

<110> CJ CHEILJEDANG CORPORATION

<120> MICROORGANISM FOR PRODUCING A MYCOSPORINE-LIKE AMINO ACID
AND METHOD FOR PRODUCING A MYCOSPORINE-LIKE AMINO ACID USING THE
SAME

<130> OPA18235-PCT

<150> KR10-2017-0103795

<151> 2017-08-16

<160> 104

<170> KopatentIn 2.0

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<211> 6461

<212> DNA

<213> *Anabaena variabilis* ATCC29413

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 Gly Arg Cys Leu Ala Ile Val Asp Ala Asn Val Ser Arg Leu Tyr Gly
 50 55 60
 Asn Gln Ile Gln Ala Tyr Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu
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 Phe Pro Ile Thr Ile Thr Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu
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 Arg Val Ile Asp Val Phe Ala Asp Phe Lys Leu Val Arg Lys Glu Pro
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Val Leu Val Val Gly Gly Gly Leu Ile Thr Asp Val Val Gly Phe Ala
115 120 125

Cys Ser Thr Tyr Arg Arg Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr
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His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Ser Arg Lys
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Val Phe Leu Asp Phe Ser Leu Leu Arg Thr Leu Pro Thr Asp Gln Val
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Arg Asn Gly Met Ala Glu Leu Val Lys Ile Ala Val Val Ala His Gln
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Glu Val Phe Glu Leu Leu Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr
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His Phe Gly Asn Ile Asp Ala Thr Pro Glu Ile Lys Glu Ile Ala His
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Arg Leu Thr Tyr Lys Ala Ile His Lys Met Leu Glu Leu Glu Val Pro
245 250 255

Asn Leu His Glu Leu Asp Leu Asp Arg Val Ile Ala Tyr Gly His Thr
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Trp Ser Pro Thr Leu Glu Leu Ala Pro Arg Leu Pro Met Phe His Gly
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His Ala Val Asn Val Asp Met Ala Phe Ser Ala Thr Ile Ala Ala Arg
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Arg Gly Tyr Ile Thr Ile Ala Glu Arg Asp Arg Ile Leu Gly Leu Met
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Ser Arg Val Gly Leu Ser Leu Asp His Pro Met Leu Asp Ile Asp Ile
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Gln Pro Thr Ala Arg Pro Val Thr Pro Leu Gly Ile Leu Thr Lys Gln		
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Glu Leu Ile Ala Asn Ile His Gln Ala Trp Arg Leu Ala Ala Gly Ile		
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Asp Pro Tyr Leu Glu Glu Cys Thr Thr Pro Glu Ser Pro Glu Leu Ala		
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Gly Gly Thr Thr Val Arg Pro Leu Glu Gln Glu Met Leu Ser Gly His		
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Ile Glu Gly Gln Thr Leu Lys Met Phe Val His Met Thr Lys Ala Lys		
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Lys Val Leu Glu Ile Gly Met Phe Thr Gly Tyr Ser Ala Leu Ala Met		
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Pro Tyr Ala Ala Glu Ile Gly Gln Lys Ala Phe Gln Gln Ser Pro His		
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Gly Gly Lys Ile Arg Val Glu Leu Asp Ala Ala Leu Ala Thr Leu Asp
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Lys Leu Ala Glu Ala Gly Glu Ser Phe Asp Leu Val Phe Ile Asp Ala
595 600 605

Asp Lys Lys Glu Tyr Val Ala Tyr Phe His Lys Leu Leu Gly Ser Ser
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Leu Leu Ala Pro Asp Gly Phe Ile Cys Val Asp Asn Thr Leu Leu Gln
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Gly Glu Val Tyr Leu Pro Ala Glu Glu Arg Ser Val Asn Gly Glu Ala
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Ile Ala Gln Phe Asn His Thr Val Ala Ile Asp Pro Arg Val Glu Gln
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Val Leu Leu Pro Leu Arg Asp Gly Leu Thr Ile Ile Arg Arg Ile Gln
675 680 685

Pro Met Ala Gln Ser Leu Pro Leu Ser Ser Ala Pro Ala Thr Pro Ser
690 695 700

Leu Pro Ser Gln Thr Lys Ile Ala Ala Ile Ile Gln Asn Ile Cys Thr
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Leu Ala Leu Leu Leu Leu Ala Leu Pro Ile Asn Ala Thr Ile Val Phe
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Ile Ser Leu Leu Val Phe Arg Pro Gln Lys Val Lys Ala Ala Asn Pro
740 745 750

Gln Thr Ile Leu Ile Ser Gly Gly Lys Met Thr Lys Ala Leu Gln Leu
755 760 765

Ala Arg Ser Phe His Ala Ala Gly His Arg Val Val Leu Val Glu Thr
770 775 780

His Lys Tyr Trp Leu Thr Gly His Arg Phe Ser Gln Ala Val Asp Lys
785 790 795 800

Phe Tyr Thr Val Pro Ala Pro Gln Asp Asn Pro Gln Ala Tyr Ile Gln
805 810 815

Ala Leu Val Asp Ile Val Lys Gln Glu Asn Ile Asp Val Tyr Ile Pro
820 825 830

Val Thr Ser Pro Val Gly Ser Tyr Tyr Asp Ser Leu Ala Lys Pro Glu
835 840 845

Leu Ser His Tyr Cys Glu Val Phe His Phe Asp Ala Asp Ile Thr Gln
850 855 860

Met Leu Asp Asp Lys Phe Ala Leu Thr Gln Lys Ala Arg Ser Leu Gly
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Leu Ser Val Pro Lys Ser Phe Lys Ile Thr Ser Pro Glu Gln Val Ile
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Asn Phe Asp Phe Ser Gly Glu Thr Arg Lys Tyr Ile Leu Lys Ser Ile
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Pro Tyr Asp Ser Val Arg Arg Leu Asp Leu Thr Lys Leu Pro Cys Ala
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Thr Pro Glu Glu Thr Ala Ala Phe Val Arg Ser Leu Pro Ile Thr Pro
930 935 940

Glu Lys Pro Trp Ile Met Gln Glu Phe Ile Pro Gly Lys Glu Phe Cys
945 950 955 960

Thr His Ser Thr Val Arg Asn Gly Glu Leu Arg Leu His Cys Cys Cys
965 970 975

Glu Ser Ser Ala Phe Gln Val Asn Tyr Glu Asn Val Asn Asn Pro Gln
980 985 990

Ile Thr Glu Trp Val Gln His Phe Val Lys Glu Leu Lys Leu Thr Gly
995 1000 1005

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

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

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Glu Ile Lys Ile Ile Asp Val Pro Gly Asn His Tyr Ser Phe Val Leu
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35 40 45

Gly Arg Cys Leu Thr Val Ile Asp Ala Asn Val Asn Arg Leu Tyr Gly
50 55 60

Lys Gln Ile Lys Ser Tyr Phe Arg His Tyr Gly Ile Asp Leu Thr Val
65 70 75 80

Val Pro Ile Val Ile Thr Glu Pro Thr Lys Thr Leu Ala Thr Phe Glu
85 90 95

Lys Ile Val Asp Ala Phe Ser Asp Phe Gly Leu Ile Arg Lys Glu Pro
100 105 110

Val Leu Val Val Gly Gly Gly Leu Thr Thr Asp Val Ala Gly Phe Ala
115 120 125

Cys Ala Ala Tyr Arg Arg Lys Ser Asn Tyr Ile Arg Val Pro Thr Thr
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Leu Ile Gly Leu Ile Asp Ala Gly Val Ala Ile Lys Val Ala Val Asn
145 150 155 160

His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Pro Leu Lys
165 170 175

Val Ile Leu Asp Phe Ser Phe Leu Gln Thr Leu Pro Thr Ala Gln Val
180 185 190

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

Glu Val Phe Glu Leu Leu Tyr Glu Tyr Gly Glu Glu Leu Leu Ser Thr
210 215 220

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

Lys Leu Asn Tyr Glu Ala Ile Lys Thr Met Leu Glu Leu Glu Thr Pro
245 250 255

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

Trp Ser Pro Thr Leu Glu Leu Ala Pro Met Ile Pro Leu Phe His Gly
275 280 285

His Ala Val Asn Ile Asp Met Ala Leu Ser Ala Thr Ile Ala Ala Arg
290 295 300

Arg Gly Tyr Ile Thr Ser Gly Glu Arg Asp Arg Ile Leu Ser Leu Met
305 310 315 320

Ser Arg Ile Gly Leu Ser Ile Asp His Pro Leu Leu Asp Gly Asp Leu
325 330 335

Leu Trp Tyr Ala Thr Gln Ser Ile Ser Leu Thr Arg Asp Gly Lys Gln
340 345 350

Arg Ala Ala Met Pro Lys Pro Ile Gly Glu Cys Phe Phe Val Asn Asp
355 360 365

Phe Thr Arg Glu Glu Leu Asp Ala Ala Leu Ala Glu His Lys Arg Leu
370 375 380

Cys Ala Thr Tyr Pro Arg Gly Gly Asp Gly Ile Asp Ala Tyr Ile Glu
385 390 395 400

Thr Gln Glu Glu Ser Lys Leu Leu Gly Val Met Thr Ser Ile Leu Gly
405 410 415

Arg Asp Thr Ala Arg Pro Ile Thr Pro His Ser Ile Leu Val Ala Gln
420 425 430

Leu Gln Lys Thr Leu Arg Met Ala Glu Glu Ser Asn Ile Pro Ser Glu
435 440 445

Ile Leu Thr Ser Leu Arg Gln Gly Leu Gln Leu Ala Ala Gly Leu Asp
450 455 460

Pro Tyr Leu Asp Asp Cys Thr Thr Pro Glu Ser Thr Ala Leu Thr Ala
465 470 475 480

Leu Ala Gln Lys Thr Ser Ile Glu Asp Trp Ser Lys Arg Phe Ser Asp
485 490 495

Gly Glu Thr Val Arg Gln Leu Glu Gln Glu Met Leu Ser Gly His Leu
500 505 510

Glu Gly Gln Thr Leu Lys Met Phe Val His Ile Thr Lys Ala Lys Ser
515 520 525

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Tyr Val Ala Glu Phe Ala Gln Thr Cys Phe Gln Glu Ser Pro His Gly
565 570 575

Arg Lys Ile Val Val Glu Val Ala Pro Ala Leu Glu Thr Leu His Lys
580 585 590

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595 600 605

Lys Lys Glu Tyr Ile Glu Tyr Phe Gln Ile Ile Leu Asp Ser His Leu
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Leu Ala Pro Asp Gly Leu Ile Cys Val Asp Asn Thr Leu Leu Gln Gly
625 630 635 640

Gln Val Tyr Leu Pro Ser Glu Gln Arg Thr Ala Asn Gly Glu Ala Ile
645 650 655

Ala Gln Phe Asn Arg Ile Val Ala Ala Asp Pro Arg Val Glu Gln Val
660 665 670

Leu Leu Pro Ile Arg Asp Gly Ile Thr Leu Ile Arg Arg Leu Val Met
675 680 685

Ala Gln Ser Ile Ser Leu Ser Leu Pro Gln Ser Thr Thr Pro Ser Lys

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Ile Leu Leu Leu Ile Ala Leu Pro Leu Asn Ala Leu Ile Val Leu Ile			
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Ser Leu Met Cys Arg Pro Phe Thr Lys Lys Pro Ala Val Ala Thr His			
	740	745	750
Pro Gln Asn Ile Leu Val Ser Gly Gly Lys Met Thr Lys Ala Leu Gln			
	755	760	765
Leu Ala Arg Ser Phe His Ala Ala Gly His Arg Val Ile Leu Ile Glu			
	770	775	780
Gly His Lys Tyr Trp Leu Ser Gly His Arg Phe Ser Asn Ser Val Ser			
785	790	795	800
Arg Phe Tyr Thr Val Pro Ala Pro Gln Asp Asp Pro Glu Gly Tyr Thr			
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Gln Ala Leu Leu Glu Ile Val Lys Arg Glu Lys Ile Asp Val Tyr Val			
	820	825	830
Pro Val Cys Ser Pro Val Ala Ser Tyr Tyr Asp Ser Leu Ala Lys Ser			
	835	840	845
Ala Leu Ser Glu Tyr Cys Glu Val Phe His Phe Asp Ala Asp Ile Thr			
	850	855	860
Lys Met Leu Asp Asp Lys Phe Ala Phe Thr Asp Arg Ala Arg Ser Leu			
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Gly Leu Ser Ala Pro Lys Ser Phe Lys Ile Thr Asp Pro Glu Gln Val			
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	900	905	910
Ile Ser Tyr Asp Ser Val Arg Arg Leu Asn Leu Thr Lys Leu Pro Cys			
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Asp Thr Pro Glu Glu Thr Ala Ala Phe Val Lys Ser Leu Pro Ile Ser
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Pro Glu Lys Pro Trp Ile Met Gln Glu Phe Ile Pro Gly Lys Glu Leu
945 950 955 960

Cys Thr His Ser Thr Val Arg Asp Gly Glu Leu Arg Leu His Cys Cys
965 970 975

Ser Asn Ser Ser Ala Phe Gln Ile Asn Tyr Glu Asn Val Glu Asn Pro
980 985 990

Gln Ile Gln Glu Trp Val Gln His Phe Val Lys Ser Leu Arg Leu Thr
995 1000 1005

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Ala Ile Glu Cys Asn Pro Arg Thr His Ser Ala Ile Thr Met Phe Tyr
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Ala Pro Leu Glu Pro Leu Ala Asp Ser Lys Pro Thr Tyr Trp Ile Tyr
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His Glu Ile Trp Arg Leu Thr Gly Ile Arg Ser Gly Gln Gln Leu Gln
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Thr Trp Phe Gly Arg Leu Val Arg Gly Thr Asp Ala Ile Tyr Arg Leu
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Asp Asp Pro Ile Pro Phe Leu Thr Leu His His Trp Gln Ile Thr Leu
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Leu Leu Leu Gln Asn Leu Gln Arg Leu Lys Gly Trp Val Lys Ile Asp
1125 1130 1135

Phe Asn Ile Gly Lys Leu Val Glu Leu Gly Gly Asp Met Pro Val Leu
1140 1145 1150

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1155 1160 1165

Leu Ser Arg Leu Tyr Ala Gln Asp Cys Leu Ala Ala Thr Ala Asp Pro
1170 1175 1180

Ser Leu Tyr Asn Phe Gln Ile Ala Tyr Ile Thr Pro Asp Arg Gln Trp
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Arg Phe Pro Asp Ser Leu Ser Arg Glu Asp Ile Ala Leu Thr Lys Pro
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Ile Pro Val Phe Asp Ala Ile Gln Phe Leu Thr Gly Gln Asn Ile Asp
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Met Met Leu Pro Gln Met Phe Cys Ile Pro Gly Met Thr Gln Tyr Arg
1235 1240 1245

Ala Leu Phe Asp Leu Leu Lys Ile Pro Tyr Ile Gly Asn Thr Pro Asp
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Ile Met Ala Ile Ala Ala His Lys Ala Arg Ala Lys Ala Ile Val Glu
1265 1270 1275 1280

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

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Ile Asp Pro Lys Gly Gln Pro Trp Phe Leu Glu Ala Gly Leu Tyr Cys		
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Ser Phe Ala Pro Lys Ser Val Ile Ser Ser Met Ala Lys Ala Ala Gly		
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<211> 36

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<211> 71

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cttcgaagtt c 71

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<210> 15

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<400> 18
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pSKH130-deltafhuA-Pn-aroG-Pn-ppsA-Pn-tktA plasmid

<400> 19
gaaaatgccg atgggtaccg 20

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<210> 21
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<210> 28
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<400> 28
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<210> 29
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<400> 31
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<210> 32
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<400> 32
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<210> 33
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<210> 34

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<210> 35

<211> 58

<212> DNA

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<223> forward primer for CJ7 promoter fragment

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<210> 36

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<210> 37

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> forward primer for lysc8 promoter fragment

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47

<210> 38

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> reverse primer for lysc8 promoter fragment

<400> 38

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48

<210> 39

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for O2 promoter fragment

<400> 39

ccaaacacca acaaaaggct ctacccatat gcaataatcg tgaatttgg cagc

54

<210> 40
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for O2 promoter fragment

<400> 40
caaactttgc ttggacgata ctcatgttt tgatctctc caataatcta tgc 53

<210> 41
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for aroD genes to construct pDC delta aroD

<400> 41
gatcggatcc cactggacgt ttgggtgaga cc 32

<210> 42
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for aroD genes to construct pDC delta aroD

<400> 42
gatcggatcc actagtttta ggtccattt ctaattg 37

<210> 43
<211> 29
<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for aroD genes to construct pDC delta aroD

<400> 43

gatcactagt atgaacgaca gtattctcc

29

<210> 44

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for aroD genes to construct pDC delta aroD

<400> 44

gatcaagctt gttacatcct gacgttgtagg

30

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for Ava_A

<400> 45

cgcggatcca tgagtatcgt ccaagcaaag

30

<210> 46

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for Ava_A

<400> 46
cgctcgagt tatttaacac tccgattaa ttc 33

<210> 47
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for Ava_B

<400> 47
cgcgatcca tgacaaatgt gattgtccaa c 31

<210> 48
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for Ava_B

<400> 48
cgctcgagt taagggtgta ttctcgcat aattg 35

<210> 49
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for Ava_C

<400> 49
cgcgatcca tggcacaatc cttccctt tc 32

<210> 50
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> reverse primer for Ava_C

<400> 50
 cgctcgagc taatctccc ccaattccac c 31

<210> 51
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> forward primer for Ava_D

<400> 51
 cgcgatcca tgcagactat agattttaat attc 34

<210> 52
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> reverse primer for Ava_D

<400> 52
 cgctcgagt tatgaattat ttccagaca atc 33

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> forward primer for Npr_A

<400> 53

cgcggatcca tgagtaatgt tcaagcatcg

30

<210> 54

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for Npr_A

<400> 54

cgctctgagt cacactccca atagtttg

29

<210> 55

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for Npr_B

<400> 55

cgcggatcca tgaccagtat ttaggacga g

31

<210> 56

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for Npr_B

<400> 56

cgctctgagt tataccaagc gtctaadc 28

<210> 57

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for Npr_C

<400> 57

cgcgatcca tggcacaatc aatctcttta tc 32

<210> 58

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer for Npr_C

<400> 58

cgctctgagt tagtcgcccc ctaattccac g 31

<210> 59

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer for Npr_D

<400> 59

cgcgatcca tgccagtact taatctctt c 31

<210> 60

<211> 35

<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for Npr_D

<400> 60
cgctcgagt caatttgta acacctttt attac

35

<210> 61
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for pGPD

<400> 61
acgtaagata attgtatatt acgcagtta tcattatcaa tactcgcc

48

<210> 62
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for pGPD

<400> 62
gtaacgacaa tcctctccat gtggtcttga atcaaagctg

40

<210> 63
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for LoxP(Ura)

<400> 63
ccgattgtca atcagcgtaa cagctgaagc ttcgtacgc 39

<210> 64
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for LoxP(Ura)

<400> 64
ttgtttggc cagtcggcaa gggcataggc cactagtggg tctg 44

<210> 65
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for aroB

<400> 65
cagctttgat tcaagaccac atggagagga ttgtcggtac 40

<210> 66
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for aroB

<400> 66
gcgtacgaag cttcagctgt tacgctgatt gacaatcgg 39

<210> 67
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for ARO1 fragment 1

<400> 67
accattcaag agtatatgag agaaggaaaa ct 32

<210> 68
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for ARO1 fragment 1

<400> 68
ggcgagtatt gataatgata aactgcgtaa tatacaatta tcttacg 47

<210> 69
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for ARO1 fragment 2

<400> 69
cagatccact agtggcctat gcccttgccg actggccaaa acaa 44

<210> 70
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> reverse primer for ARO1 fragment 2

<400> 70

caaatatcaa tggcacgttg

20

<210> 71

<211> 759

<212> DNA

<213> Escherichia coli W3110

<400> 71

atgaaaaccg taactgtaaa agatctcgtc attggtacgg gcgcacctaa aatcatcgtc	60
tcgctgatgg cgaaagatat cgccagcgtg aaatccgaag ctctgccta tcgtgaagcg	120
gactttgata ttctggaatg gcgtgtggac cactatgccg acctctcaa tgtggagtct	180
gtcatggcgg cagcaaaaat tctccgtgag accatgccag aaaaaccgct gctgtttacc	240
ttccgcagtg ccaaagaagg cggcgagcag gcgattcca ccgaggctta tattgcactc	300
aatcgtgcag ccatcgacag cggcctggtt gatatgatcg atctggagt atttaccggt	360
gatgatcagg ttaaagaaac cgtcgcctac gccacgcgc atgatgtgaa agtagtcatg	420
tccaacatg acttcataa aacgccggaa gccgaagaaa tcattgcccg tctgcgcaaa	480
atgcaatcct tcgacgccga tattcctaag attgcgctga tgccgcaaag taccagcgat	540
gtgctgacgt tgcttgccgc gaccctggag atgcaggagc agtatgccga tcgtccaatt	600
atcacgatgt cgatggcaaa aactggcgta atttctcgtc tggctggtga agtatttggc	660
tcggcggcaa cttttggtgc ggtaaaaaaa gcgtctgcgc cagggcaa atctcggtaaat	720
gatttgcgca cggtattaac tattttacac caggcataa	759

<210> 72

<211> 252

<212> PRT

<213> Escherichia coli W3110

<400> 72

Met Lys Thr Val Thr Val Lys Asp Leu Val Ile Gly Thr Gly Ala Pro
1 5 10 15

Lys Ile Ile Val Ser Leu Met Ala Lys Asp Ile Ala Ser Val Lys Ser
20 25 30

Glu Ala Leu Ala Tyr Arg Glu Ala Asp Phe Asp Ile Leu Glu Trp Arg
35 40 45

Val Asp His Tyr Ala Asp Leu Ser Asn Val Glu Ser Val Met Ala Ala
50 55 60

Ala Lys Ile Leu Arg Glu Thr Met Pro Glu Lys Pro Leu Leu Phe Thr
65 70 75 80

Phe Arg Ser Ala Lys Glu Gly Gly Glu Gln Ala Ile Ser Thr Glu Ala
85 90 95

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

Ile Asp Leu Glu Leu Phe Thr Gly Asp Asp Gln Val Lys Glu Thr Val
115 120 125

Ala Tyr Ala His Ala His Asp Val Lys Val Val Met Ser Asn His Asp
130 135 140

Phe His Lys Thr Pro Glu Ala Glu Glu Ile Ile Ala Arg Leu Arg Lys
145 150 155 160

Met Gln Ser Phe Asp Ala Asp Ile Pro Lys Ile Ala Leu Met Pro Gln
165 170 175

Ser Thr Ser Asp Val Leu Thr Leu Leu Ala Ala Thr Leu Glu Met Gln
180 185 190

Glu Gln Tyr Ala Asp Arg Pro Ile Ile Thr Met Ser Met Ala Lys Thr
195 200 205

Gly Val Ile Ser Arg Leu Ala Gly Glu Val Phe Gly Ser Ala Ala Thr

210	215	220	
Phe Gly Ala Val Lys Lys Ala Ser Ala Pro Gly Gln Ile Ser Val Asn			
225	230	235	240
Asp Leu Arg Thr Val Leu Thr Ile Leu His Gln Ala			
	245	250	

<210> 73
 <211> 1053
 <212> DNA
 <213> Escherichia coli W3110

<400> 73

atgaattatc agaacgacga ttacgcatc aaagaaatca aagagttact tcctcctgtc	60
gcattgctgg aaaaattccc cgctactgaa aatgccgcga atacggttgc ccatgcccga	120
aaagcgatcc ataagatcct gaaaggtaat gatgatcgcc tgttggttgt gattggccca	180
tgctcaattc atgatcctgt cgcggaacaa gagtatgcca ctgcttgct ggcgctgcgt	240
gaagagctga aagatgagct ggaaatcgta atgcgcgtct atttgaaaa gccgcgtacc	300
acggtgggct ggaaagggct gattaacgat ccgcatatgg ataatagctt ccagatcaac	360
gacggtctgc gtatagcccc taaattgctg ctgatatta acgacagcgg tctgccagcg	420
gcaggtgagt ttctcgatat gatcacccca caatatctcg ctgacctgat gagctggggc	480
gcaattggcg cacgtaccac cgaatcgag gtgcaccgcg aactggcatc agggctttct	540
tgtccggctg gttcaaaaa tggcaccgac ggtacgatta aagtggctat cgatgccatt	600
aatgccgccg gtgcgccgca ctgcttctg tccgtaacga aatgggggca ttcggcgatt	660
gtgaatacca gcggtaacgg cgattgccat atcattctgc gcggcggtaa agagcctaac	720
tacagcgca agcacgttg tgaagtgaag gaagggtga acaaacgagg cctgccagca	780
caggtgatga tcgatttcag ccatgctaac tcgtccaaac aattcaaaaa gcagatggat	840
gtttgtgctg acgtttgcc gcagattgcc ggtggcgaaa aggccattat tggcgtgatg	900

gtggaaagcc atctggtgga aggcaatcag agcctcgaga gcggggagcc gctggcctac 960
 ggtaagagca tcaccgatgc ctgcatcggc tgggaagata ccgatgctct gttacgtcaa 1020
 ctggcgaatg cagtaaaagc gcgtcgcggg taa 1053

<210> 74
 <211> 350
 <212> PRT
 <213> Escherichia coli W3110

<400> 74
 Met Asn Tyr Gln Asn Asp Asp Leu Arg Ile Lys Glu Ile Lys Glu Leu
 1 5 10 15

Leu Pro Pro Val Ala Leu Leu Glu Lys Phe Pro Ala Thr Glu Asn Ala
 20 25 30

Ala Asn Thr Val Ala His Ala Arg Lys Ala Ile His Lys Ile Leu Lys
 35 40 45

Gly Asn Asp Asp Arg Leu Leu Val Val Ile Gly Pro Cys Ser Ile His
 50 55 60

Asp Pro Val Ala Ala Lys Glu Tyr Ala Thr Arg Leu Leu Ala Leu Arg
 65 70 75 80

Glu Glu Leu Lys Asp Glu Leu Glu Ile Val Met Arg Val Tyr Phe Glu
 85 90 95

Lys Pro Arg Thr Thr Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His
 100 105 110

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

Leu Leu Leu Asp Ile Asn Asp Ser Gly Leu Pro Ala Ala Gly Glu Phe
 130 135 140

Leu Asp Met Ile Thr Pro Gln Tyr Leu Ala Asp Leu Met Ser Trp Gly
 145 150 155 160

Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Glu Leu Ala
165 170 175

Ser Gly Leu Ser Cys Pro Val Gly Phe Lys Asn Gly Thr Asp Gly Thr
180 185 190

Ile Lys Val Ala Ile Asp Ala Ile Asn Ala Ala Gly Ala Pro His Cys
195 200 205

Phe Leu Ser Val Thr Lys Trp Gly His Ser Ala Ile Val Asn Thr Ser
210 215 220

Gly Asn Gly Asp Cys His Ile Ile Leu Arg Gly Gly Lys Glu Pro Asn
225 230 235 240

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

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

Lys Gln Phe Lys Lys Gln Met Asp Val Cys Ala Asp Val Cys Gln Gln
275 280 285

Ile Ala Gly Gly Glu Lys Ala Ile Ile Gly Val Met Val Glu Ser His
290 295 300

Leu Val Glu Gly Asn Gln Ser Leu Glu Ser Gly Glu Pro Leu Ala Tyr
305 310 315 320

Gly Lys Ser Ile Thr Asp Ala Cys Ile Gly Trp Glu Asp Thr Asp Ala
325 330 335

Leu Leu Arg Gln Leu Ala Asn Ala Val Lys Ala Arg Arg Gly
340 345 350

<210> 75

<211> 2379

<212> DNA

<213> Escherichia coli W3110

<400> 75

atgtccaaca atggctcgtc accgctgggtg ctttggtata accaactcgg catgaatgat

60

gtagacaggg ttgggggcaa aaatgcctcc ctgggtgaaa tgattactaa tctttccgga	120
atgggtgttt ccgttccgaa tggtttcgcc acaaccgccg acgcgtttaa ccagtttctg	180
gaccaaagcg gcgtaaacca gcgcatttat gaactgctgg ataaaacgga tattgacgat	240
gttactcagc ttgcgaaagc gggcgcgcaa atccgccagt ggattatcga cactcccttc	300
cagcctgagc tggaaaacgc catccgcgaa gcctatgcac agctttccgc cgatgacgaa	360
aacgcctctt ttgcggtgcg ctctccgcc accgcagaag atatgccgga cgcttctttt	420
gccggtcagc aggaaacctt cctcaacgtt cagggttttg acgccgttct cgtggcagtg	480
aaacatgtat ttgcttctct gttaacgat cgcgccatct ctatcgtgt gcaccagggt	540
tacgatcacc gtggtgtggc gctctccgcc ggtgttcaac ggatggtgcg ctctgacctc	600
gcatcatctg gcgtgatgtt ctccattgat accgaatccg gctttgacca ggtggtgttt	660
atcacttccg catggggcct tggtagatg gtcgtgcagg gtgcggttaa cccggatgag	720
ttttacgtgc ataaaccgac actggcggcg aatcgcccgg ctatcgtgcg ccgcaccatg	780
gggtcgaaaa aaatccgcat ggtttacgcg ccgaccagg agcacggcaa gcagggtaaa	840
atcgaagacg taccgcagga acagcgtgac atcttctcgc tgaccaacga agaagtgcag	900
gaactggcaa aacaggccgt acaaattgag aaacactacg gtcgcccgat ggatattgag	960
tgggcgaaag atggccacac cggtaaactg ttcatgtgc aggcgcgtcc ggaaaccgtg	1020
cgctcacgcg gtcaggatcat ggagcgttat acgctgcatt cacagggtaa gattatcgcc	1080
gaaggccgtg ctatcggta tcgcatcggg gcgggtccgg tgaaagtcac ccatgacatc	1140
agcgaaatga accgcatcga acctggcgac gtgctgggta ctgacatgac cgaccggac	1200
tgggaaccga tcatgaagaa agcatctgcc atcgtcacca accgtggcgg tcgtacctgt	1260
cacgcggcga tcatcgctcg tgaactgggc attccggcgg tagtgggctg tggagatgca	1320
acagaacgga tgaaagacgg tgagaacgtc actgtttctt gtgccgaagg tgataccggt	1380

tacgtctatg cggagttgct ggaatttagc gtgaaaagct ccagcgtaga aacgatgccg	1440
gatctgccgt tgaaagtgat gatgaacgtc ggtaacccgg accgtgcttt cgacttcgcc	1500
tgctaccga acgaaggcgt gggccttgcg cgtctggaat ttatcatcaa ccgatgatt	1560
ggcgtccacc cacgcgcact gcttgagttt gacgatcagg aaccgcagtt gcaaaacgaa	1620
atccgcgaga tgatgaaagg ttttgattct ccgcgtgaat ttacgttgg tcgtctgact	1680
gaagggatcg cgacgtggg tgccgcgttt tatccgaagc gcgtcattgt ccgtctctct	1740
gattttaaat cgaacgaata tgccaacctg gtcggtggcg agcggtacga gccagatgaa	1800
gagaaccca tgctcggctt ccgtggcgcg ggccgctatg tttccgacag cttccgcgac	1860
tgtttcgcbc tggagtgtga agcagtgaag cgtgtgcgca acgacatggg actgaccaac	1920
gttgagatca tgatcccggt cgtgcgtacc gtagatcagg cgaaagcggg ggttgaagaa	1980
ctggcgcgctc aggggctgaa acgtggcgag aacgggctga aaatcatcat gatgtgtgaa	2040
atcccgcca acgccttgct ggccgagcag ttctcgaat attcgacgg cttctcaatt	2100
ggctcaaacg atatgacgca gctggcgctc ggtctggacc gtgactccgg cgtggtgtct	2160
gaattgttcg atgagcgcaa cgatgcggcg aaagcactgc tgcgatggc tatccgtgcc	2220
gcgaagaaac agggcaaata tgcgggatt tgcggtcagg gtccgtccga ccacgaagac	2280
tttgccgcac ggttgatgga agaggggatc gatagcctgt ctctgaaccc ggacaccgtg	2340
gtgcaaacct ggtaagcct ggctgaactg aagaaataa	2379

<210> 76
 <211> 792
 <212> PRT
 <213> Escherichia coli W3110

<400> 76
 Met Ser Asn Asn Gly Ser Ser Pro Leu Val Leu Trp Tyr Asn Gln Leu
 1 5 10 15

Gly Met Asn Asp Val Asp Arg Val Gly Gly Lys Asn Ala Ser Leu Gly
20 25 30

Glu Met Ile Thr Asn Leu Ser Gly Met Gly Val Ser Val Pro Asn Gly
35 40 45

Phe Ala Thr Thr Ala Asp Ala Phe Asn Gln Phe Leu Asp Gln Ser Gly
50 55 60

Val Asn Gln Arg Ile Tyr Glu Leu Leu Asp Lys Thr Asp Ile Asp Asp
65 70 75 80

Val Thr Gln Leu Ala Lys Ala Gly Ala Gln Ile Arg Gln Trp Ile Ile
85 90 95

Asp Thr Pro Phe Gln Pro Glu Leu Glu Asn Ala Ile Arg Glu Ala Tyr
100 105 110

Ala Gln Leu Ser Ala Asp Asp Glu Asn Ala Ser Phe Ala Val Arg Ser
115 120 125

Ser Ala Thr Ala Glu Asp Met Pro Asp Ala Ser Phe Ala Gly Gln Gln
130 135 140

Glu Thr Phe Leu Asn Val Gln Gly Phe Asp Ala Val Leu Val Ala Val
145 150 155 160

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

Val His Gln Gly Tyr Asp His Arg Gly Val Ala Leu Ser Ala Gly Val
180 185 190

Gln Arg Met Val Arg Ser Asp Leu Ala Ser Ser Gly Val Met Phe Ser
195 200 205

Ile Asp Thr Glu Ser Gly Phe Asp Gln Val Val Phe Ile Thr Ser Ala
210 215 220

Trp Gly Leu Gly Glu Met Val Val Gln Gly Ala Val Asn Pro Asp Glu
225 230 235 240

Phe Tyr Val His Lys Pro Thr Leu Ala Ala Asn Arg Pro Ala Ile Val

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

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

Phe Asp Phe Ala Cys Leu Pro Asn Glu Gly Val Gly Leu Ala Arg Leu
500 505 510

Glu Phe Ile Ile Asn Arg Met Ile Gly Val His Pro Arg Ala Leu Leu
515 520 525

Glu Phe Asp Asp Gln Glu Pro Gln Leu Gln Asn Glu Ile Arg Glu Met
530 535 540

Met Lys Gly Phe Asp Ser Pro Arg Glu Phe Tyr Val Gly Arg Leu Thr
545 550 555 560

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

Val Arg Leu Ser Asp Phe Lys Ser Asn Glu Tyr Ala Asn Leu Val Gly
580 585 590

Gly Glu Arg Tyr Glu Pro Asp Glu Glu Asn Pro Met Leu Gly Phe Arg
595 600 605

Gly Ala Gly Arg Tyr Val Ser Asp Ser Phe Arg Asp Cys Phe Ala Leu
610 615 620

Glu Cys Glu Ala Val Lys Arg Val Arg Asn Asp Met Gly Leu Thr Asn
625 630 635 640

Val Glu Ile Met Ile Pro Phe Val Arg Thr Val Asp Gln Ala Lys Ala
645 650 655

Val Val Glu Glu Leu Ala Arg Gln Gly Leu Lys Arg Gly Glu Asn Gly
660 665 670

Leu Lys Ile Ile Met Met Cys Glu Ile Pro Ser Asn Ala Leu Leu Ala
675 680 685

Glu Gln Phe Leu Glu Tyr Phe Asp Gly Phe Ser Ile Gly Ser Asn Asp
690 695 700

Met Thr Gln Leu Ala Leu Gly Leu Asp Arg Asp Ser Gly Val Val Ser
705 710 715 720

Glu Leu Phe Asp Glu Arg Asn Asp Ala Val Lys Ala Leu Leu Ser Met
725 730 735

Ala Ile Arg Ala Ala Lys Lys Gln Gly Lys Tyr Val Gly Ile Cys Gly
740 745 750

Gln Gly Pro Ser Asp His Glu Asp Phe Ala Ala Trp Leu Met Glu Glu
755 760 765

Gly Ile Asp Ser Leu Ser Leu Asn Pro Asp Thr Val Val Gln Thr Trp
770 775 780

Leu Ser Leu Ala Glu Leu Lys Lys
785 790

<210> 77

<211> 1992

<212> DNA

<213> Escherichia coli W3110

<400> 77

atgtcctcac gtaaagagct tgccaatgct attcgtgctg tgagcatgga cgcagtacag	60
aaagccaaat ccggtcaccc ggggtgccct atgggtatgg ctgacattgc cgaagtctctg	120
tggcgtgatt tctgaaaca caaccgcag aatccgtctt gggctgaccg tgaccgttc	180
gtgctgtcca acggccacgg ctccatgctg atctacagcc tgctgcacct caccggttac	240
gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac	300
ccggaagtgg gttacaccgc tgggtgggaa accaccaccg gtccgctggg tcagggtatt	360
gccaacgcag tcggtatggc gattgcagaa aaaacgctgg cggcgcagtt taaccgtccg	420
ggccacgaca ttgtcgacca ctacacctac gccttcatgg gcgacggctg catgatggaa	480
ggcatctccc acgaagtttg ctctctggcg ggtacgtga agctgggtaa actgattgca	540
ttctacgatg acaacgggtat ttctatcgat gggtcacgttg aaggctgggt caccgacgac	600
accgcaatgc gtttcgaagc ttacggctgg caggtatttc gcgacatcga cgggtcatgac	660

gcggcatcta tcaaacgcgc agtagaagaa gcgcgcgcag tgactgacaa accttcctg	720
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cacggtgcgc cgctgggcga cgctgaaatt gccctgaccc gcgaacaact gggctggaaa	840
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ctgccgaaag cggttactgc acgcgttgct gtagaagcgg gtattgctga ctactggtac	1860
aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ccttcggtga atctgctccg	1920
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gaactgctgt aa

1992

<210> 78

<211> 663

<212> PRT

<213> Escherichia coli W3110

<400> 78

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Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
100 105 110

Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile
115 120 125

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

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
145 150 155 160

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

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His

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

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
500 505 510

Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg
515 520 525

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
625 630 635 640

Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val
645 650 655

Ala Lys Ala Lys Glu Leu Leu
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<211> 438
<212> DNA
<213> *Corynebacterium glutamicum* ATCC 13032

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gcgaagcacg gccttgaggt tgaggcgctg cagagcaatc acgaaggtga gctaatacgat 180
gcgctgcaca acgctcgcgg cacccacatc ggttgctgta ttaacccgg cggcctgact 240
cacacttcgg tggcgctttt ggatgctgtg aaggcgtctg agcttcctac cgttgagggtg 300
cacatttcca atccgcatgc ccgtgaagag ttccgccacc attcttacet ttcctcggc 360
gcggtctccg ttatcgctgg cgctggcatc caggggtacc gtttcgcggt cgatatcctg 420
gcaaattctca aaaagtag 438

<210> 80
<211> 145
<212> PRT
<213> *Corynebacterium glutamicum* ATCC 13032

<400> 80
Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu
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20 25 30
Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
35 40 45
Ala Leu Gln Ser Asn His Glu Gly Glu Leu Ile Asp Ala Leu His Asn

50 55 60
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80
 His Thr Ser Val Ala Leu Leu Asp Ala Val Lys Ala Ser Glu Leu Pro
 85 90 95
 Thr Val Glu Val His Ile Ser Asn Pro His Ala Arg Glu Glu Phe Arg
 100 105 110
 His His Ser Tyr Ile Ser Leu Ala Ala Val Ser Val Ile Ala Gly Ala
 115 120 125
 Gly Ile Gln Gly Tyr Arg Phe Ala Val Asp Ile Leu Ala Asn Leu Lys
 130 135 140
 Lys
 145

<210> 81
 <211> 4767
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 81
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 tgcaatgata cgaacttgag taaagttcca tactaccagc aattagtcct ggaattcaag 180
 gcttctttgc cagaaggctc tcgtttactt acttatgttg ttaaaccagg tgagacaagt 240
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 gatacggtta tggtagcgat cggtggtggt gttattggtg acatgattgg gttcgttgca 360
 tctacattta tgagaggtgt tcgtgtgtgc caagtaccaa catccttatt ggcaatggtc 420
 gattcctcca ttggtggtaa aactgctatt gacactcctc taggtaaaaa ctttattggt 480
 gcattttggc aacaaaaatt tgtccttgta gatattaaat ggctagaaac gttagccaag 540

agagagttta tcaatgggat ggcagaagtt atcaagactg cttgtatttg gaacgctgac	600
gaatttacta gattagaatc aaacgcttcg ttgttcttaa atgttgtaa tggggcaaaa	660
aatgtcaagg ttaccaatca attgacaaac gagattgacg agatatcgaa tacagatatt	720
gaagctatgt tggatcatatc atataagtta gttcttgaga gtattaaggt caaagcggaa	780
gttgtctctt cggatgaacg tgaatccagt ctaagaaacc tttgaactt cggacattct	840
attggtcatg cttatgaagc tatactaacc ccacaagcat tacatggtga atgtgtgtcc	900
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gaaaaattcg gtatcaatgt tgaaacttct actacagaac cttaactta ttatattcca	1920
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<210> 82
 <211> 1588
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 82
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 Cys Pro Ser Ser Thr Tyr Val Ile Cys Asn Asp Thr Asn Leu Ser Lys
 35 40 45
 Val Pro Tyr Tyr Gln Gln Leu Val Leu Glu Phe Lys Ala Ser Leu Pro
 50 55 60
 Glu Gly Ser Arg Leu Leu Thr Tyr Val Val Lys Pro Gly Glu Thr Ser
 65 70 75 80
 Lys Ser Arg Glu Thr Lys Ala Gln Leu Glu Asp Tyr Leu Leu Val Glu
 85 90 95
 Gly Cys Thr Arg Asp Thr Val Met Val Ala Ile Gly Gly Gly Val Ile
 100 105 110
 Gly Asp Met Ile Gly Phe Val Ala Ser Thr Phe Met Arg Gly Val Arg
 115 120 125
 Val Val Gln Val Pro Thr Ser Leu Leu Ala Met Val Asp Ser Ser Ile
 130 135 140

Gly Gly Lys Thr Ala Ile Asp Thr Pro Leu Gly Lys Asn Phe Ile Gly
145 150 155 160

Ala Phe Trp Gln Pro Lys Phe Val Leu Val Asp Ile Lys Trp Leu Glu
165 170 175

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

Thr Ala Cys Ile Trp Asn Ala Asp Glu Phe Thr Arg Leu Glu Ser Asn
195 200 205

Ala Ser Leu Phe Leu Asn Val Val Asn Gly Ala Lys Asn Val Lys Val
210 215 220

Thr Asn Gln Leu Thr Asn Glu Ile Asp Glu Ile Ser Asn Thr Asp Ile
225 230 235 240

Glu Ala Met Leu Asp His Thr Tyr Lys Leu Val Leu Glu Ser Ile Lys
245 250 255

Val Lys Ala Glu Val Val Ser Ser Asp Glu Arg Glu Ser Ser Leu Arg
260 265 270

Asn Leu Leu Asn Phe Gly His Ser Ile Gly His Ala Tyr Glu Ala Ile
275 280 285

Leu Thr Pro Gln Ala Leu His Gly Glu Cys Val Ser Ile Gly Met Val
290 295 300

Lys Glu Ala Glu Leu Ser Arg Tyr Phe Gly Ile Leu Ser Pro Thr Gln
305 310 315 320

Val Ala Arg Leu Ser Lys Ile Leu Val Ala Tyr Gly Leu Pro Val Ser
325 330 335

Pro Asp Glu Lys Trp Phe Lys Glu Leu Thr Leu His Lys Lys Thr Pro
340 345 350

Leu Asp Ile Leu Leu Lys Lys Met Ser Ile Asp Lys Lys Asn Glu Gly
355 360 365

Ser Lys Lys Lys Val Val Ile Leu Glu Ser Ile Gly Lys Cys Tyr Gly

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

Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys Phe Gly
610 615 620

Ile Asn Val Glu Thr Ser Thr Thr Glu Pro Tyr Thr Tyr Tyr Ile Pro
625 630 635 640

Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser Asp Ala
645 650 655

Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly Thr Thr
660 665 670

Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp Ala Arg
675 680 685

Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr Gln Thr
690 695 700

Ala Thr Ser Thr Thr Val Ser Gly Pro Pro Val Gly Thr Leu Lys Pro
705 710 715 720

Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu Thr Ala
725 730 735

Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser Ala Asn
740 745 750

Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu Cys Asn
755 760 765

Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val Lys Thr
770 775 780

Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser Ile Lys
785 790 795 800

Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val Cys Thr
805 810 815

Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala Gly Met
820 825 830

Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val Arg Ile
835 840 845

Leu Glu Arg His Cys Thr Gly Lys Thr Trp Pro Gly Trp Trp Asp Val
850 855 860

Leu His Ser Glu Leu Gly Ala Lys Leu Asp Gly Ala Glu Pro Leu Glu
865 870 875 880

Cys Thr Ser Lys Lys Asn Ser Lys Lys Ser Val Val Ile Ile Gly Met
885 890 895

Arg Ala Ala Gly Lys Thr Thr Ile Ser Lys Trp Cys Ala Ser Ala Leu
900 905 910

Gly Tyr Lys Leu Val Asp Leu Asp Glu Leu Phe Glu Gln Gln His Asn
915 920 925

Asn Gln Ser Val Lys Gln Phe Val Val Glu Asn Gly Trp Glu Lys Phe
930 935 940

Arg Glu Glu Glu Thr Arg Ile Phe Lys Glu Val Ile Gln Asn Tyr Gly
945 950 955 960

Asp Asp Gly Tyr Val Phe Ser Thr Gly Gly Gly Ile Val Glu Ser Ala
965 970 975

Glu Ser Arg Lys Ala Leu Lys Asp Phe Ala Ser Ser Gly Gly Tyr Val
980 985 990

Leu His Leu His Arg Asp Ile Glu Glu Thr Ile Val Phe Leu Gln Ser
995 1000 1005

Asp Pro Ser Arg Pro Ala Tyr Val Glu Glu Ile Arg Glu Val Trp Asn
1010 1015 1020

Arg Arg Glu Gly Trp Tyr Lys Glu Cys Ser Asn Phe Ser Phe Phe Ala
1025 1030 1035 1040

Pro His Cys Ser Ala Glu Ala Glu Phe Gln Ala Leu Arg Arg Ser Phe
1045 1050 1055

Ser Lys Tyr Ile Ala Thr Ile Thr Gly Val Arg Glu Ile Glu Ile Pro
1060 1065 1070

Ser Gly Arg Ser Ala Phe Val Cys Leu Thr Phe Asp Asp Leu Thr Glu

1075	1080	1085
Gln Thr Glu Asn Leu Thr Pro Ile Cys Tyr Gly Cys Glu Ala Val Glu		
1090	1095	1100
Val Arg Val Asp His Leu Ala Asn Tyr Ser Ala Asp Phe Val Ser Lys		
1105	1110	1115 1120
Gln Leu Ser Ile Leu Arg Lys Ala Thr Asp Ser Ile Pro Ile Ile Phe		
1125	1130	1135
Thr Val Arg Thr Met Lys Gln Gly Gly Asn Phe Pro Asp Glu Glu Phe		
1140	1145	1150
Lys Thr Leu Arg Glu Leu Tyr Asp Ile Ala Leu Lys Asn Gly Val Glu		
1155	1160	1165
Phe Leu Asp Leu Glu Leu Thr Leu Pro Thr Asp Ile Gln Tyr Glu Val		
1170	1175	1180
Ile Asn Lys Arg Gly Asn Thr Lys Ile Ile Gly Ser His His Asp Phe		
1185	1190	1195 1200
Gln Gly Leu Tyr Ser Trp Asp Asp Ala Glu Trp Glu Asn Arg Phe Asn		
1205	1210	1215
Gln Ala Leu Thr Leu Asp Val Asp Val Val Lys Phe Val Gly Thr Ala		
1220	1225	1230
Val Asn Phe Glu Asp Asn Leu Arg Leu Glu His Phe Arg Asp Thr His		
1235	1240	1245
Lys Asn Lys Pro Leu Ile Ala Val Asn Met Thr Ser Lys Gly Ser Ile		
1250	1255	1260
Ser Arg Val Leu Asn Asn Val Leu Thr Pro Val Thr Ser Asp Leu Leu		
1265	1270	1275 1280
Pro Asn Ser Ala Ala Pro Gly Gln Leu Thr Val Ala Gln Ile Asn Lys		
1285	1290	1295
Met Tyr Thr Ser Met Gly Gly Ile Glu Pro Lys Glu Leu Phe Val Val		
1300	1305	1310

Gly Lys Pro Ile Gly His Ser Arg Ser Pro Ile Leu His Asn Thr Gly
1315 1320 1325

Tyr Glu Ile Leu Gly Leu Pro His Lys Phe Asp Lys Phe Glu Thr Glu
1330 1335 1340

Ser Ala Gln Leu Val Lys Glu Lys Leu Leu Asp Gly Asn Lys Asn Phe
1345 1350 1355 1360

Gly Gly Ala Ala Val Thr Ile Pro Leu Lys Leu Asp Ile Met Gln Tyr
1365 1370 1375

Met Asp Glu Leu Thr Asp Ala Ala Lys Val Ile Gly Ala Val Asn Thr
1380 1385 1390

Val Ile Pro Leu Gly Asn Lys Lys Phe Lys Gly Asp Asn Thr Asp Trp
1395 1400 1405

Leu Gly Ile Arg Asn Ala Leu Ile Asn Asn Gly Val Pro Glu Tyr Val
1410 1415 1420

Gly His Thr Ala Gly Leu Val Ile Gly Ala Gly Gly Thr Ser Arg Ala
1425 1430 1435 1440

Ala Leu Tyr Ala Leu His Ser Leu Gly Cys Lys Lys Ile Phe Ile Ile
1445 1450 1455

Asn Arg Thr Thr Ser Lys Leu Lys Pro Leu Ile Glu Ser Leu Pro Ser
1460 1465 1470

Glu Phe Asn Ile Ile Gly Ile Glu Ser Thr Lys Ser Ile Glu Glu Ile
1475 1480 1485

Lys Glu His Val Gly Val Ala Val Ser Cys Val Pro Ala Asp Lys Pro
1490 1495 1500

Leu Asp Asp Glu Leu Leu Ser Lys Leu Glu Arg Phe Leu Val Lys Gly
1505 1510 1515 1520

Ala His Ala Ala Phe Val Pro Thr Leu Leu Glu Ala Ala Tyr Lys Pro
1525 1530 1535

Ser Val Thr Pro Val Met Thr Ile Ser Gln Asp Lys Tyr Gln Trp His
1540 1545 1550

Val Val Pro Gly Ser Gln Met Leu Val His Gln Gly Val Ala Gln Phe
1555 1560 1565

Glu Lys Trp Thr Gly Phe Lys Gly Pro Phe Lys Ala Ile Phe Asp Ala
1570 1575 1580

Val Thr Lys Glu
1585

<210> 83

<211> 1089

<212> DNA

<213> Escherichia coli W3110

<400> 83

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accaacgaaa ccttggtccc tctgtatctc gataaggctc gcggcggtact tgaacaggcg	180
ggtgttaacg tcgatagcgt tatcctccct gacggcgagc agtataaaag cctggctgta	240
ctcgataccg tctttacggc gttgttaca aaaccgcatt gtcgcgatac tacgctggtg	300
gcgcttggtg gcggcgtagt gggcgatctg accggcttcg cggcggcgag ttatcagcgc	360
ggtgtccgtt tcattcaagt cccgacgacg ttactgtcgc aggtcgattc ctccgttggc	420
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gggctggcag aagtcacaa atacggcatt attcttgacg gtgcgtttt taactggctg	600
gaagagaatc tggatgcgtt gttgcgtctg gacgggtccg caatggcgta ctgtattcgc	660
cgttgttgtg aactgaaggc agaagttgtc gccgccgacg agcgcgaaac cgggttacgt	720
gctttactga atctgggaca caccttgggt catgccattg aagctgaaat ggggtatggc	780
aattggttac atggtgaagc ggtcgctgcg ggtatggtga tggcgggcgc gacgtcgga	840

cgtctcgggc agtttagttc tgccgaaacg cagcgtatta taaccctgct caagcgggct 900
 gggttaccgg tcaatgggcc gcgcgaaatg tccgcgcagg cgtatttacc gcatatgctg 960
 cgtgacaaga aagtccttgc gggagagatg cgcttaattc ttccgttggc aattggttaag 1020
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 tcagcgtaa 1089

<210> 84
 <211> 362
 <212> PRT
 <213> Escherichia coli W3110

<400> 84
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 Ile Ala Ser Gly Leu Phe Asn Glu Pro Ala Ser Phe Leu Pro Leu Lys
 20 25 30
 Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu
 35 40 45
 Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val
 50 55 60
 Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val
 65 70 75 80
 Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp
 85 90 95
 Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly
 100 105 110
 Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro
 115 120 125
 Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala
 130 135 140

Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro
145 150 155 160

Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg
165 170 175

Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu
180 185 190

Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu
195 200 205

Arg Leu Asp Gly Pro Ala Met Ala Tyr Cys Ile Arg Arg Cys Cys Glu
210 215 220

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

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

Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met
260 265 270

Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala
275 280 285

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

Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu
305 310 315 320

Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
325 330 335

Ala Ile Gly Lys Ser Glu Val Arg Ser Gly Val Ser His Glu Leu Val
340 345 350

Leu Asn Ala Ile Ala Asp Cys Gln Ser Ala
355 360

<210> 85
 <211> 2247
 <212> DNA
 <213> *Anabaena variabilis* ATCC29413

<400> 85

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ctagcagatg tatatcaagg ttttggacga tgcttggcga ttgtagatgc taacgtcagt	180
cggttgtatg gtaatcaaat tcaggcatat ttccagtatt atggtataga actgaggcta	240
tttctatta ccattactga accagataag actattcaaa ctttcgagag agttatagat	300
gtctttgcag atttcaaatt agtccgcaaa gaaccagtat tagtcgtggg tggcggttta	360
attacagatg ttgtcggcctt tgcttgttct acatatcgtc gcagcagcaa ttacatccgc	420
attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat	480
catcgcaaac tgaaaaaccg tttgggtgct tatcatgctt ctcgcaaagt attttagat	540
ttctccttgt tgcgtactct ccctacagac caagtacgta acgggatggc ggaattggta	600
aaaatcgctg tagtagcgca tcaagaagtt ttgaattgt tggagaagta cggcgaagaa	660
ttactacgta ctcatTTTgg caatatagat gcaactccag agattaaaga aatagcccat	720
cgtttgactt acaaagctat ccataagatg ttggaattgg aagttccaa cctgcatgag	780
ttagacctag ataggggtgat tgcttacggt cacacttggga gtccacctt ggaacttgcg	840
cctcgtctac ccatgttcca cggacacgcc gttaatgtag atatggcttt ctcggcaacg	900
atcgccgccc gtagaggata tattacaatt gcagaacgcg atcgtatttt aggattaatg	960
agtcgcgttg gtctatccct cgaccatccc atgttgata tagatatttt gtggcgtggt	1020
actgaatcta tcacattaac tcgtgatggt ttgttaagag ctgctatgcc aaaaccatt	1080
ggtgattgtg tcttcgtaa tgacctgaca agagaagaat tagcagccgc attagctgac	1140

cacaaagaac tttgtaccag ttatccccgt ggtggtgaag gtgtggatgt gtatcccgtt	1200
tatcaaaaag aattaatcgg gagtggttaa taatgacttt ttgaattca aaatgcaaaa	1260
tactccacgg atacactgcg cgagcgcggt agcatttctg ttcgcggagc gtcccgtagg	1320
gaaagagaag gctacgcaaa taatcggaca ctaattgtct ttaatttga attttgaatt	1380
ttgaattttg aattggagcg aagcgacttg acaaatgtga ttgtccaacc aacagctaga	1440
cctgttacac cattgggaat ttaaccaag cagttagaag ccatagtcca agaggttaag	1500
caacatccag atttacctgg ggaattgata gcaaacatcc atcaggcttg gcgtttagcc	1560
gcaggtatag acccttattt ggaagaatgc accactccag aatctcctga actcgctgca	1620
ttggcaaaaa ccacagccac cgaagcctgg ggagaacact tccacggagg tacaaccgtc	1680
cgtcctctag aacaagagat gctttctggt catatcgaag gacaaacctt aaagatgttt	1740
gttcacatga ccaaagctaa aaaagtctta gaaattggga tgtttaccgg ttattcggcg	1800
ctggcgatgg cggaagcatt accagaggat ggactgcttg tggcttgtga agttgacctt	1860
tacgcggcgg aaattggaca gaaagccttt caacaatctc cccacgggtg aaagattcgt	1920
gtggaattgg atgcagcctt agcaactctt gataagttag cagaagctgg ggagtctttt	1980
gacttggtat ttatcgacgc agataaaaaa gagtatgtag cctattttca caagttgcta	2040
ggtagcagtt tgtagcacc agatggcttt atttgtgtag ataacacctt attacaaggg	2100
gaagtttatc taccagcaga ggaacgtagc gtcaatggtg aagcgatcgc gcaatttaat	2160
catacagtag ctatagaccc ccgtgtagaa caggttttgt tgccgtgcg agatggttta	2220
acaattatcc gcagaataca accttaa	2247

<210> 86
 <211> 820
 <212> PRT
 <213> Anabaena variabilis ATCC29413

<400> 86

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

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

Gly Arg Cys Leu Ala Ile Val Asp Ala Asn Val Ser Arg Leu Tyr Gly
50 55 60

Asn Gln Ile Gln Ala Tyr Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu
65 70 75 80

Phe Pro Ile Thr Ile Thr Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu
85 90 95

Arg Val Ile Asp Val Phe Ala Asp Phe Lys Leu Val Arg Lys Glu Pro
100 105 110

Val Leu Val Val Gly Gly Gly Leu Ile Thr Asp Val Val Gly Phe Ala
115 120 125

Cys Ser Thr Tyr Arg Arg Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr
130 135 140

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

His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Ser Arg Lys
165 170 175

Val Phe Leu Asp Phe Ser Leu Leu Arg Thr Leu Pro Thr Asp Gln Val
180 185 190

Arg Asn Gly Met Ala Glu Leu Val Lys Ile Ala Val Val Ala His Gln
195 200 205

Glu Val Phe Glu Leu Leu Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr
210 215 220

His Phe Gly Asn Ile Asp Ala Thr Pro Glu Ile Lys Glu Ile Ala His

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

Val Asp Ala Asn Val Ser Arg Leu Tyr Gly Asn Gln Ile Gln Ala Tyr
465 470 475 480

Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu Phe Pro Ile Thr Ile Thr
485 490 495

Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu Arg Val Ile Asp Val Phe
500 505 510

Ala Asp Phe Lys Leu Val Arg Lys Glu Pro Val Leu Val Val Gly Gly
515 520 525

Gly Leu Ile Thr Asp Val Val Gly Phe Ala Cys Ser Thr Tyr Arg Arg
530 535 540

Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr Leu Ile Gly Leu Ile Asp
545 550 555 560

Ala Ser Val Ala Ile Lys Val Ala Val Asn His Arg Lys Leu Lys Asn
565 570 575

Arg Leu Gly Ala Tyr His Ala Ser Arg Lys Val Phe Leu Asp Phe Ser
580 585 590

Leu Leu Arg Thr Leu Pro Thr Asp Gln Val Arg Asn Gly Met Ala Glu
595 600 605

Leu Val Lys Ile Ala Val Val Ala His Gln Glu Val Phe Glu Leu Leu
610 615 620

Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr His Phe Gly Asn Ile Asp
625 630 635 640

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

Ile His Lys Met Leu Glu Leu Glu Val Pro Asn Leu His Glu Leu Asp
660 665 670

Leu Asp Arg Val Ile Ala Tyr Gly His Thr Trp Ser Pro Thr Leu Glu
675 680 685

Leu Ala Pro Arg Leu Pro Met Phe His Gly His Ala Val Asn Val Asp
690 695 700

Met Ala Phe Ser Ala Thr Ile Ala Ala Arg Arg Gly Tyr Ile Thr Ile
705 710 715 720

Ala Glu Arg Asp Arg Ile Leu Gly Leu Met Ser Arg Val Gly Leu Ser
725 730 735

Leu Asp His Pro Met Leu Asp Ile Asp Ile Leu Trp Arg Gly Thr Glu
740 745 750

Ser Ile Thr Leu Thr Arg Asp Gly Leu Leu Arg Ala Ala Met Pro Lys
755 760 765

Pro Ile Gly Asp Cys Val Phe Val Asn Asp Leu Thr Arg Glu Glu Leu
770 775 780

Ala Ala Ala Leu Ala Asp His Lys Glu Leu Cys Thr Ser Tyr Pro Arg
785 790 795 800

Gly Gly Glu Gly Val Asp Val Tyr Pro Val Tyr Gln Lys Glu Leu Ile
805 810 815

Gly Ser Val Lys
820

<210> 87

<211> 3638

<212> DNA

<213> *Anabaena variabilis* ATCC29413

<400> 87

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ctagcagatg tatatcaagg ttttgacga tgctggcga tttagatgc taacgtcagt 180

cggttgatg gtaatcaaat tcaggcatat ttccagtatt atggtataga actgaggcta 240

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attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat	480
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aaaatcgctg tagtagcgca tcaagaagtt ttgaattgt tggagaagta cggcgaagaa	660
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gtttaactgg tatccgttct ttacccagt tgcaaagatg gctggggaat attggcgcg	3480
ggactgatgc gatttatcag ccagatgacc ccttaccgtt ttgatggta catcattggc	3540
aaattcccct actgttattg aataattgc gtcgtcttaa aggttgagc cggatagatt	3600
tcaatattgg gaagttggtg gaattggggg gagattag	3638

<210> 88
 <211> 1099
 <212> PRT
 <213> *Anabaena variabilis* ATCC29413

<400> 88
 Met Ser Ile Val Gln Ala Lys Phe Glu Ala Lys Glu Thr Ser Phe His
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Val Glu Gly Tyr Glu Lys Ile Glu Tyr Asp Leu Val Tyr Val Asp Gly
 20 25 30

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

Gly Arg Cys Leu Ala Ile Val Asp Ala Asn Val Ser Arg Leu Tyr Gly
 50 55 60

Asn Gln Ile Gln Ala Tyr Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu
 65 70 75 80

Phe Pro Ile Thr Ile Thr Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu
85 90 95

Arg Val Ile Asp Val Phe Ala Asp Phe Lys Leu Val Arg Lys Glu Pro
100 105 110

Val Leu Val Val Gly Gly Gly Leu Ile Thr Asp Val Val Gly Phe Ala
115 120 125

Cys Ser Thr Tyr Arg Arg Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr
130 135 140

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

His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Ser Arg Lys
165 170 175

Val Phe Leu Asp Phe Ser Leu Leu Arg Thr Leu Pro Thr Asp Gln Val
180 185 190

Arg Asn Gly Met Ala Glu Leu Val Lys Ile Ala Val Val Ala His Gln
195 200 205

Glu Val Phe Glu Leu Leu Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr
210 215 220

His Phe Gly Asn Ile Asp Ala Thr Pro Glu Ile Lys Glu Ile Ala His
225 230 235 240

Arg Leu Thr Tyr Lys Ala Ile His Lys Met Leu Glu Leu Glu Val Pro
245 250 255

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

Trp Ser Pro Thr Leu Glu Leu Ala Pro Arg Leu Pro Met Phe His Gly
275 280 285

His Ala Val Asn Val Asp Met Ala Phe Ser Ala Thr Ile Ala Ala Arg
290 295 300

Arg Gly Tyr Ile Thr Ile Ala Glu Arg Asp Arg Ile Leu Gly Leu Met
305 310 315 320

Ser Arg Val Gly Leu Ser Leu Asp His Pro Met Leu Asp Ile Asp Ile
325 330 335

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

Arg Ala Ala Met Pro Lys Pro Ile Gly Asp Cys Val Phe Val Asn Asp
355 360 365

Leu Thr Arg Glu Glu Leu Ala Ala Ala Leu Ala Asp His Lys Glu Leu
370 375 380

Cys Thr Ser Tyr Pro Arg Gly Gly Glu Gly Val Asp Val Tyr Pro Val
385 390 395 400

Tyr Gln Lys Glu Leu Ile Gly Ser Val Lys Met Ser Ile Val Gln Ala
405 410 415

Lys Phe Glu Ala Lys Glu Thr Ser Phe His Val Glu Gly Tyr Glu Lys
420 425 430

Ile Glu Tyr Asp Leu Val Tyr Val Asp Gly Ile Phe Glu Ile Gln Asn
435 440 445

Ser Ala Leu Ala Asp Val Tyr Gln Gly Phe Gly Arg Cys Leu Ala Ile
450 455 460

Val Asp Ala Asn Val Ser Arg Leu Tyr Gly Asn Gln Ile Gln Ala Tyr
465 470 475 480

Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu Phe Pro Ile Thr Ile Thr
485 490 495

Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu Arg Val Ile Asp Val Phe
500 505 510

Ala Asp Phe Lys Leu Val Arg Lys Glu Pro Val Leu Val Val Gly Gly
515 520 525

Gly Leu Ile Thr Asp Val Val Gly Phe Ala Cys Ser Thr Tyr Arg Arg
530 535 540

Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr Leu Ile Gly Leu Ile Asp

545	550	555	560
Ala Ser Val Ala Ile Lys Val Ala Val Asn His Arg Lys Leu Lys Asn			
	565	570	575
Arg Leu Gly Ala Tyr His Ala Ser Arg Lys Val Phe Leu Asp Phe Ser			
	580	585	590
Leu Leu Arg Thr Leu Pro Thr Asp Gln Val Arg Asn Gly Met Ala Glu			
	595	600	605
Leu Val Lys Ile Ala Val Val Ala His Gln Glu Val Phe Glu Leu Leu			
	610	615	620
Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr His Phe Gly Asn Ile Asp			
625	630	635	640
Ala Thr Pro Glu Ile Lys Glu Ile Ala His Arg Leu Thr Tyr Lys Ala			
	645	650	655
Ile His Lys Met Leu Glu Leu Glu Val Pro Asn Leu His Glu Leu Asp			
	660	665	670
Leu Asp Arg Val Ile Ala Tyr Gly His Thr Trp Ser Pro Thr Leu Glu			
	675	680	685
Leu Ala Pro Arg Leu Pro Met Phe His Gly His Ala Val Asn Val Asp			
	690	695	700
Met Ala Phe Ser Ala Thr Ile Ala Ala Arg Arg Gly Tyr Ile Thr Ile			
705	710	715	720
Ala Glu Arg Asp Arg Ile Leu Gly Leu Met Ser Arg Val Gly Leu Ser			
	725	730	735
Leu Asp His Pro Met Leu Asp Ile Asp Ile Leu Trp Arg Gly Thr Glu			
	740	745	750
Ser Ile Thr Leu Thr Arg Asp Gly Leu Leu Arg Ala Ala Met Pro Lys			
	755	760	765
Pro Ile Gly Asp Cys Val Phe Val Asn Asp Leu Thr Arg Glu Glu Leu			
	770	775	780

Ala Ala Ala Leu Ala Asp His Lys Glu Leu Cys Thr Ser Tyr Pro Arg
785 790 795 800

Gly Gly Glu Gly Val Asp Val Tyr Pro Val Tyr Gln Lys Glu Leu Ile
805 810 815

Gly Ser Val Lys Met Thr Asn Val Ile Val Gln Pro Thr Ala Arg Pro
820 825 830

Val Thr Pro Leu Gly Ile Leu Thr Lys Gln Leu Glu Ala Ile Val Gln
835 840 845

Glu Val Lys Gln His Pro Asp Leu Pro Gly Glu Leu Ile Ala Asn Ile
850 855 860

His Gln Ala Trp Arg Leu Ala Ala Gly Ile Asp Pro Tyr Leu Glu Glu
865 870 875 880

Cys Thr Thr Pro Glu Ser Pro Glu Leu Ala Ala Leu Ala Lys Thr Thr
885 890 895

Ala Thr Glu Ala Trp Gly Glu His Phe His Gly Gly Thr Thr Val Arg
900 905 910

Pro Leu Glu Gln Glu Met Leu Ser Gly His Ile Glu Gly Gln Thr Leu
915 920 925

Lys Met Phe Val His Met Thr Lys Ala Lys Lys Val Leu Glu Ile Gly
930 935 940

Met Phe Thr Gly Tyr Ser Ala Leu Ala Met Ala Glu Ala Leu Pro Glu
945 950 955 960

Asp Gly Leu Leu Val Ala Cys Glu Val Asp Pro Tyr Ala Ala Glu Ile
965 970 975

Gly Gln Lys Ala Phe Gln Gln Ser Pro His Gly Gly Lys Ile Arg Val
980 985 990

Glu Leu Asp Ala Ala Leu Ala Thr Leu Asp Lys Leu Ala Glu Ala Gly
995 1000 1005

Glu Ser Phe Asp Leu Val Phe Ile Asp Ala Asp Lys Lys Glu Tyr Val
1010 1015 1020

Ala Tyr Phe His Lys Leu Leu Gly Ser Ser Leu Leu Ala Pro Asp Gly
 1025 1030 1035 1040

Phe Ile Cys Val Asp Asn Thr Leu Leu Gln Gly Glu Val Tyr Leu Pro
 1045 1050 1055

Ala Glu Glu Arg Ser Val Asn Gly Glu Ala Ile Ala Gln Phe Asn His
 1060 1065 1070

Thr Val Ala Ile Asp Pro Arg Val Glu Gln Val Leu Leu Pro Leu Arg
 1075 1080 1085

Asp Gly Leu Thr Ile Ile Arg Arg Ile Gln Pro
 1090 1095

<210> 89

<211> 1233

<212> DNA

<213> *Anabaena variabilis* ATCC29413

<400> 89

atgagtatcg tccaagcaaa gtttgaagct aaggaaacat ctttcatgt agaaggttac	60
gaaaagattg agtatgattt ggtgtatgta gatggtattt ttgaaatcca gaattctgca	120
ctagcagatg tatatcaagg ttttggacga tgcttggcga ttgtagatgc taacgtcagt	180
cggttgtatg gtaatcaaatt tcaggcatat ttccagtatt atggtataga actgaggcta	240
tttctatta ccattactga accagataag actattcaaa ctttcgagag agttatagat	300
gtctttgcag atttcaaatt agtccgcaaa gaaccagtat tagtcgtggg tggcgggtta	360
attacagatg ttgtcggctt tgcttgttct acatatcgtc gcagcagcaa ttacatccgc	420
attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat	480
catcgcaaac tgaaaaaccg tttgggtgct tatcatgctt ctcgcaaagt attttagat	540
ttctccttgt tgcgtactct ccctacagac caagtacgta acgggatggc ggaattggta	600
aaaatcgctg tagtagcgca tcaagaagtt ttgaattgt tggagaagta cggcgaagaa	660

ttactacgta ctcattttgg caatatagat gcaactccag agattaaaga aatagcccat	720
cgtttgactt acaaagctat ccataagatg ttggaattgg aagttcccaa cctgcatgag	780
ttagacctag ataggggtgat tgcttacggg cacacttgga gtcccacctt ggaacttgcg	840
cctcgtctac ccatgttcca cggacacgcc gttaatgtag atatggcttt ctcggcaacg	900
atcgccgccc gtagaggata tattacaatt gcagaacgcg atcgtatttt aggattaatg	960
agtcgcgttg gtctatccct cgaccatccc atgttgata tagatatattt gtggcgtggt	1020
actgaatcta tcacattaac tcgtgatggg ttgttaagag ctgctatgcc aaaaccatt	1080
gggtgatttg tcttcgtcaa tgacctgaca agagaagaat tagcagccgc attagctgac	1140
cacaaagaac tttgtaccag ttatccccgt ggtggtgaag gtgtggatgt gtatcccgtt	1200
tatcaaaaag aattaatcgg gagtgtaaa taa	1233

<210> 90
 <211> 410
 <212> PRT
 <213> Anabaena variabilis ATCC29413

<400> 90
 Met Ser Ile Val Gln Ala Lys Phe Glu Ala Lys Glu Thr Ser Phe His
 1 5 10 15
 Val Glu Gly Tyr Glu Lys Ile Glu Tyr Asp Leu Val Tyr Val Asp Gly
 20 25 30
 Ile Phe Glu Ile Gln Asn Ser Ala Leu Ala Asp Val Tyr Gln Gly Phe
 35 40 45
 Gly Arg Cys Leu Ala Ile Val Asp Ala Asn Val Ser Arg Leu Tyr Gly
 50 55 60
 Asn Gln Ile Gln Ala Tyr Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu
 65 70 75 80
 Phe Pro Ile Thr Ile Thr Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu

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

Ser Arg Val Gly Leu Ser Leu Asp His Pro Met Leu Asp Ile Asp Ile
 325 330 335

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

Arg Ala Ala Met Pro Lys Pro Ile Gly Asp Cys Val Phe Val Asn Asp
 355 360 365

Leu Thr Arg Glu Glu Leu Ala Ala Ala Leu Ala Asp His Lys Glu Leu
 370 375 380

Cys Thr Ser Tyr Pro Arg Gly Gly Glu Gly Val Asp Val Tyr Pro Val
 385 390 395 400

Tyr Gln Lys Glu Leu Ile Gly Ser Val Lys
 405 410

<210> 91

<211> 840

<212> DNA

<213> *Anabaena variabilis* ATCC29413

<400> 91

ttgacaaatg tgattgtcca accaacagct agacctgtta caccattggg aattttaacc	60
aagcagttag aagccatagt ccaagaggtt aagcaacatc cagatttacc tggggaattg	120
atagcaaaca tccatcaggc ttggcgttta gccgcaggta tagaccctta ttggaagaa	180
tgcaccactc cagaatctcc tgaactcgct gcattggcaa aaaccacagc caccgaagcc	240
tggggagaac acttcacgg aggtacaacc gtccgtctc tagaacaaga gatgctttct	300
ggtcatatcg aaggacaaac cttaaagatg ttgttcaca tgaccaaagc taaaaaagtc	360
ttagaaattg ggatgtttac cggttattcg gcgctggcga tggcggaagc attaccagag	420
gatggactgc ttgtggcttg tgaagttgac cttacgcgg cggaattgg acagaaagcc	480
tttcaacaat ctccccacgg tggaagatt cgtgtggaat tggatgcagc ctagcaact	540
cttgataagt tagcagaagc tggggagtct ttgacttgg tatttatcga cgcagataaa	600

aaagagtatg tagcctatTT tcacaagttg ctaggtagca gtttgtagc accagatggc	660
tttatttgTg tagataacac cttattacaa ggggaagttt atctaccagc agaggaacgt	720
agcgtcaatg gtgaagcgat cgcgcaattt aatcatacag tagctataga cccccgtgta	780
gaacagggttT tgttgccgtt gcgagatggT ttaacaatta tccgcagaat acaaccttaa	840

840

<210> 92
 <211> 410
 <212> PRT
 <213> *Anabaena variabilis* ATCC29413

<400> 92
 Met Ser Ile Val Gln Ala Lys Phe Glu Ala Lys Glu Thr Ser Phe His
 1 5 10 15

Val Glu Gly Tyr Glu Lys Ile Glu Tyr Asp Leu Val Tyr Val Asp Gly
 20 25 30

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

Gly Arg Cys Leu Ala Ile Val Asp Ala Asn Val Ser Arg Leu Tyr Gly
 50 55 60

Asn Gln Ile Gln Ala Tyr Phe Gln Tyr Tyr Gly Ile Glu Leu Arg Leu
 65 70 75 80

Phe Pro Ile Thr Ile Thr Glu Pro Asp Lys Thr Ile Gln Thr Phe Glu
 85 90 95

Arg Val Ile Asp Val Phe Ala Asp Phe Lys Leu Val Arg Lys Glu Pro
 100 105 110

Val Leu Val Val Gly Gly Gly Leu Ile Thr Asp Val Val Gly Phe Ala
 115 120 125

Cys Ser Thr Tyr Arg Arg Ser Ser Asn Tyr Ile Arg Ile Pro Thr Thr
 130 135 140

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

His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Ser Arg Lys
165 170 175

Val Phe Leu Asp Phe Ser Leu Leu Arg Thr Leu Pro Thr Asp Gln Val
180 185 190

Arg Asn Gly Met Ala Glu Leu Val Lys Ile Ala Val Val Ala His Gln
195 200 205

Glu Val Phe Glu Leu Leu Glu Lys Tyr Gly Glu Glu Leu Leu Arg Thr
210 215 220

His Phe Gly Asn Ile Asp Ala Thr Pro Glu Ile Lys Glu Ile Ala His
225 230 235 240

Arg Leu Thr Tyr Lys Ala Ile His Lys Met Leu Glu Leu Glu Val Pro
245 250 255

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

Trp Ser Pro Thr Leu Glu Leu Ala Pro Arg Leu Pro Met Phe His Gly
275 280 285

His Ala Val Asn Val Asp Met Ala Phe Ser Ala Thr Ile Ala Ala Arg
290 295 300

Arg Gly Tyr Ile Thr Ile Ala Glu Arg Asp Arg Ile Leu Gly Leu Met
305 310 315 320

Ser Arg Val Gly Leu Ser Leu Asp His Pro Met Leu Asp Ile Asp Ile
325 330 335

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

Arg Ala Ala Met Pro Lys Pro Ile Gly Asp Cys Val Phe Val Asn Asp
355 360 365

Leu Thr Arg Glu Glu Leu Ala Ala Ala Leu Ala Asp His Lys Glu Leu

370	375	380	
Cys Thr Ser Tyr Pro Arg Gly Gly Glu Gly Val Asp Val Tyr Pro Val			
385	390	395	400
Tyr Gln Lys Glu Leu Ile Gly Ser Val Lys			
	405	410	

<210> 93
 <211> 840
 <212> DNA
 <213> *Anabaena variabilis* ATCC29413

<400> 93

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aagcagttag aagccatagt ccaagagggt aagcaacatc cagatttacc tggggaattg	120
atagcaaaca tccatcaggc ttggcggtta gccgcaggta tagaccctta ttggaagaa	180
tgcaccactc cagaatctcc tgaactcgct gcattggcaa aaaccacagc caccgaagcc	240
tggggagaac acttcacgg aggtacaacc gtccgtctc tagaacaaga gatgctttct	300
ggtcatatcg aaggacaaac cttaaagatg ttgttcaca tgaccaaagc taaaaaagtc	360
ttagaaattg ggatgtttac cggttattcg gcgctggcga tggcggaagc attaccagag	420
gatggactgc ttgtggcttg tgaagttgac cttacgcgg cggaattgg acagaaagcc	480
tttaacaat ctccccacgg tggaagatt cgtgtggaat tggatgcagc ctagcaact	540
cttgataagt tagcagaagc tggggagtct ttgacttgg tatttatcga cgcagataaa	600
aaagagtatg tagcctattt tcacaagttg ctaggtagca gtttgtagc accagatggc	660
tttatttgtag tagataacac cttattacaa ggggaagttt atctaccagc agaggaacgt	720
agcgtcaatg gtgaagcgat cgcgcaattt aatcatacag tagctataga ccccgtgta	780
gaacagggtt ttgtgccgtt gcgagatggt ttaacaatta tccgcagaat acaaccttaa	840

840

<210> 94
 <211> 279
 <212> PRT
 <213> *Anabaena variabilis* ATCC29413

<400> 94

Met Thr Asn Val Ile Val Gln Pro Thr Ala Arg Pro Val Thr Pro Leu
 1 5 10 15

Gly Ile Leu Thr Lys Gln Leu Glu Ala Ile Val Gln Glu Val Lys Gln
 20 25 30

His Pro Asp Leu Pro Gly Glu Leu Ile Ala Asn Ile His Gln Ala Trp
 35 40 45

Arg Leu Ala Ala Gly Ile Asp Pro Tyr Leu Glu Glu Cys Thr Thr Pro
 50 55 60

Glu Ser Pro Glu Leu Ala Ala Leu Ala Lys Thr Thr Ala Thr Glu Ala
 65 70 75 80

Trp Gly Glu His Phe His Gly Gly Thr Thr Val Arg Pro Leu Glu Gln
 85 90 95

Glu Met Leu Ser Gly His Ile Glu Gly Gln Thr Leu Lys Met Phe Val
 100 105 110

His Met Thr Lys Ala Lys Lys Val Leu Glu Ile Gly Met Phe Thr Gly
 115 120 125

Tyr Ser Ala Leu Ala Met Ala Glu Ala Leu Pro Glu Asp Gly Leu Leu
 130 135 140

Val Ala Cys Glu Val Asp Pro Tyr Ala Ala Glu Ile Gly Gln Lys Ala
 145 150 155 160

Phe Gln Gln Ser Pro His Gly Gly Lys Ile Arg Val Glu Leu Asp Ala
 165 170 175

Ala Leu Ala Thr Leu Asp Lys Leu Ala Glu Ala Gly Glu Ser Phe Asp
 180 185 190

Leu Val Phe Ile Asp Ala Asp Lys Lys Glu Tyr Val Ala Tyr Phe His
 195 200 205

Lys Leu Leu Gly Ser Ser Leu Leu Ala Pro Asp Gly Phe Ile Cys Val
 210 215 220

Asp Asn Thr Leu Leu Gln Gly Glu Val Tyr Leu Pro Ala Glu Glu Arg
 225 230 235 240

Ser Val Asn Gly Glu Ala Ile Ala Gln Phe Asn His Thr Val Ala Ile
 245 250 255

Asp Pro Arg Val Glu Gln Val Leu Leu Pro Leu Arg Asp Gly Leu Thr
 260 265 270

Ile Ile Arg Arg Ile Gln Pro
 275

<210> 95

<211> 2667

<212> DNA

<213> *Anabaena variabilis* ATCC29413

<400> 95

atgcagacta tagatttta tattcgttag ttactgttag agtggaacgc gaccacaga	60
gattatgatc tttccagag ttacatgaa ctaattgttag ctcaagtaga acgaacacct	120
gaggcgatcg ctgtcacctt tgacaagcaa caactaactt atcaagaact aaatcataaa	180
gcaaaccagc taggacatta ttacaaaca ttaggagtcc agccagaaac cctggtaggc	240
gtttgttag aacgttcctt agaaatgggt atctgtcttt taggaatcct caaagctggg	300
ggtgcttatg ttctattga cctgaatat cctcaagaac gcatagctta tatgctagaa	360
gattctcagg tgaagggtact actaactcaa gaaaaattac tcaatcaa tccccaccat	420
caagcacaaa ctatctgtgt agatagggaa tgggagaaaa ttccacaca agctaatacc	480
aatcccaaaa gtaatatata aacggataat ctgcttatg taatttacac ctctggttcc	540
actggtaaac caaaagggtgc aatgaacacc cacaaaggta tctgtaatcg cttattgtgg	600

atgcaggaag cttatcaaat cgattccaca gatagcattt tacaaaaaac ccccttagt	660
tttgatgttt ccgttggga gttcttttg actttattaa ctggcgcacg ttggtaata	720
gccaaaccag gcggacataa agatagtgt tacctcatcg atttaattac tcaagaacaa	780
atcactacgt tgcattttgt cccctcaatg ctgcaagtgt tttacaaaa tcgcatgta	840
agcaaagca gctctctaaa aagagttatt ttagcgggtg aagctttatc tatagattta	900
caaaatagat tttccagca ttgcaatgt gaattacata acctctatgg cccgacagaa	960
gcagcaattg atgtcacatt ttggcaatgt agaaaagata gtaatttaaa gagtgtacct	1020
attggctgct ccattgctaa tactcaaatt tatattcttg atgccgattt acaaccagta	1080
aatttggtg tctctggtga aatttatatt ggtgggtgtag ggggtgctcg tggttattg	1140
aataaagaag aattgaccaa agaaaaattt attattaatc cctttcccaa ttctgagttt	1200
aagcgacttt ataaaacagg tgatttagct cgttatttac ccgatggaaa tattgaatat	1260
cttggtagaa cagattatca agtaaaaatt cgggggtata gaattgaaat tggcgagatt	1320
gaaaatgttt tatcttcaca cccacaagtc agagaagctg tagtcatagc gcgggatgat	1380
aacgtcaag aaaaacaaat catcgcttat attacctata actccatcaa acctcagctt	1440
gataatctgc gtgatttcct aaaagcaagg ctacctgatt ttatgattcc agccgctttt	1500
gtgatgctgg agcatcttcc ttaactccc agtggttaaag tagaccgtaa ggcattacct	1560
aagcctgatt tatttaatta tagtgaacat aattcctatg tagcgctcga gaatgaagtt	1620
gaagaaaaat tagtacaaat ctggtcgaat attctgcatt tacctaaagt aggtgtgaca	1680
gaaaactttt tcgctattgg tggttaattcc ctcaaagctc tacatttaatt ttctcaaatt	1740
gaagagttat ttgctaaaga gatatcctta gcaacacttt taacaaatcc agtaattgca	1800
gatttagcca aggttattca agcaaacaac caaatccata attcaccctt agttccaatt	1860
caaccacaag gtaagcagca gcctttcttt tgtatacatc ctgctgggtg tcatgtttta	1920

tgctatttta aactcgcaaca atatatagga actgaccaac cattttatgg cttacaagct 1980
 caaggatttt atggagatga agcacccttg acgcgagttg aagatatggc tagtctctac 2040
 gtcaaaacta ttagagaatt tcaaccccaa gggccttatc gtgtcggggg gtggtcattt 2100
 ggtggagtcg tagcttatga agtagcacag cagttacata gacaaggaca agaagtatct 2160
 ttactagcaa tattagattc ttacgtaccg attctgctgg ataaacaaaa acccattgat 2220
 gacgtttatt tagttggtgt tctctccaga gttttggcg gtatgtttgg tcaagataat 2280
 ctagtcacac ctgaagaaat agaaaattta actgtagaag aaaaaattaa ttacatcatt 2340
 gataaagcac ggagcgctag aatattcccg cctgggtgtag aacgtcaaaa taatcgccgt 2400
 attcttgatg ttttggtggg aactttaaaa gcaacttatt cctatataag acaaccatat 2460
 ccaggaaaag tcactgtatt tcgagccagg gaaaaacata ttatggctcc tgacccgacc 2520
 ttagtttggg tagaattatt ttctgtaatg gcggctcaag aaattaagat tattgatgtc 2580
 cctggaaacc attattcggt tgttctagaa ccccatgtac aggttttagc acagcgttta 2640
 caagattgtc tggaaaataa ttcataa 2667

<210> 96
 <211> 888
 <212> PRT
 <213> *Anabaena variabilis* ATCC29413

<400> 96
 Met Gln Thr Ile Asp Phe Asn Ile Arg Lys Leu Leu Val Glu Trp Asn
 1 5 10 15
 Ala Thr His Arg Asp Tyr Asp Leu Ser Gln Ser Leu His Glu Leu Ile
 20 25 30
 Val Ala Gln Val Glu Arg Thr Pro Glu Ala Ile Ala Val Thr Phe Asp
 35 40 45
 Lys Gln Gln Leu Thr Tyr Gln Glu Leu Asn His Lys Ala Asn Gln Leu

50	55	60			
Gly	His	Tyr	Leu	Gln	Thr
65	70	75	80		
Val	Cys	Leu	Glu	Arg	Ser
	85	90	95		
Leu	Lys	Ala	Gly	Gly	Ala
100	105	110			
Glu	Arg	Ile	Ala	Tyr	Met
115	120	125			
Thr	Gln	Glu	Lys	Leu	Leu
130	135	140			
Ile	Cys	Val	Asp	Arg	Glu
145	150	155	160		
Asn	Pro	Lys	Ser	Asn	Ile
165	170	175			
Thr	Ser	Gly	Ser	Thr	Gly
180	185	190			
Gly	Ile	Cys	Asn	Arg	Leu
195	200	205			
Ser	Thr	Asp	Ser	Ile	Leu
210	215	220			
Val	Trp	Glu	Phe	Phe	Trp
225	230	235	240		
Ala	Lys	Pro	Gly	Gly	His
245	250	255			
Thr	Gln	Glu	Gln	Ile	Thr
260	265	270			
Val	Phe	Leu	Gln	Asn	Arg
275	280	285			

Val Ile Cys Ser Gly Glu Ala Leu Ser Ile Asp Leu Gln Asn Arg Phe
290 295 300

Phe Gln His Leu Gln Cys Glu Leu His Asn Leu Tyr Gly Pro Thr Glu
305 310 315 320

Ala Ala Ile Asp Val Thr Phe Trp Gln Cys Arg Lys Asp Ser Asn Leu
325 330 335

Lys Ser Val Pro Ile Gly Arg Pro Ile Ala Asn Thr Gln Ile Tyr Ile
340 345 350

Leu Asp Ala Asp Leu Gln Pro Val Asn Ile Gly Val Thr Gly Glu Ile
355 360 365

Tyr Ile Gly Gly Val Gly Val Ala Arg Gly Tyr Leu Asn Lys Glu Glu
370 375 380

Leu Thr Lys Glu Lys Phe Ile Ile Asn Pro Phe Pro Asn Ser Glu Phe
385 390 395 400

Lys Arg Leu Tyr Lys Thr Gly Asp Leu Ala Arg Tyr Leu Pro Asp Gly
405 410 415

Asn Ile Glu Tyr Leu Gly Arg Thr Asp Tyr Gln Val Lys Ile Arg Gly
420 425 430

Tyr Arg Ile Glu Ile Gly Glu Ile Glu Asn Val Leu Ser Ser His Pro
435 440 445

Gln Val Arg Glu Ala Val Val Ile Ala Arg Asp Asp Asn Ala Gln Glu
450 455 460

Lys Gln Ile Ile Ala Tyr Ile Thr Tyr Asn Ser Ile Lys Pro Gln Leu
465 470 475 480

Asp Asn Leu Arg Asp Phe Leu Lys Ala Arg Leu Pro Asp Phe Met Ile
485 490 495

Pro Ala Ala Phe Val Met Leu Glu His Leu Pro Leu Thr Pro Ser Gly
500 505 510

Lys Val Asp Arg Lys Ala Leu Pro Lys Pro Asp Leu Phe Asn Tyr Ser
515 520 525

Glu His Asn Ser Tyr Val Ala Pro Arg Asn Glu Val Glu Glu Lys Leu
530 535 540

Val Gln Ile Trp Ser Asn Ile Leu His Leu Pro Lys Val Gly Val Thr
545 550 555 560

Glu Asn Phe Phe Ala Ile Gly Gly Asn Ser Leu Lys Ala Leu His Leu
565 570 575

Ile Ser Gln Ile Glu Glu Leu Phe Ala Lys Glu Ile Ser Leu Ala Thr
580 585 590

Leu Leu Thr Asn Pro Val Ile Ala Asp Leu Ala Lys Val Ile Gln Ala
595 600 605

Asn Asn Gln Ile His Asn Ser Pro Leu Val Pro Ile Gln Pro Gln Gly
610 615 620

Lys Gln Gln Pro Phe Phe Cys Ile His Pro Ala Gly Gly His Val Leu
625 630 635 640

Cys Tyr Phe Lys Leu Ala Gln Tyr Ile Gly Thr Asp Gln Pro Phe Tyr
645 650 655

Gly Leu Gln Ala Gln Gly Phe Tyr Gly Asp Glu Ala Pro Leu Thr Arg
660 665 670

Val Glu Asp Met Ala Ser Leu Tyr Val Lys Thr Ile Arg Glu Phe Gln
675 680 685

Pro Gln Gly Pro Tyr Arg Val Gly Gly Trp Ser Phe Gly Gly Val Val
690 695 700

Ala Tyr Glu Val Ala Gln Gln Leu His Arg Gln Gly Gln Glu Val Ser
705 710 715 720

Leu Leu Ala Ile Leu Asp Ser Tyr Val Pro Ile Leu Leu Asp Lys Gln
725 730 735

Lys Pro Ile Asp Asp Val Tyr Leu Val Gly Val Leu Ser Arg Val Phe
740 745 750

Gly Gly Met Phe Gly Gln Asp Asn Leu Val Thr Pro Glu Glu Ile Glu

755 760 765
 Asn Leu Thr Val Glu Glu Lys Ile Asn Tyr Ile Ile Asp Lys Ala Arg
 770 775 780
 Ser Ala Arg Ile Phe Pro Pro Gly Val Glu Arg Gln Asn Asn Arg Arg
 785 790 795 800
 Ile Leu Asp Val Leu Val Gly Thr Leu Lys Ala Thr Tyr Ser Tyr Ile
 805 810 815
 Arg Gln Pro Tyr Pro Gly Lys Val Thr Val Phe Arg Ala Arg Glu Lys
 820 825 830
 His Ile Met Ala Pro Asp Pro Thr Leu Val Trp Val Glu Leu Phe Ser
 835 840 845
 Val Met Ala Ala Gln Glu Ile Lys Ile Ile Asp Val Pro Gly Asn His
 850 855 860
 Tyr Ser Phe Val Leu Glu Pro His Val Gln Val Leu Ala Gln Arg Leu
 865 870 875 880
 Gln Asp Cys Leu Glu Asn Asn Ser
 885

<210> 97
 <211> 1233
 <212> DNA
 <213> Nostoc punctiforme ATCC29133

<400> 97
 atgagtaatg ttcaagcatc gtttgaagca acggaagctg aattccgcgt ggaaggttac 60
 gaaaaaattg agtttagtct tgtctatgta aatggtgcat ttgatatcag taacagagaa 120
 attgcagaca gctatgagaa gtttggccgt tgtctgactg tgattgatgc taatgtcaac 180
 agattatatg gcaagcaa at caagtcatat ttagacact atggattatga tctgaccgta 240
 gttcccattg tgattactga gcctactaaa acccttgcaa cctttgagaa aattgttgat 300
 gcttttctg actttggttt aatccgcaag gaaccagtat tagtagtggg tgggtggtta 360

accactgatg tagctgggtt tgcgtgtgct gcttaccgtc gtaagagtaa ctatattcgg	420
gttccgacaa cgctgattgg tctgattgat gcaggtgtag cgattaaggt tgcagtcaac	480
catcgcaagt taaaaaatcg cttgggtgca tatcatgctc ctttgaaagt catcctcgat	540
ttctccttct tgcaaacatt accaacggct caagttcgta atgggatggc agagttggtc	600
aaaattgctg ttgtggcgaa ctctgaagtc tttgaattgt tgtatgaata tggcgaagag	660
ttgctttcca ctactttgg atatgtgaat ggtacaaagg aactgaaagc gatcgacat	720
aaactcaatt acgaggcaat aaaaactatg ctggagttgg aaactccaaa ctgcatgag	780
ttagacctcg atcgcgcat tgcctacggg cacacttggg gtccgacctt agaattagct	840
ccgatgatac cgttgttca cggatcatgcc gtcaatatag acatggcttt gtctgcaact	900
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agtcgtatag gtttatcaat cgatcatcct ctactagatg gcgatttgct ctggtatgct	1020
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ggtgagtgct tctttgtcaa cgatttcacc cgtgaagaac tagatgcagc ttagctgaa	1140
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<210> 98

<211> 410

<212> PRT

<213> Nostoc punctiforme ATCC29133

<400> 98

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5

10

15

Val Glu Gly Tyr Glu Lys Ile Glu Phe Ser Leu Val Tyr Val Asn Gly

20

25

30

Ala Phe Asp Ile Ser Asn Arg Glu Ile Ala Asp Ser Tyr Glu Lys Phe
35 40 45

Gly Arg Cys Leu Thr Val Ile Asp Ala Asn Val Asn Arg Leu Tyr Gly
50 55 60

Lys Gln Ile Lys Ser Tyr Phe Arg His Tyr Gly Ile Asp Leu Thr Val
65 70 75 80

Val Pro Ile Val Ile Thr Glu Pro Thr Lys Thr Leu Ala Thr Phe Glu
85 90 95

Lys Ile Val Asp Ala Phe Ser Asp Phe Gly Leu Ile Arg Lys Glu Pro
100 105 110

Val Leu Val Val Gly Gly Gly Leu Thr Thr Asp Val Ala Gly Phe Ala
115 120 125

Cys Ala Ala Tyr Arg Arg Lys Ser Asn Tyr Ile Arg Val Pro Thr Thr
130 135 140

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

His Arg Lys Leu Lys Asn Arg Leu Gly Ala Tyr His Ala Pro Leu Lys
165 170 175

Val Ile Leu Asp Phe Ser Phe Leu Gln Thr Leu Pro Thr Ala Gln Val
180 185 190

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

Glu Val Phe Glu Leu Leu Tyr Glu Tyr Gly Glu Glu Leu Leu Ser Thr
210 215 220

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

Lys Leu Asn Tyr Glu Ala Ile Lys Thr Met Leu Glu Leu Glu Thr Pro
245 250 255

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

Trp Ser Pro Thr Leu Glu Leu Ala Pro Met Ile Pro Leu Phe His Gly
 275 280 285

His Ala Val Asn Ile Asp Met Ala Leu Ser Ala Thr Ile Ala Ala Arg
 290 295 300

Arg Gly Tyr Ile Thr Ser Gly Glu Arg Asp Arg Ile Leu Ser Leu Met
 305 310 315 320

Ser Arg Ile Gly Leu Ser Ile Asp His Pro Leu Leu Asp Gly Asp Leu
 325 330 335

Leu Trp Tyr Ala Thr Gln Ser Ile Ser Leu Thr Arg Asp Gly Lys Gln
 340 345 350

Arg Ala Ala Met Pro Lys Pro Ile Gly Glu Cys Phe Phe Val Asn Asp
 355 360 365

Phe Thr Arg Glu Glu Leu Asp Ala Ala Leu Ala Glu His Lys Arg Leu
 370 375 380

Cys Ala Thr Tyr Pro Arg Gly Gly Asp Gly Ile Asp Ala Tyr Ile Glu
 385 390 395 400

Thr Gln Glu Glu Ser Lys Leu Leu Gly Val
 405 410

<210> 99

<211> 834

<212> DNA

<213> Nostoc punctiforme ATCC29133

<400> 99

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gcacagctac aaaaaaccct cagaatggca gaggaaagta atattccttc agagatactg 120

acttctctgc gccaaagggtt gcaattagca gcagggttag atccctatct ggatgattgc 180

actaccctg aatcgaccgc attgacagca ctagcgcaga agacaagcat tgaagactgg 240

agtaaaccgt tcagtgatgg tgaaacagtg cgtcaattag agcaagaaat gctctcagga 300

catcttgaag gacaaacact aaagatgttt gtgcatatca ctaaggctaa aagcatccta	360
gaagtgggaa tgttcacagg atattcagct ttggcaatgg cagaggcggt accagatgat	420
gggcgactga ttgcttgtga agtagactcc tatgtggccg agtttgctca aacttgcttt	480
caagagtctc cccacggccg caagattggt gtagaagtgg cacctgcact agagacgctg	540
cacaagctgg tggctaaaaa agaatccttt gatctgatct tcattgatgc ggataaaaag	600
gagtatatag aatacttcca aattatcttg gatagccatt tactagctcc cgacggatta	660
atctgtgtag ataatacttt gttgcaagga caagtttacc tgccatcaga acagcgtaca	720
gccaatgggtg aagcgatcgc tcaattcaac cgcattgtcg cgcagatcc tcgtgtagag	780
caagttctgt tacccatacg agatgggata accctgatta gacgcttggt ataa	834

<210> 100
 <211> 277
 <212> PRT
 <213> Nostoc punctiforme ATCC29133

<400> 100
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 Ser Ile Leu Val Ala Gln Leu Gln Lys Thr Leu Arg Met Ala Glu Glu
 20 25 30

 Ser Asn Ile Pro Ser Glu Ile Leu Thr Ser Leu Arg Gln Gly Leu Gln
 35 40 45

 Leu Ala Ala Gly Leu Asp Pro Tyr Leu Asp Asp Cys Thr Thr Pro Glu
 50 55 60

 Ser Thr Ala Leu Thr Ala Leu Ala Gln Lys Thr Ser Ile Glu Asp Trp
 65 70 75 80

 Ser Lys Arg Phe Ser Asp Gly Glu Thr Val Arg Gln Leu Glu Gln Glu
 85 90 95

Met Leu Ser Gly His Leu Glu Gly Gln Thr Leu Lys Met Phe Val His
 100 105 110

Ile Thr Lys Ala Lys Ser Ile Leu Glu Val Gly Met Phe Thr Gly Tyr
 115 120 125

Ser Ala Leu Ala Met Ala Glu Ala Leu Pro Asp Asp Gly Arg Leu Ile
 130 135 140

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

Gln Glu Ser Pro His Gly Arg Lys Ile Val Val Glu Val Ala Pro Ala
 165 170 175

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

Ile Phe Ile Asp Ala Asp Lys Lys Glu Tyr Ile Glu Tyr Phe Gln Ile
 195 200 205

Ile Leu Asp Ser His Leu Leu Ala Pro Asp Gly Leu Ile Cys Val Asp
 210 215 220

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

Ala Asn Gly Glu Ala Ile Ala Gln Phe Asn Arg Ile Val Ala Ala Asp
 245 250 255

Pro Arg Val Glu Gln Val Leu Leu Pro Ile Arg Asp Gly Ile Thr Leu
 260 265 270

Ile Arg Arg Leu Val
 275

<210> 101

<211> 1386

<212> DNA

<213> Nostoc punctiforme ATCC29133

<400> 101

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ctaaaaatag cagctctact gaagactatc gggactctaa tactactgct gatagccttg	120
ccgcttaatg ctttgatagt attgatatct ctgatgtgta ggccgtttac aaaaaaacct	180
gccgtagcca ctcatcccca gaatatcttg gtcagtggcg gcaaaatgac caaagcattg	240
caacttgccc gtccttcca tgcagccgga cacagagtta ttctgattga aggtcataaa	300
tactggttat cagggcatag attctcaaat tctgtgagtc gttttatac agttcctgca	360
ccacaagacg acccagaagg ctatacccaa gcgctattgg aaattgtcaa acgagagaag	420
attgacgttt atgtaccctg atgcagccct gtagctagtt attacgactc ttggcaaag	480
tctgcactat cagaatattg tgaggttttt cacttgatg ctgatataac caagatgctg	540
gatgataaat ttgcctttac cgatcgggcg cgatcgcttg gtttatcagc cccgaaatct	600
tttaaaatta ccgatcctga acaagttatc aacttcgatt ttagtaaaga gacgcgcaaa	660
tatattctta agagtatttc ttacgactca gttcgccgct taaatttaac caaacttct	720
tgtgataccc cagaagagac agcagcgttt gtcaagagtt taccatcag cccagaaaaa	780
ccttggatta tgcaagaatt tattctggg aaagaattat gcacccatag cacagtccga	840
gacggcgaat taagggtgca ttgctgttca aattcttcag cgtttcagat taactatgaa	900
aatgtcgaaa atcccaaatt tcaagaatgg gtacaacatt tcgtcaaaag ttacggctg	960
actggacaaa tatctcttga ctttatccaa gctgaagatg gtacagctta tgccattgaa	1020
tgtaatcctc gcaccattc ggcgatcaca atgttctaca atcaccaggg tgttgagaa	1080
gcctatcttg gtaaaactcc tctagctgca ccttgggaac ctctgcaga tagcaagccc	1140
acttactgga tatatcacga aatctggcga ttgactggga ttcgctctgg acaacaatta	1200
caaacttggg ttgggagatt agtcagaggt acagatgcca tttatcgctt ggacgatccg	1260
ataccatttt taactttgca ccattggcag attactttac ttttgctaca aaatttgcaa	1320
cgactcaaag gttgggtaaa gatcgatttt aatatcggtg aactcgtgga attagggggc	1380

gactaa

1386

<210> 102

<211> 461

<212> PRT

<213> Nostoc punctiforme ATCC29133

<400> 102

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Lys Gly Val Arg Leu Lys Ile Ala Ala Leu Leu Lys Thr Ile Gly Thr
20 25 30

Leu Ile Leu Leu Leu Ile Ala Leu Pro Leu Asn Ala Leu Ile Val Leu
35 40 45

Ile Ser Leu Met Cys Arg Pro Phe Thr Lys Lys Pro Ala Val Ala Thr
50 55 60

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

Gln Leu Ala Arg Ser Phe His Ala Ala Gly His Arg Val Ile Leu Ile
85 90 95

Glu Gly His Lys Tyr Trp Leu Ser Gly His Arg Phe Ser Asn Ser Val
100 105 110

Ser Arg Phe Tyr Thr Val Pro Ala Pro Gln Asp Asp Pro Glu Gly Tyr
115 120 125

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

Val Pro Val Cys Ser Pro Val Ala Ser Tyr Tyr Asp Ser Leu Ala Lys
145 150 155 160

Ser Ala Leu Ser Glu Tyr Cys Glu Val Phe His Phe Asp Ala Asp Ile
165 170 175

Thr Lys Met Leu Asp Asp Lys Phe Ala Phe Thr Asp Arg Ala Arg Ser

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

Leu Asp Asp Pro Ile Pro Phe Leu Thr Leu His His Trp Gln Ile Thr
 420 425 430

Leu Leu Leu Leu Gln Asn Leu Gln Arg Leu Lys Gly Trp Val Lys Ile
 435 440 445

Asp Phe Asn Ile Gly Lys Leu Val Glu Leu Gly Gly Asp
 450 455 460

<210> 103

<211> 1047

<212> DNA

<213> Nostoc punctiforme ATCC29133

<400> 103

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tttcaaattg catatatcac acccgatcgg cagtggcgat ttctgactc tctcagtcga	180
gaagatatgg ctcttaccaa accgattcct gtgtttgatg ccatacaatt tctaacaggc	240
caaacattg acatgatgtt accacaaatg tttgtattc ctggaatgac tcagtaccgt	300
gccctattcg atctgctcaa gatcccttat ataggaaata cccagatat tatggcgatc	360
gcggcccaca aagccagagc caaagcaatt gtcgaagcag caggggtaaa agtgcctcgt	420
ggagaattgc ttcgccaagg agatattcca acaattacac ctccagcagt cgtcaaacct	480
gtaagtctg acaactctt aggagtagtc ttagttaaag atgtgactga atatgatgct	540
gccttaaaga aagcattga atatgcttcg gaggtcatcg tagaagcatt catcgaactt	600
ggtcgagaag tcagatgcgg catcattgta aaagacggtg agctaataagg ttaccctt	660
gaagagtatc tggtagaccc acacgataaa cctatccgta actatgctga taaactcaa	720
caaactgacg atggcgactt gcatttgact gctaaagata atatcaaggc ttggatttta	780
gaccctaacg acccaatcac ccaaaagggt cagcaagtgg ctaaaagggtg tcatcaggct	840

ttgggtgtgc gccactacag ttatttgac ttccgaatcg atccaaaggg acaaccttgg 900
 ttcttagaag ctggattata ttgttctttt gcccccaaaa gtgtgatttc ttctatggcg 960
 aaagcagccg gaatccctct aatgattta ttaataaccg ctattaatga aacattgggt 1020
 agtaataaaa aggtgttaca aaattga 1047

<210> 104
 <211> 348
 <212> PRT
 <213> Nostoc punctiforme ATCC29133

<400> 104
 Met Pro Val Leu Asn Ile Leu His Leu Val Gly Ser Ala His Asp Lys
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 Phe Tyr Cys Asp Leu Ser Arg Leu Tyr Ala Gln Asp Cys Leu Ala Ala
 20 25 30
 Thr Ala Asp Pro Ser Leu Tyr Asn Phe Gln Ile Ala Tyr Ile Thr Pro
 35 40 45
 Asp Arg Gln Trp Arg Phe Pro Asp Ser Leu Ser Arg Glu Asp Ile Ala
 50 55 60
 Leu Thr Lys Pro Ile Pro Val Phe Asp Ala Ile Gln Phe Leu Thr Gly
 65 70 75 80
 Gln Asn Ile Asp Met Met Leu Pro Gln Met Phe Cys Ile Pro Gly Met
 85 90 95
 Thr Gln Tyr Arg Ala Leu Phe Asp Leu Leu Lys Ile Pro Tyr Ile Gly
 100 105 110
 Asn Thr Pro Asp Ile Met Ala Ile Ala Ala His Lys Ala Arg Ala Lys
 115 120 125
 Ala Ile Val Glu Ala Ala Gly Val Lys Val Pro Arg Gly Glu Leu Leu
 130 135 140
 Arg Gln Gly Asp Ile Pro Thr Ile Thr Pro Pro Ala Val Val Lys Pro
 145 150 155 160

Val Ser Ser Asp Asn Ser Leu Gly Val Val Leu Val Lys Asp Val Thr
165 170 175

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

Ile Val Glu Ala Phe Ile Glu Leu Gly Arg Glu Val Arg Cys Gly Ile
195 200 205

Ile Val Lys Asp Gly Glu Leu Ile Gly Leu Pro Leu Glu Glu Tyr Leu
210 215 220

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

Gln Thr Asp Asp Gly Asp Leu His Leu Thr Ala Lys Asp Asn Ile Lys
245 250 255

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

Val Ala Lys Arg Cys His Gln Ala Leu Gly Cys Arg His Tyr Ser Leu
275 280 285

Phe Asp Phe Arg Ile Asp Pro Lys Gly Gln Pro Trp Phe Leu Glu Ala
290 295 300

Gly Leu Tyr Cys Ser Phe Ala Pro Lys Ser Val Ile Ser Ser Met Ala
305 310 315 320

Lys Ala Ala Gly Ile Pro Leu Asn Asp Leu Leu Ile Thr Ala Ile Asn
325 330 335

Glu Thr Leu Gly Ser Asn Lys Lys Val Leu Gln Asn
340 345