

1447SeqListing_ST25
SEQUENCE LISTING

<110> ILLUMINA, INC.
<120> RECOMBINASE MUTANTS
<130> 531.14470201
<150> 62/314,273
<151> 2016-03-28
<160> 36
<170> PatentIn version 3.5
<210> 1
<211> 356
<212> PRT
<213> Enterobacteria phage RB49
<400> 1

Met Ser Val Leu Glu Lys Leu Lys Lys Asn Ser Thr Leu Lys Thr Thr
1 5 10 15

Ala Val Leu Ser Lys Ser Ser Phe Phe Asn Glu Lys Thr Asn Thr Arg
20 25 30

Thr Lys Ile Pro Met Leu Asn Ile Ala Phe Ser Gly Asp Leu Lys Lys
35 40 45

Gly Phe Gln Ser Gly Leu Ile Phe Phe Ala Gly Pro Ser Lys His Phe
50 55 60

Lys Ser Asn Met Gly Leu Thr Cys Val Ser Ala Tyr Met Lys Gln Asn
65 70 75 80

Pro Asp Ala Ala Cys Leu Phe Phe Asp Ser Glu Phe Gly Ile Thr Ser
85 90 95

Ala Tyr Leu Glu Ser Met Gly Val Asp Pro Asp Arg Val Val His Val
100 105 110

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Pro Ile Lys Asn Ile Glu Glu Leu Lys Phe Glu Ile Met Asn Gln Leu
115 120 125

Glu Gln Ile Thr Arg Glu Asp Lys Val Ile Ile Phe Ile Asp Ser Ile
130 135 140

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

Ser Ala Gln Asp Met Thr Arg Ala Lys Ala Leu Lys Gly Leu Phe Arg
165 170 175

Met Val Thr Pro Tyr Leu Thr Met Asn Asp Ile Pro Cys Ile Ala Ile
180 185 190

Asn His Thr Tyr Glu Thr Gln Glu Met Phe Ser Lys Thr Val Met Ser
195 200 205

Gly Gly Thr Gly Ala Met Tyr Ser Ala Asn Glu Val Phe Ile Ile Gly
210 215 220

Arg Arg Gln Gln Lys Glu Gly Thr Glu Ile Thr Gly Tyr Asp Phe Ile
225 230 235 240

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

Ile Ser Val Thr Phe Ser Gly Gly Ile Asp Pro Tyr Ser Gly Leu Leu
260 265 270

Glu Leu Ala Val Glu Leu Gly Trp Val Val Lys Pro Ser Asn Gly Trp
275 280 285

Tyr Ser Arg Ser Ile Leu Asn Thr Glu Thr Gly Glu Met Glu Thr Glu
290 295 300

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Glu Arg Lys Phe Arg Ala Lys Glu Thr Asn Ser Ile Glu Phe Trp Lys
305 310 315 320

Pro Leu Leu Thr Asn Asp Lys Phe Asn Glu Ala Ile Asn Asp His Tyr
325 330 335

Lys Leu Gly Gln Val Ile Ser Asp Glu Ala Val Asp Lys Glu Ile Glu
340 345 350

Asp Met Leu Ala
355

<210> 2
<211> 356
<212> PRT
<213> Enterobacteria phage RB49

<400> 2

Met Ser Val Leu Glu Lys Leu Lys Lys Asn Ser Thr Leu Lys Thr Thr
1 5 10 15

Ala Val Leu Ser Lys Ser Ser Phe Phe Asn Glu Lys Thr Asn Thr Arg
20 25 30

Thr Lys Ile Pro Met Leu Asn Ile Ala Phe Ser Gly Asp Leu Lys Lys
35 40 45

Gly Phe Gln Ser Gly Leu Ile Phe Phe Ala Gly Pro Ser Lys Ser Phe
50 55 60

Lys Ser Asn Met Gly Leu Thr Cys Val Ser Ala Tyr Met Lys Gln Asn
65 70 75 80

Pro Asp Ala Ala Cys Leu Phe Phe Asp Ser Glu Phe Gly Ile Thr Ser
85 90 95

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Ala Tyr Leu Glu Ser Met Gly Val Asp Pro Asp Arg Val Val His Val
100 105 110

Pro Ile Lys Asn Ile Glu Glu Leu Lys Phe Glu Ile Met Asn Gln Leu
115 120 125

Glu Gln Ile Thr Arg Glu Asp Lys Val Ile Ile Phe Ile Asp Ser Ile
130 135 140

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

Ser Ala Gln Asp Met Thr Arg Ala Lys Ala Leu Lys Gly Leu Phe Arg
165 170 175

Met Val Thr Pro Tyr Leu Thr Met Asn Asp Ile Pro Cys Ile Ala Ile
180 185 190

Asn His Thr Tyr Glu Thr Gln Glu Met Phe Ser Lys Thr Val Met Ser
195 200 205

Gly Gly Thr Gly Ala Met Tyr Ser Ala Asn Glu Val Phe Ile Ile Gly
210 215 220

Arg Arg Gln Gln Lys Glu Gly Thr Glu Ile Thr Gly Tyr Asp Phe Ile
225 230 235 240

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

Ile Ser Val Thr Phe Ser Gly Gly Ile Asp Pro Tyr Ser Gly Leu Leu
260 265 270

Glu Leu Ala Val Glu Leu Gly Trp Val Val Lys Pro Ser Asn Gly Trp
275 280 285

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Tyr Ser Arg Ser Ile Leu Asn Thr Glu Thr Gly Glu Met Glu Thr Glu
290 295 300

Glu Arg Lys Phe Arg Ala Lys Glu Thr Asn Ser Ile Glu Phe Trp Lys
305 310 315 320

Lys Leu Leu Thr Asn Asp Lys Phe Asn Glu Ala Ile Asn Asp His Tyr
325 330 335

Lys Leu Gly Gln Val Ile Ser Asp Glu Ala Val Asp Lys Glu Ile Glu
340 345 350

Asp Met Leu Ala
355

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Semi Conserved Domain

<400> 3

Phe Trp Gly Pro Leu
1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Semi Conserved Domain

<220>
<221> VARIANT
<222> (3)..(3)
<223> X = G, K, R

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<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> X = P, D

<220>
 <221> VARIANT
 <222> (5)..(5)
 <223> X = L, M, I

<220>
 <221> VARIANT
 <222> (6)..(6)
 <223> X = F, L, I

<400> 4

Phe Trp Xaa Xaa Xaa Xaa
 1 5

<210> 5
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Semi Conserved Domain

<400> 5

Ala Ile Lys Arg Ala Tyr
 1 5

<210> 6
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Semi Conserved Domain

<220>
 <221> VARIANT
 <222> (3)..(3)

<223> X = K, N, E

<220>

<221> VARIANT

<222> (4)..(4)

<223> X = R, T, D

<220>

<221> VARIANT

<222> (5)..(5)

<223> X = H, A, R, K

<400> 6

Ala Ile Xaa Xaa Xaa Tyr
1 5

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Semi Conserved Domain

<220>

<221> VARIANT

<222> (1)..(1)

<223> X = F, L

<220>

<221> VARIANT

<222> (2)..(2)

<223> X = R, K, M, L, N

<220>

<221> VARIANT

<222> (3)..(3)

<223> X = D, K, T, E

<220>

<221> VARIANT

<222> (4)..(4)

<223> X = A, G, I

<220>

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<221> VARIANT
 <222> (5)..(5)
 <223> X = I, C, V

<220>
 <221> VARIANT
 <222> (6)..(6)
 <223> X = K, E, S, Q, N

<220>
 <221> VARIANT
 <222> (7)..(7)
 <223> X = R, T, D, N, E, K

<220>
 <221> VARIANT
 <222> (8)..(8)
 <223> X = A, R, K, M, I, H, E

<220>
 <221> VARIANT
 <222> (9)..(9)
 <223> X = Y, F

<400> 7

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 8
 <211> 391
 <212> PRT
 <213> Enterobacteria phage T4

<400> 8

Met Ser Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser Lys Leu
 1 5 10 15

Thr Ala Glu Leu Thr Ala Ser Lys Phe Phe Asn Glu Lys Asp Val Val
 20 25 30

Arg Thr Lys Ile Pro Met Met Asn Ile Ala Leu Ser Gly Glu Ile Thr
 35 40 45

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Gly Gly Met Gln Ser Gly Leu Leu Ile Leu Ala Gly Pro Ser Lys Ser
50 55 60

Phe Lys Ser Asn Phe Gly Leu Thr Met Val Ser Ser Tyr Met Arg Gln
65 70 75 80

Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly Ile Thr
85 90 95

Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val Ile His
100 105 110

Thr Pro Val Gln Ser Leu Glu Gln Leu Arg Ile Asp Met Val Asn Gln
115 120 125

Leu Asp Ala Ile Glu Arg Gly Glu Lys Val Val Val Phe Ile Asp Ser
130 135 140

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

Lys Val Val Ser Asp Met Thr Arg Ala Lys Thr Met Lys Ser Leu Phe
165 170 175

Arg Ile Val Thr Pro Tyr Phe Ser Thr Lys Asn Ile Pro Cys Ile Ala
180 185 190

Ile Asn His Thr Tyr Glu Thr Gln Glu Met Phe Ser Lys Thr Val Met
195 200 205

Gly Gly Gly Thr Gly Pro Met Tyr Ser Ala Asp Thr Val Phe Ile Ile
210 215 220

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

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Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser Lys Phe
 245 250 255

Phe Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser Gly Leu
 260 265 270

Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys Asn Gly
 275 280 285

Trp Tyr Ala Arg Glu Phe Leu Asp Glu Glu Thr Gly Glu Met Ile Arg
 290 295 300

Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr Phe Trp
 305 310 315 320

Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys Arg Ala
 325 330 335

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

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

Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln Leu Ser
 370 375 380

Asp Met Glu Glu Phe Asn Glu
 385 390

<210> 9
 <211> 393
 <212> PRT
 <213> Enterobacteria phage T6
 <400> 9

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Met Ser Ile Ala Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser
1 5 10 15

Lys Met Thr Ala Glu Leu Thr Thr Ser Lys Phe Phe Asn Glu Lys Asp
20 25 30

Val Ile Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala
35 40 45

Ile Asp Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser
50 55 60

Lys His Phe Lys Ser Asn Met Ser Leu Thr Met Val Ala Ala Tyr Leu
65 70 75 80

Asn Lys Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly
85 90 95

Ile Thr Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val
100 105 110

Ile His Thr Pro Ile Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val
115 120 125

Asn Gln Leu Glu Ala Ile Glu Arg Gly Glu Lys Val Ile Val Phe Ile
130 135 140

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

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

Leu Phe Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys
180 185 190

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Val Ala Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr
195 200 205

Val Met Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe
210 215 220

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

Gln Phe Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser
245 250 255

Lys Phe Phe Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser
260 265 270

Gly Leu Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys
275 280 285

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

Ile Arg Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr
305 310 315 320

Phe Trp Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys
325 330 335

Arg Ala Tyr Gln Leu Gly Ala Ile Asp Ser Asn Glu Ile Val Glu Ala
340 345 350

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

Glu Ser Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln
370 375 380

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Leu Ser Asp Met Glu Glu Phe Asn Glu
385 390

<210> 10
<211> 387
<212> PRT
<213> Acinetobacter phage 133

<400> 10

Met Ser Ser Leu Lys Glu Arg Leu Ile Lys Ala Ser Thr Ser Lys Met
1 5 10 15

Thr Ala Glu Leu Thr Lys Ser Lys Phe Phe Asn Asp Lys Thr Val Val
20 25 30

Arg Thr Arg Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala Leu Asn
35 40 45

Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser Lys His
50 55 60

Phe Lys Ser Asn Met Gly Leu Thr Met Val Ala Ala Tyr Met Lys Ala
65 70 75 80

Phe Pro Asp Ala Val Cys Met Phe Tyr Asp Ser Glu Phe Gly Ile Thr
85 90 95

Pro Ala Tyr Leu Lys Ala Met Gly Val Asp Pro Asp Arg Val Ile His
100 105 110

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

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

Ile Gly Asn Leu Ala Ser Lys Lys Glu Thr Glu Asp Ala Leu Asn Glu

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

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340

345

350

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

Pro Ala Glu Ser Ala Ala Asp Lys Glu Gln Gln Leu Glu Asp Phe Val
370 375 380

Asp Glu Asp
385

<210> 11
<211> 390
<212> PRT
<213> Enterobacteria phage RB69

<400> 11

Met Ser Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser Lys Met
1 5 10 15

Thr Ala Asp Leu Thr Lys Ser Lys Leu Phe Asn Asn Arg Asp Glu Val
20 25 30

Pro Thr Arg Ile Pro Met Leu Asn Ile Ala Leu Gly Gly Ala Leu Asn
35 40 45

Ala Gly Leu Gln Ser Gly Leu Thr Ile Phe Ala Ala Pro Ser Lys His
50 55 60

Phe Lys Thr Leu Phe Gly Leu Thr Met Val Ala Ala Tyr Met Lys Lys
65 70 75 80

Tyr Lys Asp Ala Ile Cys Leu Phe Tyr Asp Ser Glu Phe Gly Ala Ser
85 90 95

Glu Ser Tyr Phe Arg Ser Met Gly Val Asp Leu Asp Arg Val Val His
100 105 110

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

Leu Asp Ala Ile Glu Arg Gly Asp Lys Val Ile Ile Phe Ile Asp Ser
130 135 140

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

Lys Val Val Gly Asp Met Ser Arg Ala Lys Ala Leu Lys Ser Leu Phe
165 170 175

Arg Ile Val Thr Pro Tyr Leu Thr Ile Lys Asp Ile Pro Cys Val Ala
180 185 190

Ile Asn His Thr Ala Met Glu Ile Gly Gly Leu Tyr Pro Lys Glu Ile
195 200 205

Met Gly Gly Gly Thr Gly Ile Leu Tyr Ser Ala Asn Thr Val Phe Phe
210 215 220

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

Phe Thr Leu Lys Ala Glu Lys Ser Arg Thr Val Lys Glu Lys Ser Thr
245 250 255

Phe Pro Ile Thr Val Asn Phe Asp Gly Gly Ile Asp Pro Phe Ser Gly
260 265 270

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

Gly Trp Tyr Ala Arg Glu Phe Leu Asp Glu Glu Thr Gly Glu Met Ile
290 295 300

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Arg Glu Glu Lys Ser Trp Arg Ala Lys Ala Thr Asp Cys Val Glu Phe
305 310 315 320

Trp Gly Pro Leu Phe Lys His Lys Pro Phe Arg Asp Ala Ile Glu Thr
325 330 335

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

Val Asn Asp Leu Ile Asn Cys Lys Ala Thr Thr Lys Val Pro Val Lys
355 360 365

Thr Ser Asp Ala Pro Ser Ala Ala Asp Ile Glu Asn Asp Leu Asp Glu
370 375 380

Met Glu Asp Phe Asp Glu
385 390

<210> 12
<211> 411
<212> PRT
<213> Aeromonas phage Aeh1

<400> 12

Met Ala Lys Gly Ile Lys Thr Ala Lys Thr Gly Asn Leu Gly Ser Leu
1 5 10 15

Met Ser Lys Leu Ala Gly Thr Ser Ser Asn Lys Met Ser Ser Val Leu
20 25 30

Ala Asp Ser Lys Phe Phe Asn Asp Lys Asp Cys Val Arg Thr Arg Val
35 40 45

Pro Leu Leu Asn Leu Ala Met Ser Gly Glu Leu Asp Gly Gly Leu Thr
50 55 60

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Pro Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His Phe Lys Ser Asn
65 70 75 80

Leu Ser Leu Val Phe Val Ala Ala Tyr Leu Arg Lys Tyr Pro Asp Ala
85 90 95

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

Glu Ser Gln Gly Val Asp Ile Ser Arg Val Ile His Cys Pro Phe Lys
115 120 125

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

Glu Arg Gly Asp Arg Val Ile Val Phe Val Asp Ser Ile Gly Asn Ala
145 150 155 160

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

Asp Met Thr Arg Ala Lys Gln Ile Lys Ser Leu Thr Arg Met Met Thr
180 185 190

Pro Tyr Leu Thr Val Asn Asp Ile Pro Ala Ile Met Val Ala His Thr
195 200 205

Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys Val Val Ser Gly Gly Thr
210 215 220

Gly Ile Thr Tyr Ser Ser Asp Thr Val Ile Ile Ile Gly Arg Gln Gln
225 230 235 240

Glu Lys Asp Gly Lys Glu Leu Leu Gly Tyr Asn Phe Val Leu Asn Met
245 250 255

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Glu Lys Ser Arg Phe Val Lys Glu Gln Ser Lys Leu Pro Leu Glu Val
 260 265 270

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

Leu Glu Val Gly Phe Val Val Lys Pro Ser Asn Gly Trp Phe Ser Arg
 290 295 300

Ala Phe Leu Asp Glu Glu Thr Gly Glu Leu Val Glu Glu Asp Arg Lys
 305 310 315 320

Trp Arg Arg Ala Asp Thr Asn Cys Leu Glu Phe Trp Lys Pro Met Phe
 325 330 335

Ala His Gln Pro Phe Lys Thr Ala Cys Ser Asp Met Phe Lys Leu Lys
 340 345 350

Ser Val Ala Val Lys Asp Glu Val Phe Asp Glu Val Asp Glu Leu Phe
 355 360 365

Ser Gly Glu Ala Glu Met Pro Val Asn Met Gly Arg Lys Leu Asp Thr
 370 375 380

Ala Asp Gln Glu Glu Ile Asp Gln Leu Glu Glu Val Asp Val Glu Gly
 385 390 395 400

Ser Asp Ser Asp Glu Leu Phe Ala Asn Leu Asp
 405 410

<210> 13
 <211> 368
 <212> PRT
 <213> Aeromonas phage 65
 <400> 13

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Met Ala Lys Lys Ala Lys Val Val Asn Ser Gly Asp Leu Leu Glu Arg
1 5 10 15

Leu Asn Gly Thr Ser Ser Asn Lys Met Ser Ala Met Leu Ala Glu Ser
20 25 30

Ile Phe Phe Asn Glu Lys Asp Thr Ile Arg Thr Arg Val Pro Ile Ile
35 40 45

Asn Leu Met Met Ser Gly Arg Leu Asp Gly Gly Ile Thr Pro Gly Leu
50 55 60

Thr Cys Ile Ala Gly Pro Ser Lys His Phe Lys Ser Asn Leu Ser Leu
65 70 75 80

Val Met Val Ser Ala Tyr Leu Arg Lys Tyr Pro Lys Ala Val Cys Leu
85 90 95

Phe Phe Asp Asn Glu Phe Gly Ser Thr Pro Asp Tyr Phe Thr Ser Gln
100 105 110

Gly Val Asp Ile Ser Arg Val Val His Cys Pro Phe Ile Asp Val Glu
115 120 125

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

Asp Lys Val Ile Ile Tyr Ile Asp Ser Ile Gly Asn Val Ala Ser Lys
145 150 155 160

Lys Glu Leu Gln Asp Ala Lys Asp Glu Lys Ser Ala Gln Asp Met Thr
165 170 175

Arg Ala Lys Gln Ile Lys Ser Leu Phe Arg Met Val Thr Pro Tyr Leu
180 185 190

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Thr Val Leu Asp Ile Pro Cys Ile Ala Val Asn His Thr Tyr Glu Thr
195 200 205

Gln Glu Met Phe Ser Lys Thr Val Met Ser Gly Gly Thr Gly Pro Met
210 215 220

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

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

Arg Ala Ile Lys Glu Lys Ser Lys Leu Asp Leu Met Val Ser Phe Glu
260 265 270

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

Gly Phe Val Thr Lys Pro Gln Asn Ala Arg Tyr Gln Arg Asn Phe Leu
290 295 300

Asp Leu Glu Pro Gly Glu Met Val Ile Pro Glu Asp Glu Lys Lys Trp
305 310 315 320

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

His Lys Pro Phe Met Asp Ala Val Ser Asn Ala Tyr Lys Leu Lys Ala
340 345 350

Val Glu Val Ser Gln Glu Val Phe Asp Glu Val Asp Gln Leu Phe Gly
355 360 365

<210> 14
<211> 366
<212> PRT
<213> Vibrio phage KVP40

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<400> 14

Met Ser Asp Leu Met Lys Ser Leu Lys Lys Ser Ser Thr Ser Gly Tyr
1 5 10 15

Ala Gln Val Leu Ser Glu Ser Gln Phe Met Phe Asp Lys Asp His Thr
20 25 30

Arg Thr Tyr Val Pro Ala Ile Asn Ile Ala Phe Ser Gly Glu Val Asp
35 40 45

Gly Gly Leu Thr Ser Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His
50 55 60

Phe Lys Ser Asn Leu Gly Leu Val Gly Val Ala Ala Tyr Leu Lys Lys
65 70 75 80

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

Pro Ser Tyr Leu Arg Ser Gln Gly Val Asp Pro Asp Arg Val Leu His
100 105 110

Ile Gln Cys Glu Ser Val Glu Arg Met Lys Phe Glu Met Ala Asn Gln
115 120 125

Leu Lys Asp Leu Ala Glu Arg Lys Arg Ala Lys Lys Ala Gly Glu Glu
130 135 140

Pro Asp Arg Val Ile Phe Phe Ile Asp Ser Val Gly Asn Val Ala Ser
145 150 155 160

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

Ser Arg Ala Lys Gln Leu Lys Ser Leu Phe Arg Ile Ile Thr Pro Tyr

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180

185

190

Phe Thr Met Leu Asp Ile Pro Cys Ile Ala Ile Asn His Thr Tyr Gln
 195 200 205

Thr Gln Glu Ile Tyr Ser Lys Thr Val Met Ser Gly Gly Thr Gly Ile
 210 215 220

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

Asp Gly Lys Asp Ile Ile Gly Tyr His Phe Ile Met Asn Ile Glu Lys
 245 250 255

Ser Arg Phe Val Lys Glu Lys Met Lys Val Pro Leu Thr Val Thr Tyr
 260 265 270

Glu Asn Gly Ile Asp Pro Phe Ser Gly Leu Leu Asp Ile Ala Leu Gln
 275 280 285

Thr Gly His Val Val Lys Pro Ser Asn Gly Trp Tyr Gln Arg Ala Thr
 290 295 300

Val Asp Glu Glu Thr Gly Glu Met Ile Val Glu Glu Lys Lys Tyr Arg
 305 310 315 320

Ala Lys Glu Thr Gln Thr Ile Ser Phe Trp Lys Asp Ile Ile Asn Ser
 325 330 335

Pro Thr Phe Lys Glu Gly Val Lys Arg Ile Tyr Cys Leu Gly Gln Leu
 340 345 350

Asp Glu Ser Glu Leu Phe Gly Glu Val Asp Ser Leu Phe Asp
 355 360 365

<210> 15

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<211> 386

<212> PRT

<213> Enterobacteria phage RB43

<400> 15

Met Ser Asn Lys Ala Leu Leu Lys Lys Leu Ile Lys Asn Ser Asn Ser
1 5 10 15

Gln Ser Ala Ala Ile Leu Ser Glu Ser Asp Val Phe Asn Asn Ile Thr
20 25 30

Lys Thr Arg Thr Arg Val Pro Ile Leu Asn Leu Ala Leu Ser Gly Ala
35 40 45

Phe Asp Gly Gly Leu Thr Ser Gly Leu Thr Leu Phe Ala Gly Pro Ser
50 55 60

Lys His Phe Lys Ser Asn Leu Gly Leu Val Thr Val Ser Ala Tyr Leu
65 70 75 80

Lys Ala Asn Glu Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Lys Gly
85 90 95

Val Thr Lys Ser Tyr Leu Lys Ser Met Gly Val Asp Pro Asp Arg Val
100 105 110

Val Tyr Thr Arg Ile Thr Thr Val Glu Gln Leu Arg Asn Asp Val Val
115 120 125

Ser Gln Leu Asp Ala Leu Glu Arg Gly Asp Lys Val Ile Ile Phe Val
130 135 140

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

Ser Asp Asn Asp Lys Gln Asp Met Thr Arg Ala Lys Ala Leu Lys Gly
165 170 175

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Met Phe Arg Met Val Thr Pro Tyr Leu Ala Asp Leu Asp Ile Pro Met
180 185 190

Val Cys Ile Cys His Thr Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys
195 200 205

Val Ile Ser Gly Gly Thr Gly Leu Met Tyr Ser Ala Asp Thr Ala Ile
210 215 220

Ile Leu Gly Lys Gln Gln Val Lys Glu Gly Thr Glu Val Val Gly Tyr
225 230 235 240

Asp Phe Ile Met Asn Ile Glu Lys Ser Arg Phe Val Lys Glu Lys Ser
245 250 255

Lys Phe Pro Leu His Val Thr Tyr Glu Gly Gly Ile Ser Met Tyr Ser
260 265 270

Gly Leu Leu Asp Leu Ala Met Glu Met Asn Phe Val Gln Thr Pro Thr
275 280 285

Lys Gly Trp Arg Gly Arg Ala Phe Leu Asn Thr Glu Thr Gly Glu Leu
290 295 300

Glu Leu Glu Glu Lys Lys Trp Arg Glu Ser Glu Thr Asn Ser Ile Glu
305 310 315 320

Phe Trp Arg Pro Leu Phe Thr His Gln Pro Phe Leu Asp Ala Ile Gln
325 330 335

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

Glu Asp Leu Tyr Ser Thr Asp Glu Pro Glu Ser Asn Lys Ile Asp Leu
355 360 365

1447SeqListing_ST25

Asp Asp Asp Ile Pro Asp Asp Ile Gly Ile Asp Gln Asp Glu Glu Pro
 370 375 380

Ile Met
 385

<210> 16
 <211> 335
 <212> PRT
 <213> Prochlorococcus phage P-SSM2
 <400> 16

Met Asp Phe Leu Lys Glu Ile Val Lys Glu Ile Gly Asp Glu Tyr Thr
 1 5 10 15

Gln Val Ala Ala Asp Ile Gln Glu Asn Glu Arg Phe Ile Asp Thr Gly
 20 25 30

Ser Tyr Ile Phe Asn Gly Leu Val Ser Gly Ser Ile Phe Gly Gly Val
 35 40 45

Ser Ser Ser Arg Ile Thr Ala Ile Ala Gly Glu Ser Ser Thr Gly Lys
 50 55 60

Thr Tyr Phe Ser Leu Ala Val Val Lys Asn Phe Leu Asp Asn Asn Pro
 65 70 75 80

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

Leu Leu Glu Ser Arg Gly Ile Asp Met Asn Arg Leu Val Val Val Asn
 100 105 110

Val Val Thr Ile Glu Glu Phe Arg Ser Lys Ala Leu Arg Ala Val Asp
 115 120 125

1447SeqListing_ST25

Ile Tyr Leu Lys Thr Ser Glu Glu Glu Arg Lys Pro Cys Met Phe Val
130 135 140

Leu Asp Ser Leu Gly Met Leu Ser Thr Glu Lys Glu Ile Arg Asp Ala
145 150 155 160

Leu Asp Asp Lys Gln Val Arg Asp Met Thr Lys Ser Gln Leu Val Lys
165 170 175

Gly Ala Phe Arg Met Leu Thr Leu Lys Leu Gly Gln Ala Asn Ile Pro
180 185 190

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

Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ala Ala Ser Thr
210 215 220

Ile Ile Tyr Leu Ser Lys Lys Lys Glu Lys Asp Gln Lys Glu Val Ile
225 230 235 240

Gly Asn Leu Ile Lys Ala Lys Thr His Lys Ser Arg Leu Ser Lys Glu
245 250 255

Asn Lys Glu Val Gln Ile Arg Leu Tyr Tyr Asp Glu Arg Gly Leu Asp
260 265 270

Arg Tyr Tyr Gly Leu Leu Glu Leu Gly Glu Ile Gly Gly Met Trp Lys
275 280 285

Asn Val Ala Gly Arg Tyr Glu Met Asn Gly Lys Lys Ile Tyr Ala Lys
290 295 300

Glu Ile Leu Lys Asn Pro Thr Glu Tyr Phe Thr Asp Asp Ile Met Glu
305 310 315 320

1447SeqListing_ST25

Gln Leu Asp Asn Ile Ala Lys Glu His Phe Ser Tyr Gly Thr Asn
325 330 335

<210> 17
<211> 336
<212> PRT
<213> Prochlorococcus phage P-SSM4

<400> 17

Met Asn Phe Leu Lys Asp Ile Ala Lys Glu Ile Gly Asn Asp Tyr Ala
1 5 10 15

Ser Leu Val Ser Glu Gly Val Ser Ala Gly Asp Thr Ala Gly Phe Ile
20 25 30

Asp Thr Gly Ser Tyr Ile Phe Asn Ala Leu Leu Ser Gly Ser Ile Tyr
35 40 45

Gly Gly Ile Pro Asn Asn Lys Ile Thr Ala Ile Ala Gly Glu Thr Ser
50 55 60

Thr Gly Lys Thr Phe Phe Cys Leu Gly Met Val Gln His Phe Leu Glu
65 70 75 80

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

Ser Lys Gln Met Ile Glu Asp Arg Gly Ile Asp Ser Asn Arg Met Leu
100 105 110

Leu Val Pro Val Thr Thr Val Gln Glu Phe Arg Leu Gln Ala Ile Lys
115 120 125

Ile Leu Asp Lys Tyr Asn Glu Gln Thr Ala Glu Glu Arg Lys Pro Leu
130 135 140

1447SeqListing_ST25

Met Phe Val Leu Asp Ser Leu Gly Met Leu Ser Thr Ser Lys Glu Val
145 150 155 160

Glu Asp Ser Glu Ala Gly Lys Glu Thr Arg Asp Met Thr Arg Ala Gln
165 170 175

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

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

Tyr Ile Pro Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ala
210 215 220

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

Glu Val Val Gly Asn Ile Ile Lys Cys Lys Thr Ala Lys Ser Arg Leu
245 250 255

Thr Lys Glu Asn Ser Asp Val Glu Thr Arg Leu Tyr Tyr Asp Arg Gly
260 265 270

Leu Asp Arg Tyr Tyr Gly Leu Leu Glu Leu Gly Glu Lys His Gly Val
275 280 285

Phe Ser Arg Lys Gly Asn Arg Val Val Val Gly Asp Ser Ser Val Tyr
290 295 300

Pro Ser Ala Ile Leu Ala Asp Pro Asp Lys Tyr Phe Thr Glu Glu Leu
305 310 315 320

Met Glu Lys Leu Asp Glu Ala Ala Ala Lys Glu Phe Arg Tyr Gly Asn
325 330 335

1447SeqListing_ST25

<210> 18
 <211> 343
 <212> PRT
 <213> Synechococcus phage S-PM2

<400> 18

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

Ala Phe Ala Ser Glu Gly Val Ala Ala Gly Asp Val Glu Ser Phe Val
 20 25 30

Asp Thr Gly Ser Tyr Ile Phe Asn Ala Leu Val Ser Gly Ser Ile Phe
 35 40 45

Gly Gly Ile Pro Ser Asn Lys Ile Thr Ala Leu Ala Gly Glu Ser Gly
 50 55 60

Thr Gly Lys Thr Phe Phe Cys Leu Ser Val Val Arg Asn Phe Leu Asn
 65 70 75 80

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

Ser Lys Gln Met Ile Glu Ser Arg Gly Ile Asp Ser Thr Arg Met Ile
 100 105 110

Ile Phe Pro Val Asp Thr Ile Glu Asp Phe Arg Thr Gln Ala Val Arg
 115 120 125

Ile Ile Asp Lys Tyr Met Glu Gln Asn Lys Ser Glu Arg Lys Pro Leu
 130 135 140

Met Phe Val Leu Asp Ser Leu Gly Met Leu Ala Thr Lys Lys Glu Val
 145 150 155 160

Glu Asp Ala Ser Asn Asp Lys Gln Val Arg Asp Met Thr Lys Ala Gln

1447SeqListing_ST25

165

170

175

Ile Val Lys Ser Ala Phe Arg Ile Leu Thr Leu Lys Met Gly Lys Ala
180 185 190

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

Tyr Val Pro Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ser
210 215 220

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

Asp Leu Val Gly Asn Ile Ile Lys Cys Glu Ala Lys Lys Ser Arg Leu
245 250 255

Thr Arg Glu Gly Ser Lys Val Glu Thr Arg Leu Phe Phe Asp Gln Arg
260 265 270

Gly Leu Glu Arg Tyr Tyr Gly Met Leu Glu Leu Gly Glu Arg Ala Gly
275 280 285

Leu Trp Lys Asn Thr Ala Gly Arg Tyr Glu Ile Asn Gly Lys Lys Val
290 295 300

Tyr Gly Lys Gln Ile Leu Ala Asn Pro Asp Glu Phe Phe Thr Glu Glu
305 310 315 320

Ile Leu Gln Glu Leu Asp Lys Gln Ala Gln Arg Glu Phe Leu Tyr Gly
325 330 335

Ala Ser Asp Asp Gly Glu Asp
340

<210> 19

1447SeqListing_ST25

<211> 393

<212> PRT

<213> Enterobacteria phage RB32

<400> 19

Met Ser Ile Ala Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser
1 5 10 15

Lys Met Thr Ala Glu Leu Thr Thr Ser Lys Phe Phe Asn Glu Lys Asp
20 25 30

Val Ile Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala
35 40 45

Ile Asp Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser
50 55 60

Lys His Phe Lys Ser Asn Met Ser Leu Thr Met Val Ala Ala Tyr Leu
65 70 75 80

Asn Lys Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly
85 90 95

Ile Thr Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val
100 105 110

Ile His Thr Pro Ile Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val
115 120 125

Asn Gln Leu Glu Ala Ile Glu Arg Gly Glu Lys Val Ile Val Phe Ile
130 135 140

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

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

1447SeqListing_ST25

Leu Phe Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys
180 185 190

Val Ala Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr
195 200 205

Val Met Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe
210 215 220

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

Gln Phe Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser
245 250 255

Lys Phe Phe Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser
260 265 270

Gly Leu Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys
275 280 285

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

Ile Arg Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr
305 310 315 320

Phe Trp Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys
325 330 335

Arg Ala Tyr Gln Leu Gly Ala Ile Asp Ser Asn Glu Ile Val Glu Ala
340 345 350

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

1447SeqListing_ST25

Glu Ser Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln
 370 375 380

Leu Ser Asp Met Glu Glu Phe Asn Glu
 385 390

<210> 20
 <211> 366
 <212> PRT
 <213> Vibrio phage nt-1

<400> 20

Met Ser Asp Leu Leu Lys Ser Leu Lys Lys Ser Ser Thr Ser Gly Tyr
 1 5 10 15

Ala His Val Leu Ser Glu Ser Gln Phe Met Phe Glu Lys Asp His Thr
 20 25 30

Arg Thr Tyr Val Pro Ala Ile Asn Ile Ala Phe Ser Gly Glu Val Asp
 35 40 45

Gly Gly Leu Thr Ser Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His
 50 55 60

Phe Lys Ser Asn Leu Gly Leu Val Gly Val Ala Ala Tyr Leu Lys Lys
 65 70 75 80

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

Pro Ser Tyr Leu Lys Ser Gln Gly Val Asp Pro Glu Arg Val Leu His
 100 105 110

Ile Gln Cys Glu Ser Val Glu Arg Met Lys Phe Glu Met Ala Asn Gln
 115 120 125

1447SeqListing_ST25

Leu Lys Asp Leu Ala Glu Arg Lys Arg Ala Lys Lys Ala Gly Glu Glu
130 135 140

Pro Asp Arg Val Val Phe Phe Ile Asp Ser Val Gly Asn Val Ala Ser
145 150 155 160

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

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

Phe Thr Met Leu Asp Ile Pro Cys Ile Ala Ile Asn His Thr Tyr Gln
195 200 205

Thr Gln Glu Met Tyr Ser Lys Thr Val Met Ser Gly Gly Thr Gly Ile
210 215 220

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

Asp Gly Lys Glu Ile Ile Gly Tyr His Phe Ile Met Asn Ile Glu Lys
245 250 255

Ser Arg Phe Val Lys Glu Lys Met Lys Val Pro Leu Thr Val Thr Tyr
260 265 270

Glu His Gly Ile Asp Gln Phe Ser Gly Leu Leu Asp Ile Ala Leu Gln
275 280 285

Thr Gly His Val Val Lys Pro Ser Asn Gly Trp Tyr Gln Arg Ala Phe
290 295 300

Ile Asp Glu Glu Thr Gly Glu Ile Glu Ile Glu Glu Lys Lys Tyr Arg
305 310 315 320

1447SeqListing_ST25

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

Pro Thr Phe Lys Thr Gly Val Lys Arg Leu Tyr Cys Leu Gly Gln Leu
340 345 350

Asp Glu Ser Glu Leu Leu Asp Glu Val Asp Ser Leu Phe Asp
355 360 365

<210> 21

<211> 381

<212> PRT

<213> Enterobacteria phage RB16

<400> 21

Met Ser Asn Lys Ala Leu Leu Lys Lys Leu Ile Lys Asn Ser Asn Ser
1 5 10 15

Gln Ser Ala Ser Ile Leu Ser Glu Ser Asp Val Phe Asn Asn Ile Thr
20 25 30

Lys Thr Arg Thr Arg Val Pro Ile Leu Asn Leu Val Leu Ser Gly Ala
35 40 45

Phe Asp Gly Gly Leu Thr Ser Gly Leu Thr Leu Ile Ala Gly Pro Ser
50 55 60

Lys His Phe Lys Ser Asn Leu Gly Leu Val Ala Val Ala Ala Tyr Leu
65 70 75 80

Lys Ala Asn Glu Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Lys Gly
85 90 95

Val Thr Lys Ser Tyr Leu Lys Ser Met Gly Val Asp Pro Asp Arg Val
100 105 110

1447SeqListing_ST25

Val Tyr Thr Arg Ile Thr Thr Val Glu Gln Leu Arg Asn Asp Val Val
115 120 125

Ser Gln Leu Asp Ala Leu Glu Arg Gly Asp Lys Val Ile Ile Phe Val
130 135 140

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

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

Met Phe Arg Met Val Thr Pro Tyr Leu Ala Asp Ile Asp Ile Pro Met
180 185 190

Val Cys Ile Cys His Thr Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys
195 200 205

Val Ile Ser Gly Gly Thr Gly Leu Met Tyr Ser Ala Asp Thr Ala Ile
210 215 220

Ile Leu Gly Lys Gln Gln Val Lys Glu Gly Thr Glu Val Val Gly Tyr
225 230 235 240

Asp Phe Ile Met Asn Val Glu Lys Ser Arg Phe Val Lys Glu Lys Ser
245 250 255

Lys Phe Pro Leu His Val Thr Tyr Glu Gly Gly Ile Ser Met Phe Ser
260 265 270

Gly Leu Leu Asp Leu Ala Met Glu Met Asn Phe Val Gln Thr Pro Thr
275 280 285

Lys Gly Trp Arg Gly Arg Ala Phe Leu Asn Thr Glu Thr Gly Glu Leu
290 295 300

1447SeqListing_ST25

Glu Leu Glu Glu Lys Lys Trp Arg Glu Ala Glu Thr Asn Cys Ile Glu
305 310 315 320

Phe Trp Lys Pro Leu Phe Lys His Gln Pro Phe Ile Asp Ala Ile Gln
325 330 335

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

Glu Asp Leu Tyr Ser Asp Asp Val Val Glu Ser Asn Lys Val Asp Phe
355 360 365

Asp Asp Asp Ile Pro Asp Asp Val Asp Leu Met Glu Glu
370 375 380

<210> 22
<211> 391
<212> PRT
<213> Enterobacteria phage T4

<400> 22

Met Ser Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser Lys Leu
1 5 10 15

Thr Ala Glu Leu Thr Ala Ser Lys Phe Phe Asn Glu Lys Asp Val Val
20 25 30

Arg Thr Lys Ile Pro Met Met Asn Ile Ala Leu Ser Gly Glu Ile Thr
35 40 45

Gly Gly Met Gln Ser Gly Leu Leu Ile Leu Ala Gly Pro Ser Lys Ser
50 55 60

Phe Lys Ser Asn Phe Gly Leu Thr Met Val Ser Ser Tyr Met Arg Gln
65 70 75 80

Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly Ile Thr

1447SeqListing_ST25

85

90

95

Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val Ile His
 100 105 110

Thr Pro Val Gln Ser Leu Glu Gln Leu Arg Ile Asp Met Val Asn Gln
 115 120 125

Leu Asp Ala Ile Glu Arg Gly Glu Lys Val Val Val Phe Ile Asp Ser
 130 135 140

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

Lys Val Val Ser Asp Met Thr Arg Ala Lys Thr Met Lys Ser Leu Phe
 165 170 175

Arg Ile Val Thr Pro Tyr Phe Ser Thr Lys Asn Ile Pro Cys Ile Ala
 180 185 190

Ile Asn His Thr Tyr Glu Thr Gln Glu Met Phe Ser Lys Thr Val Met
 195 200 205

Gly Gly Gly Thr Gly Pro Met Tyr Ser Ala Asp Thr Val Phe Ile Ile
 210 215 220

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

Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser Lys Phe
 245 250 255

Lys Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser Gly Leu
 260 265 270

Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys Asn Gly

1447SeqListing_ST25

275

280

285

Trp Tyr Ala Arg Glu Phe Leu Asp Glu Glu Thr Gly Glu Met Ile Arg
290 295 300

Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr Phe Trp
305 310 315 320

Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys Arg Ala
325 330 335

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

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

Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln Leu Ser
370 375 380

Asp Met Glu Glu Phe Asn Glu
385 390

<210> 23

<211> 393

<212> PRT

<213> Enterobacteria phage T6

<400> 23

Met Ser Ile Ala Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser
1 5 10 15

Lys Met Thr Ala Glu Leu Thr Thr Ser Lys Phe Phe Asn Glu Lys Asp
20 25 30

Val Ile Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala
35 40 45

1447SeqListing_ST25

Ile Asp Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser
50 55 60

Lys His Phe Lys Ser Asn Met Ser Leu Thr Met Val Ala Ala Tyr Leu
65 70 75 80

Asn Lys Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly
85 90 95

Ile Thr Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val
100 105 110

Ile His Thr Pro Ile Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val
115 120 125

Asn Gln Leu Glu Ala Ile Glu Arg Gly Glu Lys Val Ile Val Phe Ile
130 135 140

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

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

Leu Phe Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys
180 185 190

Val Ala Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr
195 200 205

Val Met Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe
210 215 220

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

1447SeqListing_ST25

Gln Phe Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser
245 250 255

Lys Phe Lys Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser
260 265 270

Gly Leu Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys
275 280 285

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

Ile Arg Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr
305 310 315 320

Phe Trp Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys
325 330 335

Arg Ala Tyr Gln Leu Gly Ala Ile Asp Ser Asn Glu Ile Val Glu Ala
340 345 350

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

Glu Ser Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln
370 375 380

Leu Ser Asp Met Glu Glu Phe Asn Glu
385 390

<210> 24

<211> 387

<212> PRT

<213> Acinetobacter phage 133

<400> 24

1447SeqListing_ST25

Met Ser Ser Leu Lys Glu Arg Leu Ile Lys Ala Ser Thr Ser Lys Met
1 5 10 15

Thr Ala Glu Leu Thr Lys Ser Lys Phe Phe Asn Asp Lys Thr Val Val
20 25 30

Arg Thr Arg Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala Leu Asn
35 40 45

Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser Lys His
50 55 60

Phe Lys Ser Asn Met Gly Leu Thr Met Val Ala Ala Tyr Met Lys Ala
65 70 75 80

Phe Pro Asp Ala Val Cys Met Phe Tyr Asp Ser Glu Phe Gly Ile Thr
85 90 95

Pro Ala Tyr Leu Lys Ala Met Gly Val Asp Pro Asp Arg Val Ile His
100 105 110

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

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

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

Lys Thr Thr Ala Asp Met Thr Arg Ala Lys Ala Leu Lys Ser Leu Phe
165 170 175

Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asp Ile Pro Cys Val Ala
180 185 190

1447SeqListing_ST25

Val Asn His Thr Leu Gln Thr Leu Glu Met Phe Ser Lys Glu Val Met
195 200 205

Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe Phe Ile
210 215 220

Gly Lys Arg Gln Val Lys Asp Gly Thr Glu Leu Ala Gly Tyr Glu Phe
225 230 235 240

Ile Leu Lys Ala Glu Lys Ser Arg Met Val Lys Glu Lys Ser Val Phe
245 250 255

Lys Ile Thr Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser Gly Leu
260 265 270

Leu Glu Met Ala Thr Asp Leu Gly Phe Val Val Lys Pro Lys Val Gly
275 280 285

Trp Tyr Lys Arg Ala Met Met Val Asp Gly Val Met Gln His Glu Glu
290 295 300

Lys Ser Trp Arg Ala Lys Asp Thr Asp Ser Ile Asp Phe Trp Gly Pro
305 310 315 320

Leu Phe Lys His Asp Glu Phe Arg Lys Ala Ile Glu Thr Arg Tyr Gln
325 330 335

Leu Gly Ser Ile Glu Ser Asp Ala Glu Val Asp Ala Glu Val Asp Ala
340 345 350

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

Pro Ala Glu Ser Ala Ala Asp Lys Glu Gln Gln Leu Glu Asp Phe Val
370 375 380

1447SeqListing_ST25

Asp Glu Asp
385

<210> 25
<211> 390
<212> PRT
<213> Enterobacteria phage RB69

<400> 25

Met Ser Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser Lys Met
1 5 10 15

Thr Ala Asp Leu Thr Lys Ser Lys Leu Phe Asn Asn Arg Asp Glu Val
20 25 30

Pro Thr Arg Ile Pro Met Leu Asn Ile Ala Leu Gly Gly Ala Leu Asn
35 40 45

Ala Gly Leu Gln Ser Gly Leu Thr Ile Phe Ala Ala Pro Ser Lys His
50 55 60

Phe Lys Thr Leu Phe Gly Leu Thr Met Val Ala Ala Tyr Met Lys Lys
65 70 75 80

Tyr Lys Asp Ala Ile Cys Leu Phe Tyr Asp Ser Glu Phe Gly Ala Ser
85 90 95

Glu Ser Tyr Phe Arg Ser Met Gly Val Asp Leu Asp Arg Val Val His
100 105 110

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

Leu Asp Ala Ile Glu Arg Gly Asp Lys Val Ile Ile Phe Ile Asp Ser
130 135 140

1447SeqListing_ST25

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

Lys Val Val Gly Asp Met Ser Arg Ala Lys Ala Leu Lys Ser Leu Phe
 165 170 175

Arg Ile Val Thr Pro Tyr Leu Thr Ile Lys Asp Ile Pro Cys Val Ala
 180 185 190

Ile Asn His Thr Ala Met Glu Ile Gly Gly Leu Tyr Pro Lys Glu Ile
 195 200 205

Met Gly Gly Gly Thr Gly Ile Leu Tyr Ser Ala Asn Thr Val Phe Phe
 210 215 220

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

Phe Thr Leu Lys Ala Glu Lys Ser Arg Thr Val Lys Glu Lys Ser Thr
 245 250 255

Phe Lys Ile Thr Val Asn Phe Asp Gly Gly Ile Asp Pro Phe Ser Gly
 260 265 270

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

Gly Trp Tyr Ala Arg Glu Phe Leu Asp Glu Glu Thr Gly Glu Met Ile
 290 295 300

Arg Glu Glu Lys Ser Trp Arg Ala Lys Ala Thr Asp Cys Val Glu Phe
 305 310 315 320

Trp Gly Pro Leu Phe Lys His Lys Pro Phe Arg Asp Ala Ile Glu Thr
 325 330 335

1447SeqListing_ST25

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

Val Asn Asp Leu Ile Asn Cys Lys Ala Thr Thr Lys Val Pro Val Lys
355 360 365

Thr Ser Asp Ala Pro Ser Ala Ala Asp Ile Glu Asn Asp Leu Asp Glu
370 375 380

Met Glu Asp Phe Asp Glu
385 390

<210> 26

<211> 411

<212> PRT

<213> Aeromonas phage Aeh1

<400> 26

Met Ala Lys Gly Ile Lys Thr Ala Lys Thr Gly Asn Leu Gly Ser Leu
1 5 10 15

Met Ser Lys Leu Ala Gly Thr Ser Ser Asn Lys Met Ser Ser Val Leu
20 25 30

Ala Asp Ser Lys Phe Phe Asn Asp Lys Asp Cys Val Arg Thr Arg Val
35 40 45

Pro Leu Leu Asn Leu Ala Met Ser Gly Glu Leu Asp Gly Gly Leu Thr
50 55 60

Pro Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His Phe Lys Ser Asn
65 70 75 80

Leu Ser Leu Val Phe Val Ala Ala Tyr Leu Arg Lys Tyr Pro Asp Ala
85 90 95

Val Cys Ile Phe Phe Asp Asn Glu Phe Gly Ser Thr Pro Gly Tyr Phe

1447SeqListing_ST25

100

105

110

Glu Ser Gln Gly Val Asp Ile Ser Arg Val Ile His Cys Pro Phe Lys
 115 120 125

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

Glu Arg Gly Asp Arg Val Ile Val Phe Val Asp Ser Ile Gly Asn Ala
 145 150 155 160

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

Asp Met Thr Arg Ala Lys Gln Ile Lys Ser Leu Thr Arg Met Met Thr
 180 185 190

Pro Tyr Leu Thr Val Asn Asp Ile Pro Ala Ile Met Val Ala His Thr
 195 200 205

Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys Val Val Ser Gly Gly Thr
 210 215 220

Gly Ile Thr Tyr Ser Ser Asp Thr Val Ile Ile Ile Gly Arg Gln Gln
 225 230 235 240

Glu Lys Asp Gly Lys Glu Leu Leu Gly Tyr Asn Phe Val Leu Asn Met
 245 250 255

Glu Lys Ser Arg Phe Val Lys Glu Gln Ser Lys Leu Lys Leu Glu Val
 260 265 270

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

Leu Glu Val Gly Phe Val Val Lys Pro Ser Asn Gly Trp Phe Ser Arg

1447SeqListing_ST25

290

295

300

Ala Phe Leu Asp Glu Glu Thr Gly Glu Leu Val Glu Glu Asp Arg Lys
 305 310 315 320

Trp Arg Arg Ala Asp Thr Asn Cys Leu Glu Phe Trp Lys Pro Met Phe
 325 330 335

Ala His Gln Pro Phe Lys Thr Ala Cys Ser Asp Met Phe Lys Leu Lys
 340 345 350

Ser Val Ala Val Lys Asp Glu Val Phe Asp Glu Val Asp Glu Leu Phe
 355 360 365

Ser Gly Glu Ala Glu Met Pro Val Asn Met Gly Arg Lys Leu Asp Thr
 370 375 380

Ala Asp Gln Glu Glu Ile Asp Gln Leu Glu Glu Val Asp Val Glu Gly
 385 390 395 400

Ser Asp Ser Asp Glu Leu Phe Ala Asn Leu Asp
 405 410

<210> 27

<211> 368

<212> PRT

<213> Aeromonas phage 65

<400> 27

Met Ala Lys Lys Ala Lys Val Val Asn Ser Gly Asp Leu Leu Glu Arg
 1 5 10 15

Leu Asn Gly Thr Ser Ser Asn Lys Met Ser Ala Met Leu Ala Glu Ser
 20 25 30

Ile Phe Phe Asn Glu Lys Asp Thr Ile Arg Thr Arg Val Pro Ile Ile
 35 40 45

1447SeqListing_ST25

Asn Leu Met Met Ser Gly Arg Leu Asp Gly Gly Ile Thr Pro Gly Leu
50 55 60

Thr Cys Ile Ala Gly Pro Ser Lys His Phe Lys Ser Asn Leu Ser Leu
65 70 75 80

Val Met Val Ser Ala Tyr Leu Arg Lys Tyr Pro Lys Ala Val Cys Leu
85 90 95

Phe Phe Asp Asn Glu Phe Gly Ser Thr Pro Asp Tyr Phe Thr Ser Gln
100 105 110

Gly Val Asp Ile Ser Arg Val Val His Cys Pro Phe Ile Asp Val Glu
115 120 125

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

Asp Lys Val Ile Ile Tyr Ile Asp Ser Ile Gly Asn Val Ala Ser Lys
145 150 155 160

Lys Glu Leu Gln Asp Ala Lys Asp Glu Lys Ser Ala Gln Asp Met Thr
165 170 175

Arg Ala Lys Gln Ile Lys Ser Leu Phe Arg Met Val Thr Pro Tyr Leu
180 185 190

Thr Val Leu Asp Ile Pro Cys Ile Ala Val Asn His Thr Tyr Glu Thr
195 200 205

Gln Glu Met Phe Ser Lys Thr Val Met Ser Gly Gly Thr Gly Pro Met
210 215 220

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

1447SeqListing_ST25

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

Arg Ala Ile Lys Glu Lys Ser Lys Leu Lys Leu Met Val Ser Phe Glu
260 265 270

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

Gly Phe Val Thr Lys Pro Gln Asn Ala Arg Tyr Gln Arg Asn Phe Leu
290 295 300

Asp Leu Glu Pro Gly Glu Met Val Ile Pro Glu Asp Glu Lys Lys Trp
305 310 315 320

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

His Lys Pro Phe Met Asp Ala Val Ser Asn Ala Tyr Lys Leu Lys Ala
340 345 350

Val Glu Val Ser Gln Glu Val Phe Asp Glu Val Asp Gln Leu Phe Gly
355 360 365

<210> 28
<211> 366
<212> PRT
<213> Vibrio phage KVP40

<400> 28

Met Ser Asp Leu Met Lys Ser Leu Lys Lys Ser Ser Thr Ser Gly Tyr
1 5 10 15

Ala Gln Val Leu Ser Glu Ser Gln Phe Met Phe Asp Lys Asp His Thr
20 25 30

1447SeqListing_ST25

Arg Thr Tyr Val Pro Ala Ile Asn Ile Ala Phe Ser Gly Glu Val Asp
35 40 45

Gly Gly Leu Thr Ser Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His
50 55 60

Phe Lys Ser Asn Leu Gly Leu Val Gly Val Ala Ala Tyr Leu Lys Lys
65 70 75 80

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

Pro Ser Tyr Leu Arg Ser Gln Gly Val Asp Pro Asp Arg Val Leu His
100 105 110

Ile Gln Cys Glu Ser Val Glu Arg Met Lys Phe Glu Met Ala Asn Gln
115 120 125

Leu Lys Asp Leu Ala Glu Arg Lys Arg Ala Lys Lys Ala Gly Glu Glu
130 135 140

Pro Asp Arg Val Ile Phe Phe Ile Asp Ser Val Gly Asn Val Ala Ser
145 150 155 160

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

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

Phe Thr Met Leu Asp Ile Pro Cys Ile Ala Ile Asn His Thr Tyr Gln
195 200 205

Thr Gln Glu Ile Tyr Ser Lys Thr Val Met Ser Gly Gly Thr Gly Ile
210 215 220

1447SeqListing_ST25

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

Asp Gly Lys Asp Ile Ile Gly Tyr His Phe Ile Met Asn Ile Glu Lys
245 250 255

Ser Arg Phe Val Lys Glu Lys Met Lys Val Lys Leu Thr Val Thr Tyr
260 265 270

Glu Asn Gly Ile Asp Pro Phe Ser Gly Leu Leu Asp Ile Ala Leu Gln
275 280 285

Thr Gly His Val Val Lys Pro Ser Asn Gly Trp Tyr Gln Arg Ala Thr
290 295 300

Val Asp Glu Glu Thr Gly Glu Met Ile Val Glu Glu Lys Lys Tyr Arg
305 310 315 320

Ala Lys Glu Thr Gln Thr Ile Ser Phe Trp Lys Asp Ile Ile Asn Ser
325 330 335

Pro Thr Phe Lys Glu Gly Val Lys Arg Ile Tyr Cys Leu Gly Gln Leu
340 345 350

Asp Glu Ser Glu Leu Phe Gly Glu Val Asp Ser Leu Phe Asp
355 360 365

<210> 29
<211> 386
<212> PRT
<213> Enterobacteria phage RB43

<400> 29

Met Ser Asn Lys Ala Leu Leu Lys Lys Leu Ile Lys Asn Ser Asn Ser
1 5 10 15

1447SeqListing_ST25

Gln Ser Ala Ala Ile Leu Ser Glu Ser Asp Val Phe Asn Asn Ile Thr
 20 25 30

Lys Thr Arg Thr Arg Val Pro Ile Leu Asn Leu Ala Leu Ser Gly Ala
 35 40 45

Phe Asp Gly Gly Leu Thr Ser Gly Leu Thr Leu Phe Ala Gly Pro Ser
 50 55 60

Lys His Phe Lys Ser Asn Leu Gly Leu Val Thr Val Ser Ala Tyr Leu
 65 70 75 80

Lys Ala Asn Glu Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Lys Gly
 85 90 95

Val Thr Lys Ser Tyr Leu Lys Ser Met Gly Val Asp Pro Asp Arg Val
 100 105 110

Val Tyr Thr Arg Ile Thr Thr Val Glu Gln Leu Arg Asn Asp Val Val
 115 120 125

Ser Gln Leu Asp Ala Leu Glu Arg Gly Asp Lys Val Ile Ile Phe Val
 130 135 140

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

Ser Asp Asn Asp Lys Gln Asp Met Thr Arg Ala Lys Ala Leu Lys Gly
 165 170 175

Met Phe Arg Met Val Thr Pro Tyr Leu Ala Asp Leu Asp Ile Pro Met
 180 185 190

Val Cys Ile Cys His Thr Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys
 195 200 205

1447SeqListing_ST25

Val Ile Ser Gly Gly Thr Gly Leu Met Tyr Ser Ala Asp Thr Ala Ile
210 215 220

Ile Leu Gly Lys Gln Gln Val Lys Glu Gly Thr Glu Val Val Gly Tyr
225 230 235 240

Asp Phe Ile Met Asn Ile Glu Lys Ser Arg Phe Val Lys Glu Lys Ser
245 250 255

Lys Phe Lys Leu His Val Thr Tyr Glu Gly Gly Ile Ser Met Tyr Ser
260 265 270

Gly Leu Leu Asp Leu Ala Met Glu Met Asn Phe Val Gln Thr Pro Thr
275 280 285

Lys Gly Trp Arg Gly Arg Ala Phe Leu Asn Thr Glu Thr Gly Glu Leu
290 295 300

Glu Leu Glu Glu Lys Lys Trp Arg Glu Ser Glu Thr Asn Ser Ile Glu
305 310 315 320

Phe Trp Arg Pro Leu Phe Thr His Gln Pro Phe Leu Asp Ala Ile Gln
325 330 335

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

Glu Asp Leu Tyr Ser Thr Asp Glu Pro Glu Ser Asn Lys Ile Asp Leu
355 360 365

Asp Asp Asp Ile Pro Asp Asp Ile Gly Ile Asp Gln Asp Glu Glu Pro
370 375 380

Ile Met
385

1447SeqListing_ST25

<210> 30

<211> 335

<212> PRT

<213> Prochlorococcus phage P-SSM2

<400> 30

Met Asp Phe Leu Lys Glu Ile Val Lys Glu Ile Gly Asp Glu Tyr Thr
1 5 10 15

Gln Val Ala Ala Asp Ile Gln Glu Asn Glu Arg Phe Ile Asp Thr Gly
20 25 30

Ser Tyr Ile Phe Asn Gly Leu Val Ser Gly Ser Ile Phe Gly Gly Val
35 40 45

Ser Ser Ser Arg Ile Thr Ala Ile Ala Gly Glu Ser Ser Thr Gly Lys
50 55 60

Thr Tyr Phe Ser Leu Ala Val Val Lys Asn Phe Leu Asp Asn Asn Pro
65 70 75 80

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

Leu Leu Glu Ser Arg Gly Ile Asp Met Asn Arg Leu Val Val Val Asn
100 105 110

Val Val Thr Ile Glu Glu Phe Arg Ser Lys Ala Leu Arg Ala Val Asp
115 120 125

Ile Tyr Leu Lys Thr Ser Glu Glu Glu Arg Lys Pro Cys Met Phe Val
130 135 140

Leu Asp Ser Leu Gly Met Leu Ser Thr Glu Lys Glu Ile Arg Asp Ala
145 150 155 160

Leu Asp Asp Lys Gln Val Arg Asp Met Thr Lys Ser Gln Leu Val Lys

1447SeqListing_ST25

165

170

175

Gly Ala Phe Arg Met Leu Thr Leu Lys Leu Gly Gln Ala Asn Ile Pro
 180 185 190

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

Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ala Ala Ser Thr
 210 215 220

Ile Ile Tyr Leu Ser Lys Lys Lys Glu Lys Asp Gln Lys Glu Val Ile
 225 230 235 240

Gly Asn Leu Ile Lys Ala Lys Thr His Lys Ser Arg Leu Ser Lys Glu
 245 250 255

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

Arg Tyr Tyr Gly Leu Leu Glu Leu Gly Glu Ile Gly Gly Met Trp Lys
 275 280 285

Asn Val Ala Gly Arg Tyr Glu Met Asn Gly Lys Lys Ile Tyr Ala Lys
 290 295 300

Glu Ile Leu Lys Asn Pro Thr Glu Tyr Phe Thr Asp Asp Ile Met Glu
 305 310 315 320

Gln Leu Asp Asn Ile Ala Lys Glu His Phe Ser Tyr Gly Thr Asn
 325 330 335

<210> 31

<211> 336

<212> PRT

<213> Prochlorococcus phage P-SSM4

1447SeqListing_ST25

<400> 31

Met Asn Phe Leu Lys Asp Ile Ala Lys Glu Ile Gly Asn Asp Tyr Ala
 1 5 10 15

Ser Leu Val Ser Glu Gly Val Ser Ala Gly Asp Thr Ala Gly Phe Ile
 20 25 30

Asp Thr Gly Ser Tyr Ile Phe Asn Ala Leu Leu Ser Gly Ser Ile Tyr
 35 40 45

Gly Gly Ile Pro Asn Asn Lys Ile Thr Ala Ile Ala Gly Glu Thr Ser
 50 55 60

Thr Gly Lys Thr Phe Phe Cys Leu Gly Met Val Gln His Phe Leu Glu
 65 70 75 80

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

Ser Lys Gln Met Ile Glu Asp Arg Gly Ile Asp Ser Asn Arg Met Leu
 100 105 110

Leu Val Pro Val Thr Thr Val Gln Glu Phe Arg Leu Gln Ala Ile Lys
 115 120 125

Ile Leu Asp Lys Tyr Asn Glu Gln Thr Ala Glu Glu Arg Lys Pro Leu
 130 135 140

Met Phe Val Leu Asp Ser Leu Gly Met Leu Ser Thr Ser Lys Glu Val
 145 150 155 160

Glu Asp Ser Glu Ala Gly Lys Glu Thr Arg Asp Met Thr Arg Ala Gln
 165 170 175

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

1447SeqListing_ST25

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

Tyr Ile Pro Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ala
210 215 220

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

Glu Val Val Gly Asn Ile Ile Lys Cys Lys Thr Ala Lys Ser Arg Leu
245 250 255

Thr Lys Glu Asn Ser Asp Val Lys Thr Arg Leu Tyr Tyr Asp Arg Gly
260 265 270

Leu Asp Arg Tyr Tyr Gly Leu Leu Glu Leu Gly Glu Lys His Gly Val
275 280 285

Phe Ser Arg Lys Gly Asn Arg Val Val Val Gly Asp Ser Ser Val Tyr
290 295 300

Pro Ser Ala Ile Leu Ala Asp Pro Asp Lys Tyr Phe Thr Glu Glu Leu
305 310 315 320

Met Glu Lys Leu Asp Glu Ala Ala Ala Lys Glu Phe Arg Tyr Gly Asn
325 330 335

<210> 32
<211> 343
<212> PRT
<213> Synechococcus phage S-PM2

<400> 32

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

1447SeqListing_ST25

Ala Phe Ala Ser Glu Gly Val Ala Ala Gly Asp Val Glu Ser Phe Val
20 25 30

Asp Thr Gly Ser Tyr Ile Phe Asn Ala Leu Val Ser Gly Ser Ile Phe
35 40 45

Gly Gly Ile Pro Ser Asn Lys Ile Thr Ala Leu Ala Gly Glu Ser Gly
50 55 60

Thr Gly Lys Thr Phe Phe Cys Leu Ser Val Val Arg Asn Phe Leu Asn
65 70 75 80

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

Ser Lys Gln Met Ile Glu Ser Arg Gly Ile Asp Ser Thr Arg Met Ile
100 105 110

Ile Phe Pro Val Asp Thr Ile Glu Asp Phe Arg Thr Gln Ala Val Arg
115 120 125

Ile Ile Asp Lys Tyr Met Glu Gln Asn Lys Ser Glu Arg Lys Pro Leu
130 135 140

Met Phe Val Leu Asp Ser Leu Gly Met Leu Ala Thr Lys Lys Glu Val
145 150 155 160

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

Ile Val Lys Ser Ala Phe Arg Ile Leu Thr Leu Lys Met Gly Lys Ala
180 185 190

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

1447SeqListing_ST25

Tyr Val Pro Thr Lys Glu Met Gly Gly Gly Ser Gly Leu Lys Tyr Ser
 210 215 220

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

Asp Leu Val Gly Asn Ile Ile Lys Cys Glu Ala Lys Lys Ser Arg Leu
 245 250 255

Thr Arg Glu Gly Ser Lys Val Lys Thr Arg Leu Phe Phe Asp Gln Arg
 260 265 270

Gly Leu Glu Arg Tyr Tyr Gly Met Leu Glu Leu Gly Glu Arg Ala Gly
 275 280 285

Leu Trp Lys Asn Thr Ala Gly Arg Tyr Glu Ile Asn Gly Lys Lys Val
 290 295 300

Tyr Gly Lys Gln Ile Leu Ala Asn Pro Asp Glu Phe Phe Thr Glu Glu
 305 310 315 320

Ile Leu Gln Glu Leu Asp Lys Gln Ala Gln Arg Glu Phe Leu Tyr Gly
 325 330 335

Ala Ser Asp Asp Gly Glu Asp
 340

<210> 33
 <211> 393
 <212> PRT
 <213> Enterobacteria phage RB32

<400> 33

Met Ser Ile Ala Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser
 1 5 10 15

1447SeqListing_ST25

Lys Met Thr Ala Glu Leu Thr Thr Ser Lys Phe Phe Asn Glu Lys Asp
 20 25 30

Val Ile Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala
 35 40 45

Ile Asp Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser
 50 55 60

Lys His Phe Lys Ser Asn Met Ser Leu Thr Met Val Ala Ala Tyr Leu
 65 70 75 80

Asn Lys Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly
 85 90 95

Ile Thr Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val
 100 105 110

Ile His Thr Pro Ile Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val
 115 120 125

Asn Gln Leu Glu Ala Ile Glu Arg Gly Glu Lys Val Ile Val Phe Ile
 130 135 140

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

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

Leu Phe Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys
 180 185 190

Val Ala Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr
 195 200 205

1447SeqListing_ST25

Val Met Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe
 210 215 220

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

Gln Phe Val Leu Asn Val Glu Lys Ser Arg Thr Val Lys Glu Lys Ser
 245 250 255

Lys Phe Lys Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser
 260 265 270

Gly Leu Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys
 275 280 285

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

Ile Arg Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr
 305 310 315 320

Phe Trp Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys
 325 330 335

Arg Ala Tyr Gln Leu Gly Ala Ile Asp Ser Asn Glu Ile Val Glu Ala
 340 345 350

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

Glu Ser Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln
 370 375 380

Leu Ser Asp Met Glu Glu Phe Asn Glu
 385 390

1447SeqListing_ST25

<210> 34
 <211> 366
 <212> PRT
 <213> Vibrio phage nt-1

<400> 34

Met Ser Asp Leu Leu Lys Ser Leu Lys Lys Ser Ser Thr Ser Gly Tyr
 1 5 10 15

Ala His Val Leu Ser Glu Ser Gln Phe Met Phe Glu Lys Asp His Thr
 20 25 30

Arg Thr Tyr Val Pro Ala Ile Asn Ile Ala Phe Ser Gly Glu Val Asp
 35 40 45

Gly Gly Leu Thr Ser Gly Leu Thr Val Leu Ala Gly Pro Ser Lys His
 50 55 60

Phe Lys Ser Asn Leu Gly Leu Val Gly Val Ala Ala Tyr Leu Lys Lys
 65 70 75 80

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

Pro Ser Tyr Leu Lys Ser Gln Gly Val Asp Pro Glu Arg Val Leu His
 100 105 110

Ile Gln Cys Glu Ser Val Glu Arg Met Lys Phe Glu Met Ala Asn Gln
 115 120 125

Leu Lys Asp Leu Ala Glu Arg Lys Arg Ala Lys Lys Ala Gly Glu Glu
 130 135 140

Pro Asp Arg Val Val Phe Phe Ile Asp Ser Val Gly Asn Val Ala Ser
 145 150 155 160

Ala Lys Glu Ile Asp Asp Ala Gln Asn Glu Lys Ser Val Ala Asp Met

1447SeqListing_ST25

165

170

175

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

Phe Thr Met Leu Asp Ile Pro Cys Ile Ala Ile Asn His Thr Tyr Gln
 195 200 205

Thr Gln Glu Met Tyr Ser Lys Thr Val Met Ser Gly Gly Thr Gly Ile
 210 215 220

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

Asp Gly Lys Glu Ile Ile Gly Tyr His Phe Ile Met Asn Ile Glu Lys
 245 250 255

Ser Arg Phe Val Lys Glu Lys Met Lys Val Lys Leu Thr Val Thr Tyr
 260 265 270

Glu His Gly Ile Asp Gln Phe Ser Gly Leu Leu Asp Ile Ala Leu Gln
 275 280 285

Thr Gly His Val Val Lys Pro Ser Asn Gly Trp Tyr Gln Arg Ala Phe
 290 295 300

Ile Asp Glu Glu Thr Gly Glu Ile Glu Ile Glu Glu Lys Lys Tyr Arg
 305 310 315 320

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

Pro Thr Phe Lys Thr Gly Val Lys Arg Leu Tyr Cys Leu Gly Gln Leu
 340 345 350

Asp Glu Ser Glu Leu Leu Asp Glu Val Asp Ser Leu Phe Asp

1447SeqListing_ST25

355

360

365

<210> 35
 <211> 381
 <212> PRT
 <213> Enterobacteria phage RB16
 <400> 35

Met Ser Asn Lys Ala Leu Leu Lys Lys Leu Ile Lys Asn Ser Asn Ser
 1 5 10 15

Gln Ser Ala Ser Ile Leu Ser Glu Ser Asp Val Phe Asn Asn Ile Thr
 20 25 30

Lys Thr Arg Thr Arg Val Pro Ile Leu Asn Leu Val Leu Ser Gly Ala
 35 40 45

Phe Asp Gly Gly Leu Thr Ser Gly Leu Thr Leu Ile Ala Gly Pro Ser
 50 55 60

Lys His Phe Lys Ser Asn Leu Gly Leu Val Ala Val Ala Ala Tyr Leu
 65 70 75 80

Lys Ala Asn Glu Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Lys Gly
 85 90 95

Val Thr Lys Ser Tyr Leu Lys Ser Met Gly Val Asp Pro Asp Arg Val
 100 105 110

Val Tyr Thr Arg Ile Thr Thr Val Glu Gln Leu Arg Asn Asp Val Val
 115 120 125

Ser Gln Leu Asp Ala Leu Glu Arg Gly Asp Lys Val Ile Ile Phe Val
 130 135 140

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

1447SeqListing_ST25

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

Met Phe Arg Met Val Thr Pro Tyr Leu Ala Asp Ile Asp Ile Pro Met
180 185 190

Val Cys Ile Cys His Thr Tyr Asp Thr Gln Glu Met Tyr Ser Lys Lys
195 200 205

Val Ile Ser Gly Gly Thr Gly Leu Met Tyr Ser Ala Asp Thr Ala Ile
210 215 220

Ile Leu Gly Lys Gln Gln Val Lys Glu Gly Thr Glu Val Val Gly Tyr
225 230 235 240

Asp Phe Ile Met Asn Val Glu Lys Ser Arg Phe Val Lys Glu Lys Ser
245 250 255

Lys Phe Lys Leu His Val Thr Tyr Glu Gly Gly Ile Ser Met Phe Ser
260 265 270

Gly Leu Leu Asp Leu Ala Met Glu Met Asn Phe Val Gln Thr Pro Thr
275 280 285

Lys Gly Trp Arg Gly Arg Ala Phe Leu Asn Thr Glu Thr Gly Glu Leu
290 295 300

Glu Leu Glu Glu Lys Lys Trp Arg Glu Ala Glu Thr Asn Cys Ile Glu
305 310 315 320

Phe Trp Lys Pro Leu Phe Lys His Gln Pro Phe Ile Asp Ala Ile Gln
325 330 335

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

1447SeqListing_ST25

Glu Asp Leu Tyr Ser Asp Asp Val Val Glu Ser Asn Lys Val Asp Phe
355 360 365

Asp Asp Asp Ile Pro Asp Asp Val Asp Leu Met Glu Glu
370 375 380

<210> 36

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Semi Conserved Domain

<400> 36

Phe Arg Asp Ala Ile Lys Arg Ala Tyr
1 5