

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
Page 34

eolf-seq1

625		630		635		640
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Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
645 650

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

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys Asn
65 70 75 80

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
115 120 125

Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His Asp
130 135 140

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

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

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Gln Leu
180 185 190

eof-seq1

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
 195 200 205
 Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
 210 215 220
 Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
 225 230 235 240
 Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
 245 250 255
 Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
 260 265 270
 Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
 275 280 285
 Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
 290 295 300
 Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
 305 310 315 320
 Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
 325 330 335
 Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
 340 345 350
 Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
 355 360 365
 Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
 370 375 380
 Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
 385 390 395 400
 Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
 405 410 415
 Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
 420 425 430
 Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro

eolf-seql

435 440 445

Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
450 455 460

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
465 470 475 480

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
485 490 495

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
500 505 510

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
515 520 525

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
530 535 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545 550 555 560

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

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
580 585 590

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
595 600 605

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
610 615 620

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
625 630 635 640

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
645 650

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eolf-seql

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Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
65 70 75 80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
85 90 95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
100 105 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
115 120 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
130 135 140

Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
145 150 155 160

Pro Thr Pro Asn Thr Gly Glu Leu Leu Arg Pro Lys Asp Ala Lys Lys
165 170 175

Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp
180 185 190

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

Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile
210 215 220

Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr
225 230 235 240

Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu

245										eol f-seq1 250					255				
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Asn	Glu	Val	Leu	Trp	Tyr	His	Pro	Thr	Asp	Tyr	Val	Glu	Trp	His	Cys				
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Gly	Asn	Gln	Trp	Ala	Asn	Ala	Asn	Leu	Ile	Gly	Phe	Glu	Val	Cys	Glu				
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Ser	Tyr	Pro	Gly	Arg	Ile	Ser	Asp	Lys	Leu	Phe	Leu	Glu	Asn	Glu	Glu				
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Cys	Pro	His	Arg	Ser	Trp	Asp	Leu	His	Val	Gly	Lys	Gly	Glu	Pro	Tyr				
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Thr	Thr	Thr	Asn	Ile	Asn	Lys	Met	Lys	Asp	Tyr	Phe	Ile	Lys	Arg	Ile				
	370					375					380								
Lys	His	Tyr	Tyr	Asp	Gly	Gly	Lys	Leu	Glu	Val	Ser	Lys	Ala	Ala	Thr				
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Ile	Lys	Gln	Ser	Asp	Val	Lys	Gln	Glu	Val	Lys	Lys	Gln	Glu	Ala	Lys				
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Gln	Ile	Val	Lys	Ala	Thr	Asp	Trp	Lys	Gln	Asn	Lys	Asp	Gly	Ile	Trp				
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Tyr	Lys	Ala	Glu	His	Ala	Ser	Phe	Thr	Val	Thr	Ala	Pro	Glu	Gly	Ile				
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Ile	Thr	Arg	Tyr	Lys	Gly	Pro	Trp	Thr	Gly	His	Pro	Gln	Ala	Gly	Val				
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Leu	Gln	Lys	Gly	Gln	Thr	Ile	Lys	Tyr	Asp	Glu	Val	Gln	Lys	Phe	Asp				
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Gly	His	Val	Trp	Val	Ser	Trp	Glu	Thr	Phe	Glu	Gly	Glu	Thr	Val	Tyr				
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 500 505 510

Trp Gly Glu Ile Lys
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 <223> His-tagged LST_LST

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Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
 20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
 35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
 50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
 65 70 75 80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
 85 90 95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
 100 105 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
 115 120 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
 130 135 140

Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
 145 150 155 160

Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr
 165 170 175

Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg

eolf-seql

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Thr	Thr	Gly	Pro	Phe	Arg	Ser	Met	Pro	Gln	Ser	Gly	Val	Leu	Lys	Ala				
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Gly	Gln	Thr	Ile	His	Tyr	Asp	Glu	Val	Met	Lys	Gln	Asp	Gly	His	Val				
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Trp	Val	Gly	Tyr	Thr	Gly	Asn	Ser	Gly	Gln	Arg	Ile	Tyr	Leu	Pro	Val				
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Arg	Thr	Trp	Asn	Lys	Ser	Thr	Asn	Thr	Leu	Gly	Val	Leu	Trp	Gly	Thr				
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Ile	Lys	Glu	Leu	Ala	Ala	Thr	His	Glu	His	Ser	Ala	Gln	Trp	Leu	Asn				
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Asn	Tyr	Lys	Lys	Gly	Tyr	Gly	Tyr	Gly	Pro	Tyr	Pro	Leu	Gly	Ile	Asn				
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Arg	Gln	Trp	Tyr	Met	His	Leu	Ser	Lys	Tyr	Asn	Val	Lys	Val	Gly	Asp				
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Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
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Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
 450 455 460

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
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Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
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Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
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 20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
 35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
 50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
 65 70 75 80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
 85 90 95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
 100 105 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
 115 120 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met

eolf-seql

130 135 140

Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
145 150 155 160

Pro Thr Pro Asn Thr Gly Glu Leu Ala Ala Thr His Glu His Ser Ala
 165 170 175

Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro
 180 185 190

Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn
 195 200 205

Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala
 210 215 220

Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn
225 230 235 240

Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val
 245 250 255

Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly
 260 265 270

Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val
 275 280 285

Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys
290 295 300

Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn
305 310 315 320

Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser
 325 330 335

Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro
 340 345 350

Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile
 355 360 365

His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr
370 375 380

Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn
 385 390 395 400

Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
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 <400> 32

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Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg
 20 25 30

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
 35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
 50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
 65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
 85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
 100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
 115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
 130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
 145 150 155 160

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

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
 Page 44

eolf-seql

180	185	190	
Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro			
195	200	205	
Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met			
210	215	220	
Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly			
225	230	235	240
Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val			
245	250	255	
Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln			
260	265	270	
Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro			
275	280	285	
Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu			
290	295	300	
Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg			
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Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His			
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Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr			
340	345	350	
Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr			
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Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln			
370	375	380	
Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val			
385	390	395	400
Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala			
405	410	415	
Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg			
420	425	430	

eolf-seq1

Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
 435 440 445

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

Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
 465 470 475 480

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

Ile Lys Glu Leu Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile
 500 505 510

Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln
 515 520 525

Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr
 530 535 540

Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile
 545 550 555 560

Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu
 565 570 575

Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly
 580 585 590

His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met
 595 600 605

Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
 610 615 620

Gly Glu Ile Lys
 625

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 <211> 741
 <212> DNA
 <213> Staphylococcus simulans

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 attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180

eolf-seq1

tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatac acaatgggtat 240
atgcatctaa gtaaataataa tgtaaagta ggagattatg tcaaagctgg tcaaataatc 300
ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatgggt 360
aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420
ggaaaagcag gtgttacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 480
ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 540
acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 600
cattatgatg aagtgatgaa acaagacggg catgtttggg taggttatac aggtaacagt 660
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ctttggggaa ctataaagtg a 741

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<211> 246
<212> PRT
<213> Staphylococcus simulans
<400> 34

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
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Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

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

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
130 135 140

eolf-seq1

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr
145 150 155 160

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
165 170 175

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
180 185 190

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
195 200 205

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
210 215 220

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
225 230 235 240

Leu Trp Gly Thr Ile Lys
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<210> 35
<211> 94
<212> PRT
<213> Staphylococcus aureus bacteriophage 2638a
<400> 35

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
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Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
20 25 30

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
35 40 45

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
50 55 60

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
65 70 75 80

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
85 90

<210> 36
<211> 92

eof-seq1

<212> PRT

<213> Staphylococcus simulans

<400> 36

Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser
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Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg
20 25 30

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

Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly
50 55 60

Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser
65 70 75 80

Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
85 90

<210> 37

<211> 146

<212> PRT

<213> Staphylococcus aureus bacteriophage 2638a

<400> 37

Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser
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Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg
20 25 30

Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr
35 40 45

His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala
50 55 60

Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly
65 70 75 80

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
85 90 95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
100 105 110

eof-seq1

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
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Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
130 135 140

Lys Asp
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<210> 38
<211> 140
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<213> Staphylococcus simulans
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Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

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

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
130 135 140

<210> 39
<211> 169
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<213> Staphylococcus aureus bacteriophage 2638a
<400> 39

eolf-seq1

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
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Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
20 25 30

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
35 40 45

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
50 55 60

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
65 70 75 80

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
85 90 95

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
100 105 110

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
115 120 125

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
130 135 140

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
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Lys Arg Ile Lys His Tyr Tyr Asp Gly
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<210> 40
<211> 163
<212> PRT
<213> Staphylococcus aureus phage phi 11

<400> 40

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Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg
20 25 30

Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp
35 40 45

eolf-seq1

Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile
50 55 60

Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
65 70 75 80

Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
85 90 95

Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
100 105 110

Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
115 120 125

Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
130 135 140

Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
145 150 155 160

Tyr Met Asp

<210> 41
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<213> Staphylococcus aureus phage phi 11
<400> 41

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
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Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
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Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
 100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
 115 120 125

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 130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro
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<210> 42
 <211> 140
 <212> PRT
 <213> Staphylococcus phage Twort
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Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
 35 40 45

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
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Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
 65 70 75 80

Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
 85 90 95

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
 100 105 110

Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile
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Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile
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 <213> artificial

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<212> DNA
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<211> 2019
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<213> artificial

<220>
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<210> 46
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 <212> DNA
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<220>
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501'-seq]

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1260 aagaatggga gcgtagaaga gtgaaaacat atctattcaa accatataa agttaacaag
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<210> 47

<211> 1959

<212> DNA

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<210> 48
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<210> 49
 <211> 1887
 <212> DNA
 <213> artificial
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<212> DNA
<213> artificial

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eolf-seq1

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 <212> PRT
 <213> Staphylococcus aureus bacteriophage 2638a

<400> 51

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Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala
 35 40 45

Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly
 50 55 60

Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr
 65 70 75 80

Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser
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Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp
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<210> 52
 <211> 106
 <212> PRT
 <213> Staphylococcus simulans

<400> 52

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 20 25 30

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
 35 40 45

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
 50 55 60

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
65 70 75 80

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<212> PRT
<213> Staphylococcus aureus bacteriophage 2638a

<400> 53

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20 25 30

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35 40 45

His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala
50 55 60

Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly
65 70 75 80

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
85 90 95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
100 105 110

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
115 120 125

Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
130 135 140

Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr
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165 170 175

Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
 180 185 190

<210> 54
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 <212> PRT
 <213> Staphylococcus simulans
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 20 25 30

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

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
 50 55 60

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
 65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
 85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
 100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
 115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
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Gly Thr Val Thr Pro Thr Pro Asn Thr Gly
 145 150

<210> 55
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 <212> PRT
 <213> Staphylococcus aureus bacteriophage 2638a
 <400> 55

Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile
 1 5 10 15

Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys
 Page 65

eolf-seq1

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Glu Leu Lys His Ile Tyr Ser	Asn His Ile Lys Gly	Asn Lys Ile Thr
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Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile	His Asn Asp Tyr Gly	
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Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp	Leu Tyr Ala Arg Glu	Asn
65	70	75
Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn		
85	90	95
Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly		
100	105	110
Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser		
115	120	125
Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala		
130	135	140
Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val		
145	150	155
Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys		
165	170	175
Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr		
180	185	190
Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys		
195	200	205
His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile		
210	215	220
Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln		
225	230	235
Ile Val Lys Ala Thr Asp		
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 <211> 220
 <212> PRT
 <213> Staphylococcus aureus phage phi 11

eof-seq1

<400> 56

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20 25 30

Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
35 40 45

Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg
50 55 60

Leu Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp
65 70 75 80

Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile
85 90 95

Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
100 105 110

Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
115 120 125

Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
130 135 140

Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
145 150 155 160

Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
165 170 175

Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
180 185 190

Tyr Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser
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Ala Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala
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<210> 57

<211> 206

<212> PRT

<213> Staphylococcus aureus phage phi 11

eof-seq1

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35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
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Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
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<210> 58

<211> 187

<212> PRT

<213> Staphylococcus phage Twort

<400> 58

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eolf-seq1

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Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val			
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Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val			
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Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu			
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Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile			
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Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe			
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Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys			
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Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg			
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240 actactggaa aactaccctgt tccatggcca acaattgtca ctactttcgc gtatgttctt
300 caatgctttg cgaatatccc agatcatatg aaacagcatg actttttcaa gagtggccatg
360 ccggaaggtt atgtacagga aagaactata tttttcaag atgacgggaa ctacaagaca
420 cgtgctgaag tcaagtttga agttgatacc ctgtttaata gaatcggagt aaaagttatt
480 gattttaag aagatggaaa cattcttggc cacaatttg aatacaacta taactcacac
540 aatgtatata tcatggcaga caaacaaga aatggaatca aagttaactt caaatitaga
600 caccaacttg aagatggaa gttcaacta gcagaccat atcaacaata tactccaat
660 ggcatgtgccc ctgtcccttt accagacaac cattaccctgt ccacaactc tgcctttcgc
720 aaagatccca accgaaaag agaccacatg gtccctcttg agttgtaac agctgtggg
780 attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa
840 gcagcaacta tcaacaactc tgacgttaag caagaagtta aaaagcagga agcaaaaaca
900 atgttgaaag caacagattg gaaacagaaat aaagatggca ttgtgtataa agctgaacat
960 gcttcgttca cagtgcacgc accgagggga attatcacaa gatataaag tcccttgact
1020 ggtcacccac aagctgttgt attacaaaaa ggtcaaaaag ttaatatga tgaagttcaa
1080 aaatttgacg gtcatgtttg gttatcgttg gaaacgtttg agggcgaaac tgtatacatg
1140 ccggtacgca catgggacgc taaaacttgt aaagtgtga agttgtgggg cgaattaaa
1200 ggtaccggtg gaaagctaga agtaagcaaa gcagcaacta tcaacaactc tgacgtitaa
1260 caagaagtta aaaagcagga agcaaaaaca attgtgaaag caacagattg gaaacagaaat
1320 aaagatggca ttgtgtataa agctgaaacat gcttcgttca cagtgcacgc accagaggga
1380 attatcacaa gatcaaaag tcccttgact ggtcaccac aagctgttgt attacaaaaa
1440 ggtcaaacga ttaatatga tgaagttcaa aaatttgacg gtcatgtttg ggtatcgttg
1500 gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaacttgt

eof-seq1

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aaagttggtg agttgtgggg cgaaattaaa gtcgacggtg gaaagctaga agtaagcaaa 1560
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 1620
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat 1680
gcttcgttca cagtgcagc accagagggg attatcacia gatacaaagg tccttggtact 1740
ggtcacccac aagctgggtg attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa 1800
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1860
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<210> 64
 <211> 380
 <212> PRT
 <213> artificial

<220>
 <223> His-tagged GFP_CBD2638

<400> 64

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

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

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
85 90 95

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
100 105 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
130 135 140

eolf-seq1

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

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
165 170 175

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

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

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
210 215 220

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

Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
245 250 255

Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
260 265 270

Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
275 280 285

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
290 295 300

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
305 310 315 320

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

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
340 345 350

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
355 360 365

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
370 375 380

<210> 65
<211> 510

eof-seq1

<212> PRT
<213> artificial

<220>
<223> His-tagged GFP_CBD2638_CBD2638 var.1

<400> 65

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

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

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
85 90 95

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
100 105 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
130 135 140

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

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
165 170 175

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

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

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
210 215 220

eo1f-seq1

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 225 230 235 240
 Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
 245 250 255
 Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
 260 265 270
 Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
 275 280 285
 Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
 290 295 300
 Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
 305 310 315 320
 Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
 325 330 335
 Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
 340 345 350
 Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
 355 360 365
 Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Glu Leu Gly Gly
 370 375 380
 Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
 385 390 395 400
 Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
 405 410 415
 Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
 420 425 430
 Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
 435 440 445
 Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
 450 455 460
 Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
 465 470 475 480

eof-seq1

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
485 490 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
500 505 510

<210> 66
<211> 519
<212> PRT
<213> artificial

<220>
<223> His-tagged GFP_CBD2638_CBD2638 var. 2

<400> 66

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

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
85 90 95

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
100 105 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
130 135 140

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

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
165 170 175

eo1f-seq1

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 180 185 190
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 195 200 205
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 210 215 220
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 225 230 235 240
 Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
 245 250 255
 Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
 260 265 270
 Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
 275 280 285
 Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
 290 295 300
 Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
 305 310 315 320
 Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
 325 330 335
 Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
 340 345 350
 Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
 355 360 365
 Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Gly Thr Gly Gly
 370 375 380
 Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
 385 390 395 400
 Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
 405 410 415
 Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
 420 425 430

eof-seq1

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
435 440 445

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
450 455 460

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
465 470 475 480

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
485 490 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Val Asp
500 505 510

Leu Gln Pro Ser Leu Ile Ser
515

<210> 67

<211> 647

<212> PRT

<213> artificial

<220>

<223> His-tagged GFP_CBD2638_CBD2638_CBD2638

<400> 67

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

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

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
85 90 95

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
100 105 110

eof-seq1

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
130 135 140

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

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
165 170 175

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

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

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
210 215 220

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

Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
245 250 255

Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
260 265 270

Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
275 280 285

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
290 295 300

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
305 310 315 320

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

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
340 345 350

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
355 360 365

eof-seq1

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Gly Thr Gly Gly
370 375 380

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

Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
405 410 415

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
420 425 430

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
435 440 445

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
450 455 460

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
465 470 475 480

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
485 490 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys Val Asp
500 505 510

Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp
515 520 525

Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala
530 535 540

Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His
545 550 555 560

Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys
565 570 575

Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln
580 585 590

Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val
595 600 605

Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr

										eolf-seq1					
610					615					620					
Trp	Asp	Ala	Lys	Thr	Gly	Lys	Val	Gly	Lys	Leu	Trp	Gly	Glu	Ile	Lys
625					630					635					640
Leu Gln Pro Ser					Leu Ile Ser										
					645										