

eol-f-seq1
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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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eolf-seq1

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 <211> 279
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 <213> Staphylococcus simulans

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eof-seq1

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eolf-seq1

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 <213> Staphylococcus phage Twort

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 <211> 1851
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<220>

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1851

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 <213> artificial

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 <223> His-tagged Ply2638

<400> 21

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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
180 185 190

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

eolf-seq1

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 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

eo1f-seq1
460

450

455

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

<210> 22
<211> 361
<212> PRT
<213> artificial

<220>
<223> His-tagged Ami2638_CBD2638

<400> 22

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

Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met
20 25 30

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

Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys
50 55 60

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

His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu
85 90 95

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

Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val
115 120 125

Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe
130 135 140

Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu
145 150 155 160

eolf-seq1

Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser
165 170 175

Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe
180 185 190

Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys
195 200 205

Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe
210 215 220

Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser
225 230 235 240

Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys
245 250 255

Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys
260 265 270

Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala
275 280 285

Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro
290 295 300

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
325 330 335

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

Val Gly Lys Leu Trp Gly Glu Ile Lys
355 360

<210> 23
<211> 344
<212> PRT
<213> artificial

<220>
<223> His-tagged M23-2638_CBD2638

<400> 23

eolf-seq1

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Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1      5      10      15

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
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

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eo1f-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
340

<210> 24
<211> 986
<212> PRT
<213> artificial

<220>
<223> His-tagged Ply2638_Ply2638

<400> 24

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1 5 10 15

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

eolf-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

eolf-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

eo1f-seq1
620

610

615

Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
625 630 635 640

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
645 650 655

Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser
660 665 670

Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile
675 680 685

Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val
690 695 700

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
705 710 715 720

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
725 730 735

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
740 745 750

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
755 760 765

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
770 775 780

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
785 790 795 800

Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu
805 810 815

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
820 825 830

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
835 840 845

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
850 855 860

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

<210> 25
 <211> 672
 <212> PRT
 <213> artificial

<220>
 <223> His-tagged CHAP11_M23-2638_Ami2638_CBD2638

<400> 25

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

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-seql															
85								90				95			
Phe	Gly	Ser	Asn 100	Tyr	Gly	Ala	Gly	Tyr 105	Gly	His	Val	Ala	Trp 110	Val	Ile
Glu	Ala	Thr 115	Leu	Asp	Tyr	Ile	Ile 120	Val	Tyr	Glu	Gln	Asn 125	Trp	Leu	Gly
Gly	Gly 130	Trp	Thr	Asp	Gly	Ile 135	Glu	Gln	Pro	Gly	Trp 140	Gly	Trp	Glu	Lys
Val 145	Thr	Arg	Arg	Gln	His 150	Ala	Tyr	Asp	Phe	Pro 155	Met	Trp	Phe	Ile	Arg 160
Pro	Asn	Phe	Lys	Ser 165	Glu	Thr	Ala	Pro	Arg 170	Ser	Val	Gln	Ser	Pro 175	Thr
Gln	Ala	Pro	Lys 180	Lys	Glu	Thr	Ala	Gly 185	Ser	Met	Leu	Thr	Ala 190	Ile	Asp
Tyr	Leu	Thr 195	Lys	Lys	Gly	Trp	Lys 200	Ile	Ser	Ser	Asp	Pro 205	Arg	Thr	Tyr
Asp	Gly 210	Tyr	Pro	Lys	Asn	Tyr 215	Gly	Tyr	Arg	Asn	Tyr 220	His	Glu	Asn	Gly
Ile 225	Asn	Tyr	Asp	Glu	Phe 230	Cys	Gly	Gly	Tyr	His 235	Arg	Ala	Phe	Asp	Val 240
Tyr	Ser	Asn	Glu	Thr 245	Asn	Asp	Val	Pro	Ala 250	Val	Thr	Ser	Gly	Thr 255	Val
Ile	Glu	Ala	Asn 260	Asp	Tyr	Gly	Asn	Phe 265	Gly	Gly	Thr	Phe	Val 270	Ile	Arg
Asp	Ala	Asn 275	Asp	Asn	Asp	Trp	Ile 280	Tyr	Gly	His	Leu	Gln 285	Arg	Gly	Ser
Met	Arg 290	Phe	Val	Val	Gly	Asp 295	Lys	Val	Asn	Gln	Gly 300	Asp	Ile	Ile	Gly
Leu 305	Gln	Gly	Asn	Ser	Asn 310	Tyr	Tyr	Asp	Asn	Pro 315	Met	Ser	Val	His	Leu 320
His	Leu	Gln	Leu	Arg 325	Pro	Lys	Asp	Ala	Lys 330	Lys	Asp	Glu	Lys	Ser 335	Gln

eolf-seq1
 Val Cys Ser Gly₃₄₀ Leu Ala Met Glu Lys₃₄₅ Tyr Asp Ile Thr Asn₃₅₀ Leu Asn
 Ala Lys Gln₃₅₅ Asp Lys Ser Lys Asn₃₆₀ Gly Ser Val Lys Glu₃₆₅ Leu Lys His
 Ile Tyr Ser Asn His Ile Lys₃₇₅ Gly Asn Lys Ile Thr₃₈₀ Ala Pro Lys Pro
 Ser Ile Gln Gly Val Val₃₉₀ Ile His Asn Asp Tyr₃₉₅ Gly Ser Met Thr Pro₄₀₀
 Ser Gln Tyr Leu Pro₄₀₅ Trp Leu Tyr Ala Arg₄₁₀ Glu Asn Asn Gly Thr₄₁₅ His
 Val Asn Gly Trp₄₂₀ Ala Ser Val Tyr Ala₄₂₅ Asn Arg Asn Glu Val₄₃₀ Leu Trp
 Tyr His Pro₄₃₅ Thr Asp Tyr Val Glu₄₄₀ Trp His Cys Gly Asn₄₄₅ Gln Trp Ala
 Asn Ala Asn Leu Ile Gly Phe₄₅₅ Glu Val Cys Glu Ser₄₆₀ Tyr Pro Gly Arg
 Ile Ser Asp Lys Leu Phe₄₇₀ Leu Glu Asn Glu Glu₄₇₅ Ala Thr Leu Lys Val₄₈₀
 Ala Ala Asp Val₄₈₅ Met Lys Ser Tyr Gly Leu₄₉₀ Pro Val Asn Arg Asn₄₉₅ Thr
 Val Arg Leu His₅₀₀ Asn Glu Phe Phe Gly₅₀₅ Thr Ser Cys Pro His₅₁₀ Arg Ser
 Trp Asp Leu His Val Gly Lys Gly₅₂₀ Glu Pro Tyr Thr Thr₅₂₅ Thr Asn Ile
 Asn Lys Met Lys Asp Tyr Phe₅₃₅ Ile Lys Arg Ile Lys₅₄₀ His Tyr Tyr Asp
 Gly Gly Lys Leu Glu Val₅₅₀ Ser Lys Ala Ala Thr₅₅₅ Ile Lys Gln Ser Asp₅₆₀
 Val Lys Gln Glu Val₅₆₅ Lys Lys Gln Glu Ala₅₇₀ Lys Gln Ile Val Lys₅₇₅ Ala
 Thr Asp Trp Lys₅₈₀ Gln Asn Lys Asp Gly₅₈₅ Ile Trp Tyr Lys Ala₅₉₀ Glu His

eo1f-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
645 650 655

Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
660 665 670

<210> 26
<211> 714
<212> PRT
<213> artificial

<220>
<223> His-tagged Ami11_M23-2638_Ami2638_CBD2638

<400> 26

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

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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<211> 652
<212> PRT
<213> artificial

<220>
<223> His-tagged CHAPTw_Ami2638_M23-LST_CBD2638

<400> 27

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

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

eolf-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

eolf-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
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Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys

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

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
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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
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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
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Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
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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
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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
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Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
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Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
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eo1f-seq1

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

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Ala	Thr	Leu	Lys	Val	Ala	Ala	Asp	Val	Met	Lys	Ser	Tyr	Gly	Leu	Pro						
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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						
385					390					395					400						
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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Trp Gly Glu Ile Lys
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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 195	Pro Phe Arg Ser	Met 200	Pro Gln Ser Gly	Val 205	Leu Lys Ala	
Gly	Gln	Thr	Ile His Tyr	Asp 215	Glu Val Met Lys	Gln 220	Asp Gly His Val	
Trp	Val	Gly	Tyr Thr	Gly 230	Asn Ser Gly Gln	Arg 235	Ile Tyr Leu Pro Val	
Arg	Thr	Trp	Asn	Lys 245	Ser Thr Asn Thr	Leu 250	Gly Val Leu Trp Gly Thr	
Ile	Lys	Glu	Leu	Ala 260	Ala Thr His	Glu 265	His Ser Ala Gln Trp Leu Asn	
Asn	Tyr	Lys 275	Lys Gly Tyr	Gly	Tyr 280	Gly Pro Tyr Pro	Leu 285	Gly Ile Asn
Gly	Gly	Met	His Tyr	Gly	Val 295	Asp Phe Phe Met	Asn 300	Ile Gly Thr Pro
Val	Lys	Ala	Ile Ser	Ser 310	Gly Lys Ile Val	Glu 315	Ala Gly Trp Ser Asn	
Tyr	Gly	Gly	Gly	Asn 325	Gln Ile Gly Leu	Ile 330	Glu Asn Asp Gly Val His	
Arg	Gln	Trp	Tyr	Met	His 340	Leu Ser Lys	Tyr Asn Val Lys Val Gly Asp	
Tyr	Val	Lys 355	Ala Gly	Gln Ile	Ile 360	Gly Trp Ser Gly	Ser 365	Thr Gly Tyr
Ser	Thr	Ala	Pro	His	Leu 370	His 375	Phe Gln Arg Met Val Asn Ser Phe Ser	
Asn	Ser	Thr	Ala	Gln	Asp 385	Pro Met Pro Phe	Leu 390	Lys Ser Ala Gly Tyr
Gly	Lys	Ala	Gly	Gly	Thr 405	Val Thr Pro	Thr 410	Pro Asn Thr Gly Trp Lys
Thr	Asn	Lys	Tyr	Gly	Thr	Leu Tyr	Lys 420	Ser Glu Ser Ala Ser Phe Thr

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
 435 440 445

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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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
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eolf-seq1

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

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

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

eolf-seq1
 Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn
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Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
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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
 Page 44

eolf-seq1

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
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
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
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
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Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
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Gly Glu Ile Lys
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attggaacac cagtaaaaagc tattttcaagc ggaaaaaatag ttgaagctgg ttggagtaat 180

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atgcatctaa gtaaataataa tgtaaagta ggagattatg tcaaagctgg tcaaataatc 300
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aattcatttt caaattcaac tgccaagat ccaatgcctt tcttaaagag cgcaggatat 420
ggaaaagcag gtggtacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 480
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acgactgggc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 600
cattatgatg aagtgatgaa acaagacggt catgtttggg taggttatac aggtaacagt 660
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Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
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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

eo1f-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
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Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
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Leu Trp Gly Thr Ile Lys
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Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
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Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
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Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
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Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
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eof-seq1

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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
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Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser
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Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
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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

eo1f-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
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Lys Asp
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35 40 45

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
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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
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Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
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<400> 39

eolf-seq1
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 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
 145 150 155 160
 Lys Arg Ile Lys His Tyr Tyr Asp Gly
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 <213> Staphylococcus aureus phage phi 11
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Asn Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala
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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
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Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
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Tyr Met Asp

<210> 41
<211> 158
<212> PRT
<213> Staphylococcus aureus phage phi 11

<400> 41

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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

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
 145 150 155

<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
 50 55 60

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
 115 120 125

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile
 130 135 140

<210> 43
 <211> 12
 <212> PRT
 <213> artificial

eolf-seq1

<220>

<223> His-tag

<400> 43

Met Arg Gly Ser His His His His His His Gly Ser

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<210> 44

<211> 1497

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<213> artificial

<220>

<223> His-tagged Ply2638

<400> 44

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tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tgggtggttat	180
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aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc	360
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tatggtagta tgacacctag tcaataactta ccatgggttat atgcacgtga gaataacggt	720
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aaagcaacag attggaaaaca gaataaagat ggcattttggt ataaaagctga acatgcttcg	1260
ttcacagtga cagcaccaga ggggaattatc acaagataca aagggtccttg gactgggtcac	1320

eolf-seq1

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gacggtcatg	tttgggtatc	gtgggaaacg	tttgagggcg	aaactgtata	catgccggta	1440
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 <211> 2019
 <212> DNA
 <213> artificial

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aaaggtttag	gtgcaaaaga tattccggtc gctaacaact tcgacggatt agctactgta 240
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eolf-seq1

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gagccttaca	caactactaa	tattaataaa	atgaaagact	acttcatcaa	acgcatcaaa	1620
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tcgtgggaaa	cgtttgaggg	cgaaactgta	tacatgccgg	tacgcacatg	ggacgctaaa	1980
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 <211> 2145
 <212> DNA
 <213> artificial

<220>
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tcaggcaaca	cagtttggca agccttagat gaatcacaaag taggttggca taccgctaata 300
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gatggtaaaa	taccggttgc cactgtctct aatgagtcaa gcgcttcaag taatacagtt 660
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eolf-seq1

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gcaccagagg gaattatcac aagatacaaa ggtccttgga ctggtcacc acaagctgggt	1980
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tgggtatcgt gggaaacgtt tgagggcgaa actgtatata tgccggtacg cacatgggac	2100
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<210> 47
 <211> 1959
 <212> DNA
 <213> artificial

<220>
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tgtatggact tagcagtaga ttatatattac catgtaacag atggtaaaat aagaatgtgg	180
ggtaatgcta aggatgcat aaataactct tttggtggta ctgctacgggt atataaaaaac	240
taccctgctt ttagacctaa gtacgggtgat gtagtcgtat ggactactgg taattttgca	300
acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt	360
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eolf-seq1

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tatggtagta tgacacctag tcaataactta ccatgggttat atgcacgtga gaataacggt 720
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<210> 48
<211> 1554
<212> DNA
<213> artificial

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<220>
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<400> 48

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eolf-seq1

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cttattgaaa	atgatggagt	gcatagacaa	tggatatatg	atctaagtaa	atataatggt	300
aaagtaggag	attatgtcaa	agctgggtcaa	ataatcggtt	ggtctggaag	cactgggttat	360
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 <211> 1887
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<220>
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eof-seq1

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aaagcaacag attggaaaaca gaataaagat ggcatttggt ataaaagctga acatgcttcg	1260
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eolf-seq1

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<212> DNA
<213> artificial

<220>
<223> pQE-30 vector

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 <213> Staphylococcus aureus bacteriophage 2638a

<400> 51

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 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
 85 90 95

Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp
 100 105 110

Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
 115 120 125

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 <213> Staphylococcus simulans

<400> 52

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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

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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<213> Staphylococcus aureus bacteriophage 2638a
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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

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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Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser
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Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
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 <212> PRT
 <213> Staphylococcus simulans

<400> 54

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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

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<400> 55

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

eo1f-seq1

20

25

30

Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr
35 40 45

Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly
50 55 60

Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn
65 70 75 80

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
145 150 155 160

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
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Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln
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Ile Val Lys Ala Thr Asp
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<211> 220

<212> PRT

<213> Staphylococcus aureus phage phi 11

eolf-seq1

<400> 56

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Ile Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser
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
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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

eolf-seq1

<400> 57

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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

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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Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly
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<210> 58

<211> 187

<212> PRT

<213> Staphylococcus phage Twort

<400> 58

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn

eolf-seq1

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Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp			
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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
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			
	115	120	125
Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe			
	130	135	140
Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys			
	145	150	155
Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg			
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attaacctat	aaaaataggc	gtatcacgag	gccctttcgt	cttcac		4546

<210> 60
<211> 1143
<212> DNA
<213> artificial

<220>
<223> His-tagged GFP_CBD2638

<400> 60	
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actggagttg	tcccaattct tgttgaatta gatggatgatg ttaatgggca caaattttct 120
gtcagtgagg	aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc 180
actactggaa	aactacctgt tccatggcca acacttgtca ctactttcgc gtatgggtctt 240
caatgctttg	cgagataccc agatcatatg aaacggcatg actttttcaa gagtgccatg 300
cccgaagggt	atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360
cgtgctgaag	tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaagggtatt 420
gattttaaag	aagatggaaa cattcttggg cacaatttgg aatacaacta taactcacac 480
aatgtataca	tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540
cacaacattg	aagatgggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600
ggcgaaggcc	ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660
aaagatccca	acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720
attacacatg	gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa 780
gcagcaacta	tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 840
attgtgaaag	caacagattg gaaacagaat aaagatggca tttgggtataa agctgaacat 900
gcttcgttca	cagtgacagc accagagggg attatcacaa gatacaaagg tccttggact 960
ggtcacccac	aagctgggtgt attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa 1020

eolf-seq1

aaatttgacg gtcatgtttg ggtatcgtgg gaaacgtttg agggcgaaaac tgtatacatg	1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa	1140
taa	1143

<210> 61
 <211> 1539
 <212> DNA
 <213> artificial

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

<400> 61	
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actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct	120
gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc	180
actactggaa aactacctgt tccatggcca acacttgatc ctactttcgc gtatggtcct	240
caatgctttg cgagataccc agatcatatg aaacggcatg actttttcaa gagtgccatg	300
cccgaagggt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca	360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaagggtatt	420
gatttttaaag aagatggaaa cattcttggg cacaaaattgg aatacaacta taactcacac	480
aatgtataca tcatggcaga caaacaanaag aatgggaatca aagttaactt caaaattaga	540
cacaacattg aagatgggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt	600
ggcgtatggc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg	660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg	720
attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa	780
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaaaca	840
attgtgaaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat	900
gcttcgttca cagtgcagc accagagggg attatcaca gatacaaagg tccttggact	960
ggtcaccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa	1020
aaatttgacg gtcatgtttg ggtatcgtgg gaaacgtttg agggcgaaaac tgtatacatg	1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa	1140
gagctcggtg gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag	1200
caagaagtta aaaagcaaga agcaaaaaca atttgtgaaa caacagattg gaaacagaat	1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcagc accagagggg	1320
attatcaca gatacaaagg tccttggact ggtcaccac aagctggtgt attacaaaaa	1380
ggtcaaacga ttaaataatga tgaggttcaa aaatttgacg gtcatgtttg ggtatcgtgg	1440

eolf-seq1

```

gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt 1500
aaagttggta agttgtgggg cgaaattaaa taagtcgac 1539

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<210> 62
<211> 1560
<212> DNA
<213> artificial

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

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<400> 62
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actggagttg tccaattctt tgttgaatta gatggtgatg ttaatgggca caaattttct 120
gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc 180
actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggtcctt 240
caatgctttg cgagataccc agatcatatg aaacagcatg actttttcaa gagtgccatg 300
cccgaagggt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaagggtatt 420
gatttttaaag aagatggaaa cattcttggg cacaaaattg aatacaacta taactcacac 480
aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540
cacaacattg aagatgggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600
ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720
attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa 780
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 840
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat 900
gcttcgttca cagtgcagc accagaggga attatcacia gatacaaagg tccttggact 960
ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa 1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 1140
ggtagccgtg gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag 1200
caagaagtta aaaagcaaga agcaaaacaa attgtgaaag caacagattg gaaacagaat 1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcagc accagaggga 1320
attatcacia gatacaaagg tccttggact ggtcacccac aagctggtgt attacaaaaa 1380
ggtcaaacga ttaaataatga tgaggttcaa aaatttgacg gtcattgttg ggtatcgtgg 1440

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eolf-seq1

gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt	1500
aaagttggta agttgtgggg cgaaattaaa gtcgacctgc agccaagctt aattagctga	1560

<210> 63
 <211> 1944
 <212> DNA
 <213> artificial

<220>
 <223> His-tagged GFP_CBD2638_CBD2638_CBD2638

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gtcagtggag aggggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc	180
actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggctctt	240
caatgctttg cgagataccc agatcatatg aaacagcatg actttttcaa gagtgccatg	300
cccgaagggt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca	360
cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaagggtatt	420
gatttttaaag aagatggaaa cattcttggg cacaatttgg aatacaacta taactcacac	480
aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga	540
cacaacattg aagatgggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt	600
ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg	660
aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg	720
attacacatg gcatggatga actatacaaa gagctcgggtg gaaagctaga agtaagcaaa	780
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa	840
attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat	900
gcttcgttca cagtgcagc accagagggg attatcacaa gatacaaagg tccttggact	960
ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaataatga tgaggttcaa	1020
aaatttgacg gtcattgttg ggtatcgtgg gaaacgttg agggcgaaac tgtatacatg	1080
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa	1140
ggtagcgggt gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag	1200
caagaagtta aaaagcaaga agcaaaacaa attgtgaaag caacagattg gaaacagaat	1260
aaagatggca tttggtataa agctgaacat gcttcgttca cagtgcagc accagagggg	1320
attatcacaa gatacaaagg tccttggact ggtcacccac aagctggtgt attacaaaaa	1380
ggtcaaacga ttaaataatga tgaggttcaa aaatttgacg gtcattgttg ggtatcgtgg	1440
gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt	1500

eof-seq1

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aaagttggta agttgtgggg cgaaattaaa gtcgacgggtg gaaagctaga agtaagcaaa 1560
gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 1620
attgtgaaag caacagattg gaaacagaat aaagatggca tttgggtataa agctgaacat 1680
gcttcgttca cagtgacagc accagaggga attatcaciaa gatacaaagg tccttggact 1740
ggtcacccac aagctgggtg attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa 1800
aaatttgacg gtcattgtttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1860
ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 1920
ctgcagccaa gcttaattag ctga 1944

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<210> 64
<211> 380
<212> PRT
<213> artificial

<220>
<223> His-tagged GFP_CBD2638

<400> 64

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Met Arg Gly Ser 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 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

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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
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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 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
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

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

eolf-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

eolf-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

eolf-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

eof-seq1
620