

<110> CJ CheilJedang Corporation

<120> A microorganism producing a Mycosporine-like amino acid and a
method for producing a Mycosporine-like amino acid using the same

<130> OPA18547-PCT

<150> KR10-2018-0022185

<151> 2018-02-23

<160> 124

<170> KoPatentIn 3.0

<210> 1

<211> 1053

<212> DNA

<213> Escherichia coli W3110

<400> 1

atgaattatc agaacgacga ttacgcatc aaagaaatca aagagttact tcctcctgtc 60

gcattgctgg aaaaattccc cgctactgaa aatgccgcga atacggttgc ccatgcccga 120

aaagcgatcc ataagatcct gaaaggaat gatgatcgcc tgttggttgt gattggccca 180

tgctcaattc atgatcctgt cgcggaacaaa gagtatgcca ctcgcttgc ggcgctgcgt 240

gaagagctga aagatgagct ggaaatcgta atgcgcgtct atttgaaaa gccgcgtacc	300
acggtgggct ggaaagggt gattaacgat ccgcatatgg ataatagctt ccagatcaac	360
gacggtctgc gtatagcccg taaattgctg ctgatatta acgacagcgg tctgccagcg	420
gcaggtgagt ttctgatat gatcacccca caatatctcg ctgacctgat gagctggggc	480
gcaattggcg caggtaccac cgaatcgag gtgcaccgag aactggcatc agggctttct	540
tgtccggtcg gcttcaaaaa tggcaccgac ggtacgatta aagtggctat cgatgccatt	600
aatgccgccg gtgcgccgca ctgctcctg tccgtaacga aatgggggca ttcggcgatt	660
gtgaatacca gcgtaacgg cgattgcat atcattctgc gcggcggtaa agagcctaac	720
tacagcgca agcacgttc tgaagtgaaa gaagggtga acaaagcagg cctgccagca	780
caggtgatga tcgatttcag ccattgtaac tcgtcaaac aattcaaaaa gcagatggat	840
gtttgtctg acgttgcca gcagattgcc ggtggcgaaa aggccattat tggcgtgatg	900
gtggaaagcc atctggtgga aggcaatcag agcctcgaga gcggggagcc gctggcctac	960
ggtaagagca tcaccgatgc ctgcatcggc tgggaagata ccgatgctct gttacgtcaa	1020
ctggcgaatg cagtaaaagc gcgtcgcggt taa	1053

<210> 2
 <211> 350
 <212> PRT
 <213> Escherichia coli W3110

<400> 2

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> 3

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> fhuA arm 1_F

<400> 3

ccaagcgacg cccaacctgc catcatggcg cgttcaaaa ctgctcagc

49

<210> 4

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> fhuA arm 1_R

<400> 4

tatcctcgag actagtgagc tccttcagc gggtcggtgg

40

<210> 5

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> fhuA arm 2_F

<400> 5

ctagtctcga ggatatcgac cacaccctgc tgaccggtgt

40

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> fhuA arm 2_R

<400> 6
atagaatacc aattggcatg ctttttagaa acggaagggt gcggttgc 48

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Pn_aroG_F

<400> 7
aaaggagctc actagtagga tgctcctgtt atgg 34

<210> 8

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Pn_aroG_R

<400> 8
cagggtgtgg tcgatatctt accgcgcacg cgcttt

36

<210> 9
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Ptrc_F

<400> 9
aaaggagctc actagtccgc ttgctgcaac tctc

34

<210> 10
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Ptrc_R

<400> 10

tggacgatac tcatatgttt cctgtgtgaa attgttatcc

40

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj1_F

<400> 11

aaaggagctc actagtaccg cgggcttatt ccatt

35

<210> 12

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj1_R

<400> 12

atctatagtc tgcataatgtt aatctcctag attgggttc a

41

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> aroG_F

<400> 13

taggagatta acatatgaat tatcagaacg ac

32

<210> 14

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> certification primer

<400> 14

ggaacgctca gattgcgt

18

<210> 15

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_ABCD_F

<400> 15

acaatttcac acaggaaaga tatcatgagt atcgtccaag caaag

45

<210> 16

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_ABCD_R

<400> 16

ctcatccgcc aaaacagctc tagattatga attattttcc agaca 45

<210> 17

<211> 6461

<212> DNA

<213> Anabaena variabilis ATCC29413

<400> 17

atgagtatcg tccaagcaaa gttgaagct aaggaaacat ctttcatgt agaaggttac 60

gaaaagattg agtatgattt ggtgtatgta gatggatttt ttgaaatcca gaattctgca 120

ctagcagatg tataatcaagg ttttgacga tgctggcga ttgtagatgc taacgtcagt 180

cggttgatg gtaatcaaat tcaggcatat ttccagtatt atggtataga actgaggcta 240

ttcctatta ccattactga accagataag actattcaaa cttcgagag agttatagat 300

gtctttgcag atttcaaatt agtccgcaaa gaaccagtat tagtcgtggg tggcgggtta 360

attacagatg ttgtcggctt tgctgttct acatatcgtc gcagcagcaa ttacatccgc 420

attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat 480

catcgcaaac tgaaaaaccg ttgggtgct tatcatgctt ctcgcaaagt atttttagat 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 tgcttacggt cacacttggg gtcccacctt ggaacttgcg	840
cctcgtctac ccatgttcca cggacacgcc gtaaatgtag atatggcttt ctcggcaacg	900
atcgccgccc gtagaggata tattacaatt gcagaacgcg atcgtatTTT aggattaatg	960
agtcgcgttg gtctatccct cgaccatccc atgttggata tagatatTTT gtggcgtggt	1020
actgaatcta tcacattaac tcgtgatggt ttgttaagag ctgctatgcc aaaaccatt	1080
ggtgattgtg tcttcgtcaa tgacctgaca agagaagaat tagcagccgc attagctgac	1140
cacaaagaac ttgtaccag ttatccccgt ggtggtgaag gtgtggatgt gtatcccgtt	1200
tatcaaaaag aattaatcgg gagtgtaaa taatgacttt ttgaattca aaatcaaaa	1260
tactccacgg atacactgcg cgagcgcggt agcatttctg ttcgcggagc gtcccgtagg	1320
gaaagagaag gctacgcaaa taatcggaca ctaattgtct ttaatttga attttgaatt	1380

ttgaattttg aattggagcg aagcgacttg acaaattgtga ttgtccaacc aacagctaga	1440
cctgttacac cattgggaat ttaaccaag cagttagaag ccatagtcca agaggtaag	1500
caacatccag atttacctgg ggaattgata gcaaacaatcc atcaggcttg gcgttagcc	1560
gcaggtatag acccttattt ggaagaatgc accactccag aatctcctga actcgctgca	1620
ttggcaaaaa ccacagccac cgaagcctgg ggagaacact tccacggagg tacaaccgtc	1680
cgctctctag aacaagagat gctttctggt catatcgaag gacaaacctt aaagatgttt	1740
gttcacatga ccaaagctaa aaaagtctta gaaattggga tgtttaccgg ttattcggcg	1800
ctggcgatgg cggaagcatt accagaggat ggactgcttg tggcttgtga agttgaccct	1860
tacgcggcgg aaattggaca gaaagccttt caacaatctc cccacgggtgg aaagattcgt	1920
gtggaattgg atgcagcctt agcaactctt gataagttag cagaagctgg ggagtctttt	1980
gacttggtat ttatcgacgc agataaaaaa gagtatgtag cctattttca caagtgcta	2040
ggtagcagtt tgtagcacc agatggcctt atttgtag ataacacctt attacaaggg	2100
gaagttatc taccagcaga ggaacgtagc gtcaatggtg aagcgatcgc gcaattaat	2160
catacagtag ctatagacc ccgtgtagaa caggtttgtg tgccgttgcg agatggtta	2220

acaattatcc gcagaatata accttaattg tccaatcgac tatggcaciaa tcccttcccc	2280
ttcttccgc acctgctaca ccgtctcttc ctcccagac gaaaatagcc gcaattatcc	2340
aaaatatctg cactttggct ttgtattac tagcattgcc cattaatgcc accattgtt	2400
ttatatcctt gttagtcttc cgaccgcaaa aggtcaaagc agcaaaccac caaaccattc	2460
ttatcagtgg cggtaagatg accaaagctt tacaactagc aaggctattc cacgcggctg	2520
gacatagagt tgtcttggtg gaaaccata aatactggtt gactggcat cgttttccc	2580
aagcagtgga taagttttac acagtccccg caccacagga caatcccaa gcttacattc	2640
aggctttggt agatatcgtc aaacaagaaa acatcgatgt ttatattccc gtcaccagtc	2700
cagtgggtag ctactacgac tcattagcca aaccagagtt atcccattat tgcaaggtgt	2760
ttcactttga cgcagatatt acccaaagt tggtatgataa attgcgttg acacaaaag	2820
cgcgatcgct tggttatca gtacccaaat cctttaaata tacctacca gaacaagtca	2880
tcaacttga ttttctgga gagacacgta aatacatcct caaaagcatt ccctacgact	2940
cagtgcggcg gttggactta accaaactcc cctgtgctac tccagaggaa acagcagcat	3000
tcgtcagaag ttgccaatt actccgaaa aaccgtggat tatgcaggaa ttatccccg	3060

gtaaggaatt ctgcacccat agcaccgttc ggaatgggga actcagactg cattgctgtt	3120
gcgaatcttc agccttcaa gtaattatg agaatgtaaa taacccgcaa attaccgaat	3180
gggtacagca tttgtcaag gaactgaaac tgacaggaca gatttcctt gactttatcc	3240
aagccgaaga cggaacagtt tacgccatcg agtgaaccc ccgcacacat tcagcaatta	3300
ccacatttta cgaccacccc caggtagcag aagcgtaact gagtcaagca ccgacgactg	3360
aaaccataca accactaacg acaagcaagc ctacctattg gacttatcac gaagtttggc	3420
gtttaactgg tatccgttct ttcaccagtt tgcaaagatg gctgggggaat atttggcgcg	3480
ggactgatgc gatttatcag ccagatgacc ccttaccgtt ttgatggta catcattggc	3540
aaattcccct actgttattg aataatttgc gtcgtcttaa aggttggacg cggatagatt	3600
tcaatattgg gaagtgggtg gaattggggg gagattagtt tttaaacgca gagggacgct	3660
gaggttagcg cagcgaaaag ttctggagga gggtttcct ccgtaggaaa ctttcaaga	3720
gagagggacg cggagtgtgt tttctctgcg tctctgctg agaaattttt tattattgag	3780
caaagtaga agatatgcag actatagatt ttaatattcg taagtactt gtagagtgga	3840
acgcgacca cagagattat gatcttccc agagtttaca tgaactaatt gtagctcaag	3900

tagaacgaac acctgaggcg atcgctgtca cctttgacaa gcaacaacta acttatcaag	3960
aactaaatca taaagcaaac cagctaggac attatttaca aacattagga gtccagccag	4020
aaaccctggt aggcgtttgt ttagaacgtt cctagaaat ggttatctgt ctttaggaa	4080
tcctcaaagc tgggggtgct tatgttccta ttgacctga atacctcaa gaacgcatag	4140
cttatatgct agaagattct caggtgaagg tactactaac tcaagaaaaa ttactcaatc	4200
aaattcccca ccatcaagca caaactatct gtgtagatag ggaatgggag aaaattcca	4260
cacaagctaa taccaatccc aaaagtaata taaaaacgga taatcttgct tatgtaattt	4320
acacctctgg ttccactggt aaaccaaag gtgcaatgaa cacccacaaa ggtatctgta	4380
atcgcttatt gtggatgcag gaagcttacc aaatcgattc cacagatagc atttacaaa	4440
aaaccccctt tagttttgat gttccggtt gggagtctt ttgacttta ttaactggcg	4500
cacgtttggt aatagccaaa ccaggcggac ataaagatag tgcttacctc atcgatttaa	4560
ttactcaaga acaaactact acgttgcat tttcccctc aatgctgcaa gtgttttac	4620
aaaatcgcca tgtaagcaaa tgcagctctc taaaagagt tattttagc ggtgaagctt	4680
tatctataga ttacaaaat agattttcc agcatttgca atgtgaatta cataacctct	4740

atggcccgac agaagcagca attgatgtca cattttggca atgtagaaaa gatagtaatt	4800
taaagagtgt acctattggt cgtccattg ctaatactca aatttatatt ctgatgccg	4860
attacaacc agtaaatatt ggtgtcactg gtgaaattta tattggtggt gtaggggttg	4920
ctcgtggta ttgaataaa gaagaattga ccaaagaaaa atttattatt aatcccttc	4980
ccaattctga gttaagcga cttataaaa caggtgattt agctcgttat ttaccgatg	5040
gaaatattga atatcttgggt agaacagatt atcaagtaaa aattcgggggt tatagaattg	5100
aaattggcga gattgaaaat gtttatctt cacaccaca agtcagagaa gctgtagtca	5160
tagcgcggga tgataacgct caagaaaaac aaatcatcgc ttatattacc tataactcca	5220
tcaaacctca gcttgataat ctgcgtgatt tcctaaaagc aaggctacct gattttatga	5280
ttccagccgc tttgtgatg ctggagcatc ttccttaac tccagtggt aaagtagacc	5340
gtaaggcatt acctaagcct gatttattta attatagtg acataattcc tatgtagcgc	5400
ctcggaatga agtgaagaa aaattagtag aaatctggc gaatattctg catttaccta	5460
aagtaggtgt gacagaaaaac ttttcgcta ttggtggtaa ttcctcaaa gctctacatt	5520
taatttctca aattgaagag ttatttgcta aagagatac ctagcaaca ctttaacaa	5580

atccagtaat tgcagattta gccaaaggta ttcaagcaaa caaccaaata cataattcac	5640
ccctagtcc aattcaacca caaggtaagc agcagccttt ctttgtata catcctgctg	5700
gtggcatgt tttatgctat tttaaactcg cacaatatat aggaactgac caaccat	5760
atggcttaca agctcaagga tttatggag atgaagcacc ctgacgcga gttgaagata	5820
tggctagtct ctacgtcaaa actattagag aattcaacc ccaagggcct tatcgtgctg	5880
gggggtggc atttgggtga gtcgtagctt atgaagtagc acagcagta catagacaag	5940
gacaagaagt atcttacta gcaatattag attctacgt accgattctg ctggataaac	6000
aaaaacccat tgatgacgtt tatttagttg gtgttctctc cagagttttt ggcggtatgt	6060
ttgtcaaga taatctagtc acacctgaag aaatagaaaa tttaactgta gaagaaaaaa	6120
ttaattacat cattgataaa gcacggagcg ctagaatatt cccgcctggg gtagaacgtc	6180
aaaataatcg ccgtattctt gatgttttgg tgggaacttt aaaagcaact tattcctata	6240
taagacaacc atatccagga aaagtcactg tatttcgagc cagggaaaaa catattatgg	6300
ctctgaccc gacctagtt tgggtagaat tttttctgt aatggcggct caagaaatta	6360
agattattga tgtccctgga aaccattatt cgtttgtct agaaccat gtacaggttt	6420

tagcacagcg ttacaagat tgtctgaaa ataattcata a 6461

<210> 18

<211> 2379

<212> DNA

<213> Escherichia coli W3110

<400> 18

atgtccaaca atggctcgtc accgctgggtg ctttggtata accaactcgg catgaatgat 60

gtagacaggg ttgggggcaa aaatgcctcc ctgggtgaaa tgattactaa tcttccgga 120

atgggtgttt ccgttccgaa tggtttcgcc acaaccgccg acgcgttaa ccagtttctg 180

gaccaaagcg gcgtaaacca gcgcatttat gaactgctgg ataaaacgga tattgacgat 240

gttactcagc ttgcgaaagc gggcgcgcaa atccgccagt ggattatcga cactcccttc 300

cagcctgagc tgaaaaacgc catccgcgaa gcctatgcac agctttccgc cgatgacgaa 360

aacgcctctt ttgcggtgcg ctctccgcc accgcagaag atatgccgga cgcttctttt 420

gccggtcagc aggaaacctt cctcaacgtt cagggttttg acgccgttct cgtggcagtg 480

aaacatgtat ttgcttctt gttaacgat cgcgccatct cttatcgtgt gcaccagggt 540

tacgatcacc gtgggtggc gctctccgcc ggtgttcaac ggatgggtgc ctctgacctc 600

gcatcatctg gcgtgatgtt ctccattgat accgaatccg gctttgacca ggtggtgtt	660
atcacttccg catggggcct tggtagatg gtcgtgcagg gtgcggttaa cccgcatgag	720
tttacgtgc ataaaccgac actggcggcg aatcgcccgg ctatcgtgcg ccgcacatg	780
gggtcgaaaa aaatccgcat ggtttacgcg ccgaccagg agcacggcaa gcaggtaaa	840
atcgaagacg taccgcagga acagcgtgac atcttctgc tgaccaacga agaagtgcag	900
gaactggcaa aacaggccgt acaaattgag aaacactacg gtcgcccgat ggatattgag	960
tgggcgaaag atggccacac cggtaaactg ttcattgtgc aggcgcgtcc ggaaaccgtg	1020
cgctcacgcg gtcaggatcat ggagcgttat acgctgcatt cacagggtaa gattatgcc	1080
gaaggccgtg ctatcggta tcgcatcggg gcgggtccgg tgaaagtcat ccatgacatc	1140
agcgaaatga accgcatcga acctggcgac gtgctggta ctgacatgac cgaccggac	1200
tgggaaccga tcatgaagaa agcatctgcc atcgacacca accgtggcgg tcgtacctgt	1260
cacgcggcga tcatcgctcg tgaactgggc attccggcgg tagtgggctg tggagatgca	1320
acagaacgga tgaaagacgg tgagaacgtc actgtttctt gtccgaagg tgataccggt	1380
tacgtctatg cggagttgct ggaatttagc gtgaaaagct ccagcgtaga aacgatgccg	1440

gatctgccgt tgaaagtgat gatgaacgtc ggtaacccgg accgtgcttt cgacttcgcc	1500
tgcttaccga acgaaggcgt gggccttgcg cgtctggaat ttatcatcaa ccgtatgatt	1560
ggcgtccacc cacgcgcact gcttgagttt gacgatcagg aaccgcagtt gcaaaacgaa	1620
atccgcgaga tgatgaaagg ttttgattct ccgcgtgaat ttacgttgg tcgtctgact	1680
gaagggatcg cgacgctggg tgccgcgttt tatccgaagc gcgtcattgt ccgtctctct	1740
gattttaa at cgaacgaata tgccaacctg gtcggtggtg agcggtacga gccagatgaa	1800
gagaaccgga tgctcggctt ccgtggcgcg ggccgctatg ttccgacag cttccgcgac	1860
tgtttcgcg tgagagtga agcagtgaac cgtgtgcgca acgacatggg actgaccaac	1920
gttgagatca tgatcccgtt cgtgcgtacc gtagatcagg cgaaagcggg ggtgaagaa	1980
ctggcgcgctc aggggctgaa acgtggcgag aacgggctga aaatcatcat gatgtgtgaa	2040
atcccgtcca acgccttgct ggccgagcag ttctcgaat atttcgacgg cttctcaatt	2100
ggctcaaacg atatgacgca gctggcgctc ggtctggacc gtgactccgg cgtggtgtct	2160
gaattgttcg atgagcgcaa cgatgcggtg aaagcactgc tgcgatggc tatccgtgcc	2220
gcgaagaac agggcaaata tgcgggatt tgcggtcagg gtccgtccga ccacgaagac	2280

ttgccgcat ggtgatgga agaggggatc gatagcctgt ctctgaaccc ggacaccgtg 2340

gtgcaaacct ggtaagcct ggctgaactg aagaaataa 2379

<210> 19

<211> 792

<212> PRT

<213> Escherichia coli W3110

<400> 19

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> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-pps_F

<400> 20

aaaggagctc actagtttg ttctcccgt gatg

34

<210> 21

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-pps_R

<400> 21

cagggtgtgg tcgatatctt atttctcag tcagc

36

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> pps_F

<400> 22

taggagatta acatatgtcc aacaatggct cg

32

<210> 23

<211> 1992

<212> DNA

<213> Escherichia coli W3110

<400> 23

atgtcctcac gtaaagagct tgccaatgct attcgtgcgc tgagcatgga cgagtacag

60

aaagccaaat ccggtcaccc ggggtgccct atgggtatgg ctgacattgc cgaagtcctg

120

tggcgtgatt tctgaaaca caaccgcag aatccgtcct gggctgaccg tgaccgcttc

180

gtgctgtcca acggccacgg ctccatgctg atctacagcc tgctgcacct caccggttac

240

gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac

300

ccggaagtgg gttacaccgc tgggtgga accaccaccg gtccgctggg tcagggatt

360

gccaacgcag tcggtatggc gattgcagaa aaaacgctgg cggcgcagtt taaccgtccg

420

ggccacgaca ttgtcgacca ctacacctac gccttcatgg gcgacggctg catgatggaa

480

ggcatctccc acgaagtttg ctctctggcg ggtacgctga agctgggtaa actgattgca	540
ttctacgatg acaacgggtat ttctatcgat ggtcacgttg aaggctgggt caccgacgac	600
accgcaatgc gtttcgaagc ttacggctgg cacgttattc gcgacatcga cggtcatgac	660
gcgggcatcta tcaaacgcgc agtagaagaa gcgcgcgcag tgactgacaa accttcctg	720
ctgatgtgca aaaccatcat cggtttcggt tccccgaaca aagccggtac ccacgactcc	780
cacggtgcgc cgctgggcca cgctgaaatt gccctgacct gcgaacaact gggctggaaa	840
tatgcgccgt tcgaaatccc gtctgaaatc tatgtctagt gggatgcgaa agaagcaggc	900
caggcgaaag aatccgcatg gaacgagaaa ttcgctgctt acgcgaaagc ttatccgcag	960
gaagccgctg aatttaccg ccgtatgaaa ggcgaaatgc cgtctgactt cgacgctaaa	1020
gcgaaagagt tcatcgctaa actgcaggct aatccggcga aaatcgccag ccgtaaagcg	1080
tctcagaatg ctatcgaagc gttcgggccg ctgttgccgg aattcctcgg cggttctgct	1140
gacctggcgc cgtctaacct gacctgtgg tctggttcta aagcaatcaa cgaagatgct	1200
gcgggtaact acatccacta cgggtgtcgc gagttcggtg tgaccgcgat tgctaacggt	1260
atctccctgc acggtggcct cctgccgtac acctccacct tctgatgtt cgtggaatac	1320

gcacgtaacg ccgtacgtat ggctgcgctg atgaaacagc gtcaggtgat ggtttacacc	1380
cacgactcca tcggtctggg cgaagacggc ccgactcacc agccgggtga gcaggtcgct	1440
tctctgcgcg taaccccgaa catgtctaca tggcgtccgt gtgaccaggt tgaatccgcg	1500
gtcgcgtgga aatacgggtg tgagcgtcag gacggcccga ccgcactgat cctctcccgt	1560
cagaacctgg cgcagcagga acgaactgaa gagcaactgg caaacatcgc gcgcggtggt	1620
tatgtgctga aagactgcgc cggtcagccg gaactgattt tcatcgctac cggttcagaa	1680
gttgaactgg ctgttgctgc ctacgaaaaa ctgactgccg aaggcgtgaa agcgcgcgtg	1740
gtgtccatgc cgtctaccga cgcatttgac aagcaggatg ctgcttaccg tgaatccgta	1800
ctgccgaaag cggttactgc acgcgttgct gtagaagcgg gtattgctga ctactggtac	1860
aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ccttcggtga atctgctccg	1920
gcagagctgc tgttgaaga gttcggcttc actgttgata acgttggtgc gaaagcaaaa	1980
gaactgctgt aa	1992

<210> 24
 <211> 663
 <212> PRT

<213> Escherichia coli W3110

<400> 24

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met

1 5 10 15

Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly

20 25 30

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			
660			

<210> 25

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-tktA_F

<400> 25

aaaggagctc actagtgttt tctctccgc acaa

34

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-tktA_R

<400> 26

caggggtgtgg tcgatatctt acagcagttc tttgc

36

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> tktA_F

<400> 27

taggagatta acatatgtcc tcacgtaaag ag

32

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj1-aroG_R

<400> 28
cccgcggtt acccgcgacg cgctt

26

<210> 29
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj1-pps_F

<400> 29
gcgggtaaac cgcgggctta ttccat

26

<210> 30

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj1-pps_R

<400> 30
cccgcggtt atttctcag ttcagc

26

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj1-tktA_F

<400> 31
agaaataaac cgcgggctta ttccat

26

<210> 32
<211> 71
<212> DNA

<213> Artificial Sequence

<220>

<223> aroD deletion cassette_F

<400> 32

tcatgggggtt cggtcctga caggctgacc gcgtgcagaa agggtaaaaa gctggagctg 60

cttcgaagtt c 71

<210> 33

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD deletion cassette_R

<400> 33

atatatttt tagtcggcg gggaggggtgt tccgcccga atattattgc gccatggtcc 60

atatgaatat ctccttag 79

<210> 34

<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> aroD deletion_F

<400> 34

caaagatttc cctctggaat atg

23

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD deletion_R

<400> 35

cagatgtgat tttcctacg c

21

<210> 36

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

<400> 36

gtgagttgga cagttgatat ccctaaagaa gttctccctg attgccacc attgccagaa	60
ggcatgcagc agcagttcga ggacaccatt tcccgtgacg ctaagcagca acctacgtgg	120
gatcgtgcac aggcagaaaa cgtgcgcaag atccttgagt cggttcctcc aatcgttgtt	180
gcccctgagg tacttgagct gaagcagaag ctgctgatg ttgccaacgg taaggccttc	240
ctctgcagg gtggtgactg tgcggaaact ttcgagtcaa acactgagcc gcacattcgc	300
gccaacgtaa agactctgct gcagatggca gttgtttga cctacggtgc atccactcct	360
gtgatcaaga tggctcgtat tgctggtcag tacgcaaagc ctcgctcttc tgatctggat	420
ggaaatggtc tgccaaacta ccgtggcgat atcgtaacg gtgtggaggc aaccccagag	480
gctcgtcgcc acgatcctgc ccgcatgac cgctgttacg ctaacgcttc tgctcggatg	540
aacttggtgc gcgcgctcac cagctctggc accgctgac ttaccgtct cagcgagtgg	600
aaccgcgagt tcgttcgaa ctccccagct ggtgcacgct acgaggctct tgctcgtgag	660
atcgactccg gtctgcgctt catggaagca tgtggcgtgt ccgatgagtc cctgcgtgct	720
gcagatatct actgctcca cgaggctttg ctggtggatt acgagcgctc catgctgcgt	780

cttgcaaccg atgaggaagg caacgaggaa ctttacgac ttcagctca ccagctgtgg	840
atcggcgagc gcacccgtgg catggatgat ttccatgtga acttcgcatc catgatctct	900
aaccaatcg gcatcaagat tggtcctggg atcacccctg aagaggctgt tgcatacgct	960
gacaagctcg atccgaactt cgagcctggc cgtttgacca tcgttgctcg catgggccac	1020
gacaaggttc gtcctgtact tcctggtgtt atccaggctg ttgaggcatc cggacacaag	1080
gttatttggc agtccgatcc gatgcacggc aacactttca ccgcatcaa tggctacaag	1140
accgtcact tcgacaagggt tatcgatgag gtccagggct tcttcgaggt ccaccgcgca	1200
ttgggcaccc acccaggcgg aatccacatt gagttcactg gtgaagatgt caccgagtgc	1260
ctcgggtggcg ctgaagacat caccgatgtt gatctgccag gccgctacga gtccgcatgc	1320
gatcctcgcc tgaacactca gcagtcttg gagttggctt tcctcgttgc agaaatgctg	1380
cgtaactaa	1389

<210> 37

<211> 462

<212> PRT

<213> Corynebacterium glutamicum ATCC13032

<400> 37

Met Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro

1 5 10 15

Pro Leu Pro Glu Gly Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg

20 25 30

Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val

35 40 45

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

50 55 60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe

65 70 75 80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu

85 90 95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val

100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala

115 120 125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu

130 135 140

45

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu

145 150 155 160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala

165 170 175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala

180 185 190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser

195 200 205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly

210 215 220

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

225 230 235 240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg

245 250 255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr

260 265 270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met

275 280 285

Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly

290

295

300

Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala

305

310

315

320

Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala

325

330

335

Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln

340

345

350

Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met

355

360

365

His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe

370

375

380

Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala

385

390

395

400

Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp

405

410

415

Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu

420

425

430

Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln

435	440	445
Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn		
450	455	460

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-cgl aroG_F

<400> 38

ggtatcgata agcttgattc gatctgctcc cattcc 36

<210> 39

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-cgl aroG_R

<400> 39

cggtggcggc cgctctagtt agttacgcag catttc

36

<210> 40

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-cgl aroG_F

<400> 40

cgaaaggaaa cactcgatgt gagtggaca gttgatatc

39

<210> 41

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-cgl aroG_R

<400> 41

ccgccaaaac agctctagtt tagttacgca gcatttc

37

<210> 42

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_ABCD_F

<400> 42

ccaaacacca acaaaaaggct ctaccatat gatgagtatc gtccaagcaa agtttgaagc

60

60

<210> 43

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_ABCD_R

<400> 43

agagggtgac gctagtcaga actagtttat gaattat tttt ccagacaatc ttgtaaacgc 60

60

<210> 44

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> O2 promoter_F

<400> 44

ccaaacacca acaaaaggct ctacccatat gcaataatcg tgaattttgg cagc 54

<210> 45

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> O2 promoter_R

<400> 45

caaactttgc ttggacgata ctcattgttt tgatctcctc caataatcta tgc

53

<210> 46

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-cgl tkt_F

<400> 46

ggtatcgata agcttgataa gattgatcac acctttg

37

<210> 47

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pn-cgl tkt_R

<400> 47

cggtggcggc cgctctagtt aaccgtaat ggagtc

36

<210> 48
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj7-cgl tkt_F

<400> 48
cgaaaggaaa cactcgattt gaccaccttg acgctg 36

<210> 49
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Pcj7-cgl tkt_R

<400> 49
ccgccaaaac agctctagtt taaccgtaa tggagtc 37

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Ptrc-cgl pps_F

<400> 50
tcacacagga aagatatcat gaccaacagt ttgaac 36

<210> 51
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Ptrc-cgl pps_R

<400> 51
ccgccaaaac agctctagtt tacttcgtgc cggtcattg 39

<210> 52
<211> 36

<212> DNA
<213> Artificial Sequence

<220>

<223> Pcj7-cgl pps_F

<400> 52

cgaaaggaaa cactcgatat gaccaacagt ttgaac

36

<210> 53

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-aroG_F

<400> 53

ttagaaatgg aacctaaaag aaacatccca gcgctac

37

<210> 54

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-aroG_R

<400> 54

tagcgctggg atgtttctt agttacgcag catttc

36

<210> 55

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-tkt_F

<400> 55

gaaatgctgc gtaactaaag aaacatccca gcgcta

36

<210> 56

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-tkt_R

<400> 56

gtagcgctgg gatgtttctt taaccgttaa tggagtc

37

<210> 57

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-pps_F

<400> 57

gactccatta acggttaaag aaacatccca gcgctac

37

<210> 58

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Pcj7-pps_R

<400> 58

ggagaatact gtcgttcatt tacttcgtgc cggtcattg

39

<210> 59

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_F

<400> 59

ggatccacag ttattcctg gcatcc

26

<210> 60

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_R

<400> 60

tttgcttgga cgatactcat ttgttggtt atgtgtgtt

40

<210> 61

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_A_F

<400> 61

aaacacacat aaacaaacaa atgagtatcg tccaagcaaa

40

<210> 62

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_A_R

<400> 62

ggatgccagg aataaactgt ttatttaaca ctcccgatta

40

<210> 63
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> pGPD_F

<400> 63
taatcgggag tgftaaataa acagtttatt cctggcatcc 40

<210> 64
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> pGPD_R

<400> 64
tggacaatca catttgtcaa ttgtttgttt atgtgtgttt 40

<210> 65

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

<220>
<223> Ava_B_F

<400> 65
aaacacacat aaacaacaa ttgacaaatg tgattgtcca 40

<210> 66
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Ava_B_R

<400> 66
gtcgacttaa ggtgtattc tgcgga 26

<210> 67
<211> 26
<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_F

<400> 67

ggatccacag ttattcctg gcatcc

26

<210> 68

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_R

<400> 68

aaagagattg attgtgcat ttgttggtt atgtgtgtt

40

<210> 69

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_C_F

<400> 69

aaacacacat aaacaaacaa atggcacaat caatctcttt

40

<210> 70

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_C_R

<400> 70

ggatgccagg aataaactgt ttagtcgccc cctaattcca

40

<210> 71

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_F

<400> 71

tggaattagg gggcgactaa acagttatt cctggcatcc

40

<210> 72

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_R

<400> 72

aggatattaa gtactggcat ttgttggtt atgtgtgtt

40

<210> 73

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_D_F

<400> 73

aaacacacat aaacaaacaa atgccagtac ttaatcct

40

<210> 74

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Ava_D_R

<400> 74

gtcgactcaa tttgtaaca cctttt

26

<210> 75

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> TKL1_F

<400> 75

ggatccatga ctcaattcac tgacat

26

<210> 76
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> TKL1_R

<400> 76
gtcgacttag aaagctttt tcaaag 26

<210> 77
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> ARO4_F

<400> 77
ggatccatga gtgaatctcc aatgtt 26

<210> 78
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> ARO4_R

<400> 78
gtcgacctat ttctgttaa ctctc 26

<210> 79
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> pps_F

<400> 79
ggatccatgt ccaacaatgg ctgctc 26

<210> 80
<211> 26

<212> DNA
<213> Artificial Sequence

<220>

<223> pps_R

<400> 80

gtcgacttat ttcttcagtt cagcca

26

<210> 81

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_F

<400> 81

ggatccacag ttattcctg gcatcc

26

<210> 82

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_R

<400> 82

atgtcagtga attgagtcatttgttggtt atgtgtgtt

40

<210> 83

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> TKL1_F

<400> 83

aaacacacat aaacaaacaa atgactcaat tcactgacat

40

<210> 84

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> TKL1_R

<400> 84

ggatgccagg aataaactgt ttagaaagct ttttcaaag

40

<210> 85

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_F

<400> 85

cttgaaaaa agctttctaa acagtttatt cctggcatcc

40

<210> 86

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> pGPD_R

<400> 86

aacattggag attcactcat ttgttggtt atgtgtgtt

40

<210> 87

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> ARO4_F

<400> 87

aaacacacat aaacaaacaa atgagtgaat ctccaatgtt

40

<210> 88

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> ARO4_R

<400> 88

gtcgacctat ttctgttaa ctctc

26

<210> 89

<211> 438

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

<400> 89

atgcctggaa aaattctct cctcaacggc ccaaacctga acatgctggg caaacgcgag 60

cctgacatt acggacacga caccttgga gacgtcgtcg cgctggcaac cgctgaggct 120

gcgaagcacg gccttgaggt tgaggcgctg cagagcaatc acgaagggtga gctaactgat 180

gcgctgcaca acgctcgcgg caccacatc ggttgcgtga ttaaccccg cggcctgact 240

cacactcgg tggcgcttt ggatgctgtg aaggcgtctg agcttcctac cgttgagggt 300

cacattcca atccgcatgc ccgtgaagag ttccgccacc attcttacct tccctcgcc 360

gcggtctccg ttatcgctgg cgctggcatc cagggttacc gtttcgcggt cgatatacctg 420

gcaaactca aaaagtag 438

<210> 90

<211> 145

<212> PRT

<213> Corynebacterium glutamicum ATCC13032

<400> 90

Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu

1 5 10 15

Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val

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> 91

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD_F

<400> 91

gatcggatcc cactggacgt ttgggtgaga cc

32

<210> 92

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD_R

<400> 92

gacggatcc actagtttta ggtccattt ctaattg

37

<210> 93

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD_F

<400> 93

gacactagt atgaacgaca gtattctcc

29

<210> 94

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> aroD_D

<400> 94

gatcaagctt gttacatcct gacgttgtgg 30

<210> 95

<211> 2103

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

<400> 95

ttgaccacct tgacgctgtc acctgaactt caggcgctca ctgtacgcaa ttaccctct 60

gattggtccg atgtggacac caaggctgta gacactgttc gtgtcctcgc tgcagacgct 120

gtagaaaact gtggctccgg ccaccaggc accgcaatga gcctggctcc ccttgcatc 180

acctgtacc agcgggttat gaacgtagat ccacaggaca ccaactgggc aggccgtgac 240

cgcttcgttc ttcttgtgg cactcctct ttgaccagt acatccagct ttactgggt 300

ggattcggcc ttgagatgga tgacctgaag gctctcgca cctgggattc cttgaccca 360

ggacaccctg agtaccgcca caccaagggc gttgagatca cactggccc tcttgccag 420

ggtcttgcac ctgcagttgg tatggccatg gctgctcgtc gtgagcgtgg cctattcgac 480

ccaaccgctg ctgagggcga atccccattc gaccaccaca tctacgtcat tgcttctgat 540

ggtgacctgc aggaaggtgt cacctctgag gcaccccca tcgctggcac ccagcagctg 600

ggcaacctca tcgtgttctg ggatgacaac cgcattctcca tcgaagacaa cactgagatc	660
gctttcaacg aggacgttgt tgctcgttac aaggcttacg gctggcagac cattgaggtt	720
gaggctggcg aggacgttgc agcaatcgaa gctgcagtgg ctgaggctaa gaaggacacc	780
aagcgacctc ccttcattcg cgttcgcacc atcatcggct tcccagctcc aactatgatg	840
aacaccggtg ctgtgcacgg tgctgctctt ggcgcagctg aggttgcagc aaccaagact	900
gagcttggat tcgatcctga ggctcacttc gcgatcgacg atgaggttat cgctcacacc	960
cgctccctcg cagagcgcgc tgacagaag aaggctgcat ggcagggtcaa gttcgatgag	1020
tgggcagctg ccaaccctga gaacaaggct ctgttcgatc gctgaactc ccgtgagctt	1080
ccagcgggct acgctgacga gctcccaaca tgggatgcag atgagaaggg cgtcgcaact	1140
cgtaaggctt ccgaggctgc acttcaggca ctgggcaaga cccttctga gctgtggggc	1200
ggttcgctg acctcgcagg ttccaacaac accgtgatca agggctcccc ttccttcggc	1260
cctgagtcca tctccaccga gacctggtct gctgagcctt acggccgtaa cctgcacttc	1320
ggtatccgtg agcacgctat gggatccatc ctcaacggca ttccctcca cggtggcacc	1380
cgcccatacg gcggaacctt cctcatcttc tccgactaca tgcgtcctgc agttcgtctt	1440

gcagctctca tggagaccga cgcttactac gtctggaccc acgactccat cggctctgggc	1500
gaagatggcc caaccaccca gcctgttgaa accttggtg cactgcgcgc catcccaggt	1560
ctgtccgtcc tgcgtcctgc agatgcgaac gagaccgccc aggcttgggc tgcagcactt	1620
gagtacaagg aaggccctaa gggctctgca ctgaccgccc agaacgttc tgttctggaa	1680
ggcaccaagg agaaggctgc tgaaggcgtt cgccgcggtg gctacgtcct ggttgagggt	1740
tccaaggaaa cccagatgt gatcctcatg ggctccggtt ccgaggttca gcttgagtt	1800
aacgtgcga aggctctgga agctgagggc gttgcagctc gcgttgttc cgttcctgc	1860
atggattggt tccaggagca ggacgcagag tacatcgagt ccgttctgcc tgcagctgtg	1920
accgctcgtg tgtctgtga agctggcatc gcaatgcctt ggtaccgctt cttgggcacc	1980
cagggccgtg ctgtctccct tgagcacttc ggtgcttctg cggattacca gaccctgtt	2040
gagaagttcg gcatcaccac cgatgcagtc gtggcagcgg ccaaggactc cattaacggt	2100
taa	2103

<210> 96

<211> 700

<212> PRT

<213> Corynebacterium glutamicum ATCC13032

<400> 96

Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg

1 5 10 15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr

20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His

35 40 45

Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln

50 55 60

Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp

65 70 75 80

Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln

85 90 95

Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu

100 105 110

Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr

115 120 125

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

130

135

140

Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp

145

150

155

160

Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val

165

170

175

Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser

180

185

190

Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp

195

200

205

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

210

215

220

Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val

225

230

235

240

Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala

245

250

255

Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile

260

265

270

Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala

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

Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly

435

440

445

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

450

455

460

Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu

465

470

475

480

Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser

485

490

495

Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu

500

505

510

Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp

515

520

525

Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu

530

535

540

Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu

545

550

555

560

Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val

565

570

575

Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
580 585 590

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

Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
610 615 620

Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
625 630 635 640

Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
645 650 655

Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
660 665 670

Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp
675 680 685

Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Gly
690 695 700

<210> 97

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

<400> 97

atgaccaaca gtttgaacat cccgtttgtc cagcgcttcg atgaaggcct ggatcctgtt	60
ctagaagtac tcggtggcaa gggcgcttca ctagtacca tgacagatgc tggaatgccc	120
gttcacctg gatttggtg cactactgcc agcttggatg aattcatccg tgaagcaggg	180
gttgctgaac acatcgataa attcctaaac gatctcgatg cagaagatgt taaggaagtg	240
gatcgagttt ctgcgatcat ccgcatgag ctgtgcagtc ttgacgttcc agagaatgct	300
cgtttcgag tgcaccaggc ttatcgcat ctcattggaac gatgcggtgg cgacgtcccg	360
gttgctgtcc ggtcatggc cactgccgaa gatctgcccg atgcttcctt cgaggggcaa	420
caggacacct atctgtggca agtcggttg agcgctgtca ctgaacacat ccgtaaatgc	480
tgggcttcgc tgtcacttc ccgtgccatt atctaccgtc tgaaaaacaa catccccaat	540
gagggcctct ccatggcggg agttgttcaa aaaatgggtca actctcgtgt cgcaggcgtg	600
gcaatcacta tgaatccttc caacggcgac cgctcgaaga tcaccatcga ttctcatgg	660
gggtgtggtg aaatgggtg ctcagggtgaa gtgacaccag acaatatctt gctggacaag	720
atcacgctgc aggtgtgtc cgaacacatt ggaagcaaac acgctgaact catccccgat	780

gccaccagtg gaagcctcgt ggaaaagccc gttgatgaag aacgcgcaaa ccgccgcagt 840

ctgactgatg aggaaatgct cgctgtggca caaatggcta agcgtgcaga aaaacactac 900

aagtgcccac aagatatcga atgggcgctg gacgctgac tgccagatgg agaaaacctt 960

ctgttattgc aatcccgccc ggaaactatc cactccaacg gttgtgaagaa ggaaacccca 1020

actccgcagg ctgccaaaac cataggcacc ttcgatttca gctcaatcac cgtcgcaatg 1080

accggcacga agtaa 1095

<210> 98

<211> 364

<212> PRT

<213> Corynebacterium glutamicum ATCC13032

<400> 98

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

1 5 10 15

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

20 25 30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr

35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His

50

55

60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val

65

70

75

80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val

85

90

95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met

100

105

110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr

115

120

125

Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr

130

135

140

Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys

145

150

155

160

Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn

165

170

175

Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met

180

185

190

Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn

195

200

205

Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu

210

215

220

Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys

225

230

235

240

Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu

245

250

255

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

260

265

270

Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala

275

280

285

Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln

290

295

300

Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu

305

310

315

320

Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys

325

330

335

Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp

	340	345	350
Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys			
	355	360	
<210>	99		
<211>	3926		
<212>	DNA		
<213>	Saccharomyces cerevisiae		
<400>	99		
ttggcatgc ttatgaagct atactaacc cacaagcatt acatggtgaa tgtgtgtcca			60
ttggtatggt taaagaggcg gaattatccc gttatttcgg tattctctcc cctaccaag			120
ttgcacgtct atccaagatt ttggtgcct acgggttgcc tgttcgcct gatgagaaat			180
ggtttaaaga gctaacctta cataagaaaa caccattgga tatctattg aagaaaatga			240
gtattgacaa gaaaaacgag ggttcaaaa agaagggtgt catttagaa agtattggt			300
agtgctatgg tgactccgct caatttgta gcgatgaaga cctgagattt attctaacag			360
atgaaaccct cgttacccc ttcaaggaca tccctgctga tcaacagaaa gttgttatcc			420
cccctggttc taagtccatc tccaatcgtg cttaattct tgctgccctc ggtgaaggtc			480

aatgtaaaat caagaactta ttacattctg atgatactaa acatatgtta accgctgttc	540
atgaattgaa aggtgctacg atatcatggg aagataatgg tgagacgga gtggtggaag	600
gacatggtgg ttccacattg tcagcttggtg ctgaccctt atatctaggt aatgcaggta	660
ctgcatctag attttgact tccttggtg ccttggtcaa ttctactca agccaaaagt	720
atatcgttt aactggaac gcaagaatgc acaaagacc aattgctcct ttggtcgatt	780
cttgcggtgc taatggtact aaaattgagt acttgaataa tgaaggtcc ctgccaatca	840
aagtttatac tgattcgga ttcaaagggtg gtagaattga attagctgct acagtttctt	900
ctcagtacgt atcctctatc ttgatgtgtg ccccatagcg tgaagaacct gtaactttgg	960
ctctgttgg tggaagcca atctctaaat tgtacgtcga tatgacaata aaaatgatgg	1020
aaaaattcgg tatcaatgtt gaaacttcta ctacagaacc ttacacttat tatattccaa	1080
aggacatta tattaaccca tcagaatacg tcattgaaag tgatgcctca agtgctacat	1140
accattggc ctcgccgca atgactggta ctaccgtaac ggtccaaac attggttttg	1200
agtcgttaca aggtgatgcc agatttgcaa gagatgtctt gaaacctatg ggttgtaaaa	1260
taactcaaac ggcaactca actactgttt cgggtcctcc ttaggttact ttaaagccat	1320

taaaacatgt tgatatggag ccaatgactg atgcgttctt aactgcatgt gttgttgccg	1380
ctatttcgca cgacagtgat ccaaattctg caaatacaac caccattgaa ggtattgcaa	1440
accagcgtgt caaagagtgt aacagaattt tggccatggc tacagagctc gccaaattg	1500
gcgtaaaaac tacagaatta ccagatggta ttcaagtcca tggtttaaac tcgataaaag	1560
attgaaggt tcctccgac tctctggac ctgtcgggt atgcacatat gatgatcatc	1620
gtgtggccat gagtttctcg ctcttgacg gaatggtaaa ttctcaaat gaacgtgacg	1680
aagttgctaa tcctgtaaga atacttgaaa gacattgtac tggtaaaacc tggcctggct	1740
ggtgggatgt gttacattcc gaactagggt ccaaattaga tggtcagaa cctttagagt	1800
gcacatcaa aaagaactca aagaaaagcg ttgtcattat tggcatgaga gcagctggca	1860
aaactactat aagtaaatgg tgcgcatccg ctctgggta caaattagt gacctagacg	1920
agctgttga gcaacagcat aacaatcaaa gtgttaaaca atttgtgtg gagaacggtt	1980
gggagaagtt ccgtgaggaa gaaacaagaa tttcaagga agttattcaa aattacggcg	2040
atgatggata tgtttctca acaggtggcg gtattgtga aagcgctgag tctagaaaag	2100
ccttaaaaga tttgcctca tcaggtggat acgtttaca ctacatagg gatattgagg	2160

agacaattgt cttttacaa agtgatecct caagacctgc ctatgtggaa gaaattcgtg	2220
aagtttgaa cagaaggag ggggtgtata aagaatgctc aaatttctct ttcttgctc	2280
ctcattgctc cgcagaagct gagttccaag ctctaagaag atcgtttagt aagtacattg	2340
caaccattac aggtgtcaga gaaatagaaa ttccaagcgg aagatctgcc ttgtgtgtt	2400
taaccttga tgacttaact gaacaaactg agaattgac tccaatctgt tatggtgtg	2460
aggctgtaga ggtcagagta gaccattgg ctaattactc tgctgattc gtgagtaaac	2520
agttatctat attgcgtaaa gccactgaca gtattcctat cattttact gtgcgaacca	2580
tgaagcaagg tggcaacttt cctgatgaag agtcaaaac ctgagagag ctatacgata	2640
ttgcctgaa gaatggtgtt gaattccttg acttagaact aactttacct actgatatcc	2700
aatatgaggt tattaacaaa aggggcaaca ccaagatcat tggttcccat catgacttcc	2760
aaggattata ctctgggac gacgctgaat gggaaaacag attcaatcaa gcgttaactc	2820
ttgatgtgga tgttgtaaaa ttgtgggta cggctgttaa ttccaagat aattgagac	2880
tgaacactt tagggataca cacaagaata agcctttaat tgcagttaat atgacttcta	2940
aaggtagcat ttctcgtgtt ttgaataatg tttaacacc tgtgacatca gattattgc	3000

ctaactccgc tgcccctggc caattgacag tagcacaaat taacaagatg tatacatcta	3060
tgggaggtat cgagcctaag gaactgttg ttgttgaaa gccaatggc cactctagat	3120
cgccaatttt acataacact ggctatgaaa ttttaggttt acctcacaag ttcgataaat	3180
ttgaaactga atccgcacaa ttggtgaaag aaaaactttt ggacggaaac aagaacttg	3240
gcggtgctgc agtcacaatt cctctgaaat tagatataat gcagtacatg gatgaattga	3300
ctgatgctgc taaagttatt ggtgctgtaa acacagttat accattgggt aacaagaagt	3360
ttaaggtgta taataccgac tggtaggta tccgtaatgc ctaattaac aatggcgctc	3420
ccgaatatgt tggcatacc gctggttgg ttatcggtgc aggtggcact tctagagccg	3480
ccctttacgc ctgacacagt ttaggttgca aaaagatctt cataatcaac aggacaactt	3540
cgaaattgaa gccattaata gagtcacttc catctgaatt caacattatt ggaatagagt	3600
ccactaaatc tatagaagag attaaggaac acgttggcgt tgctgtcagc tgtgtaccag	3660
ccgacaaacc attagatgac gaactttta gtaagctgga gagattcctt gtgaaagggtg	3720
cccatgctgc tttgtacca accttattgg aagccgcata caaaccaagc gttactcccg	3780
ttatgacaat ttcacaagac aaatatcaat ggcacgttgt ccctggatca caaatgtag	3840

tacaccaagg thtagctcag ttgaaaagt ggacaggatt caagggccct ttcaaggcca	3900
ttttgatgc cgttacgaaa gagtag	3926
<210> 100	
<211> 2247	
<212> DNA	
<213> Anabaena variabilis ATCC29413	
<400> 100	
atgagtatcg tccaagcaaa gttgaagct aaggaaacat ctttcatgt agaaggttac	60
gaaaagattg agtatgattt ggtgtatgta gatggtattt ttgaaatcca gaattctgca	120
ctagcagatg tatatcaagg ttttgacga tgcttggcga ttgtagatgc taacgtcagt	180
cggttgatg gtaatcaaat tcaggcatat ttccagtatt atggtataga actgaggcta	240
tttctatta ccattactga accagataag actattcaaa ctttcgagag agttatagat	300
gtctttgcag atttcaaatt agtccgcaaa gaaccagtat tagtcgtggg tggcggttta	360
attacagatg ttgtcggctt tgcttgttct acatatcgtc gcagcagcaa ttacatccgc	420
attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat	480
catcgcaaac tgaaaaaccg ttgggtgct tatcatgctt ctcgcaaagt atttttagat	540

ttctccttgt tgcgtactct ccctacagac caagtacgta acgggatggc ggaattgga	600
aaaatcgctg tagtagcgca tcaagaagtt ttgaattgt tggagaagta cggcgaagaa	660
ttactacgta ctcatTTTgg caatatagat gcaactccag agattaaaga aatagcccat	720
cgtttgactt acaaagctat ccataagatg ttggaattgg aagttcccaa cctgcatgag	780
ttagacctag ataggggtgat tgcttacggt cacacttga gtcccacctt 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 ttgtaagag ctgctatgcc aaaaccatt	1080
ggtgattgtg tcttcgtcaa tgacctgaca agagaagaat tagcagccgc attagctgac	1140
cacaaagaac ttgtaccag ttatccccgt ggtggtgaag gtgtggatgt gtatcccggt	1200
tatcaaaaag aattaatcgg gagtgtaaa taatgacttt ttgaattca aaatgcaaaa	1260
tactccacgg atacactgcg cgagcgcggt agcatttctg ttcgcggagc gtcccgtagg	1320
gaaagagaag gctacgcaaa taatcggaca ctaattgtct ttaatttga atttgaatt	1380

ttgaatttg aattggagcg aagcgacttg acaaattga ttgtccaacc aacagctaga	1440
cctgttacac cattgggaat ttaaccaag cagttagaag ccatagtcca agaggtaag	1500
caacatccag atttacctgg ggaattgata gcaaacaatcc atcaggcttg gcgttagcc	1560
gcaggatatag acccttattt ggaagaatgc accactccag aatctcctga actcgctgca	1620
ttggcaaaaa ccacagccac cgaagcctgg ggagaacact tccacggagg tacaaccgtc	1680
cgtcctctag aacaagagat gctttctggt catatcgaag gacaaacctt aaagatgtt	1740
gttcacatga ccaaagctaa aaaagtctta gaaattggga tgtttaccgg ttattcggcg	1800
ctggcgatgg cggaagcatt accagaggat ggactgcttg tggcttgtga agttgacct	1860
tacgcggcgg aaattggaca gaaagccttt caacaatctc cccacggtgg aaagattcgt	1920
gtggaattgg atgcagcctt agcaactctt gataagttag cagaagctgg ggagtcttt	1980
gacttggtat ttatcgacgc agataaaaaa gagtatgtag cctatttca caagtgcta	2040
ggtagcagtt tgtagcacc agatggcttt atttgttag ataacacctt attacaagg	2100
gaagtttatc taccagcaga ggaacgtagc gtcaatggtg aagcgatcgc gcaattaat	2160
catacagtag ctatagaccc ccgtgtagaa caggtttgt tgccgttgcg agatggtta	2220

acaattatcc gcagaataca accttaa

2247

<210> 101

<211> 3532

<212> DNA

<213> *Anabaena variabilis* ATCC29413

<400> 101

tccagaattc tgcactagca gatgtatatc aagggtttgg acgatgcttg gcgattgtag 60

atgctaacgt cagtcggttg tatggtaatc aaattcaggc atattccag tattatggta 120

tagaactgag gctatttcct attaccatta ctgaaccaga taagactatt caaactttcg 180

agagagttat agatgtcttt gcagatttca aattagtccg caaagaacca gtattagtcg 240

tgggtggcgg ttaattaca gatgtgtcg gctttgcttg ttctacatat cgtcgcagca 300

gcaattacat ccgcattcct actacattga ttggattaat tgatgccagt gtagcaatta 360

aggtagcagt taatcatcgc aaactgaaaa accgtttggg tgcttatcat gcttctcgca 420

aagtatttt agatttctcc ttgtgcgta ctctccctac agaccaagta cgtaacggga 480

tggcgggaatt ggtaaaaatc gctgtagtag cgcacaaaga agtttttgaa ttgttgaga 540

agtacggcga agaattacta cgtactcatt ttggcaatat agatgcaact ccagagatta	600
aagaaatagc ccatcgttg acttacaag ctatccataa gatgttgaa ttggaagtc	660
ccaacctgca tgagttagac ctagataggg tgattgctta cggtcacact tggagtcca	720
ccttggaact tgcgcctcgt ctacccatgt tccacggaca cgccgtaat gtagatatgg	780
ctttctggc aacgatgcc gcccgtagag gatataattac aattgcagaa cgcgatcgta	840
tttaggatt aatgagtcgc gttggtctat ccctcgacca tcccatgttg gatatagata	900
tttgtggcg tggactgaa tctatcacat taactcgtga tggtttgta agagctgcta	960
tgccaaaacc cattggtgat tgtgtcttcg tcaatgacct gacaagagaa gaattagcag	1020
ccgcattagc tgaccacaaa gaactttgta ccagttatcc ccgtggtggt gaagggtggtg	1080
atgtgtatcc cgttatcaa aaagaattaa tcgggagtgt taaataatga ctttttgaa	1140
ttcaaatgc aaaatactcc acggatacac tgcgcgagcg cggtagcatt tctgttcgcg	1200
gagcgcccc tagggaaaga gaaggctacg caaataatcg gacactaatt gtcttaatt	1260
ttgaatttg aatttgaat ttgaattgg agcgaagcga cttgacaaat gtgattgtcc	1320
aaccaacagc tagacctgtt acaccattgg gaattttaac caagcagta gaagccatag	1380

tccaagaggt taagcaacat ccagatttac ctggggaatt gatagcaaac atccatcagg	1440
ctggcggtt agccgcaggt atagaccctt atttgaaga atgcaccact ccagaatctc	1500
ctgaactcgc tgcattggca aaaaccacag ccaccgaagc ctggggagaa cacttcacg	1560
gaggtacaac cgtccgtcct ctagaacaag agatgcttc tggatcatc gaaggacaaa	1620
ccttaaagat gttgttcac atgaccaaag ctaaaaaagt ctagaaatt gggatgtta	1680
ccggttattc ggcgctggcg atggcggaag cattaccaga ggatggactg cttgtggctt	1740
gtgaagtga ccctacgcg gcggaattg gacagaaagc cttcaacaa tctcccacg	1800
gtggaaagat tcgtgtggaa ttgatgcag ccttagcaac tctgataag ttagcagaag	1860
ctggggagtc tttgacttg gtattatcg acgcagataa aaaagagtat gtagcctatt	1920
ttcacaagtt gctaggtagc agttttag caccagatgg cttatttgt gtagataaca	1980
ccttattaca aggggaagtt tatctaccag cagaggaacg tagcgtcaat ggtgaagcga	2040
tcgcgcaatt taatcatata gtagctatag acccccggtg agaacagggt ttgtgccgt	2100
tcgagatgg ttaacaatt atccgcagaa tacaacctta attgtccaat cgactatggc	2160
acaatccctt ccccttctt ccgcacctgc tacaccgtct cttcttccc agacgaaaat	2220

agccgcaatt atccaaaata tctgcacttt ggctttgtta ttactagcat tgcccattaa	2280
tgccaccatt gttttatat ccttgtagt ctccgaccg caaaaggta aagcagcaaa	2340
ccccaaacc attctatca gtggcggtta gatgaccaa gctttacaac tagcaaggta	2400
attccacgcg gctggacata gagttgtctt ggtggaaacc cataaatact ggttgactgg	2460
tcatcgttt tccaagcag tggataagt ttacacagtc cccgcacccc aggacaatcc	2520
ccaagctac attcaggctt tgtagatat cgtcaaaca gaaaacatcg atgtttatat	2580
tcccgtaacc agtccagtgg gtagctacta cgactatta gccaaaccag agttatcca	2640
ttattgcgaa gtgttact ttgacgcaga tattaccaa atgttgatg ataaattgc	2700
gttgacaca aaagcgcat cgctgggtt atcagtacc aaatcctta aaattacctc	2760
accagaaca gtcataact tcgattttc tggagagaca cgtaaataca tcctaaaag	2820
cattccctac gactcagtgc ggcggttga ctaaccaa ctcccctgtg ctactccaga	2880
ggaaacagca gcattcgtca gaagttgcc aattactccc gaaaaccgt ggattatgca	2940
ggaattatc cccgtaagg aattctgcac ccatagcacc gtcggaatg gggaactcag	3000
actgcattgc tgtgcgaat cttagcctt ccaagtaat tatgagaatg taaataacc	3060

gcaaattacc gaatgggtac agcattttgt caaggaactg aaactgacag gacagatttc	3120
cttgacttt atccaagccg aagacggaac agtttacgcc atcgagtgt acccccgcac	3180
acattcagca attaccacat ttacgacca ccccaggta gcagaagcgt acttgagtca	3240
agcaccgacg actgaaacca tacaaccact aacgacaagc aagcctacct attggactta	3300
tcacgaagtt tggcgtttaa ctggtatccg ttcttcacc cagttgcaa gatggctggg	3360
gaatatttg cgcgggactg atgcgattta tcagccagat gacccttac cgttttgat	3420
ggtagatcat tggcaaattc ccctactgtt attgaataat ttgcgtcgtc ttaaagggtg	3480
gacgcggata gattcaata ttgggaagtt ggtggaattg gggggagatt ag	3532

<210> 102

<211> 1233

<212> DNA

<213> Anabaena variabilis ATCC29413

<400> 102

atgagtatcg tccaagcaaa gttgaagct aaggaaacat ctttcatgt agaaggttac	60
---	----

gaaaagattg agtatgattt ggtgtatgta gatggtattt ttgaaatcca gaattctgca	120
---	-----

ctagcagatg tatatcaagg ttttgacga tgcttggcga ttgtagatgc taacgtcagt	180
--	-----

cggttgatg gtaatcaaat tcaggcatat ttccagtatt atggtataga actgaggcta	240
ttcctatta ccattactga accagataag actattcaaa cttcgagag agttatagat	300
gtctttgcag atttcaaatt agtccgcaaa gaaccagtat tagtcgtggg tggcggttta	360
attacagatg ttgtcggctt tgcttgttct acatatcgtc gcagcagcaa ttacatccgc	420
attcctacta cattgattgg attaattgat gccagtgtag caattaaggt agcagttaat	480
catcgcaaac tgaaaaaccg ttgggtgct tatcatgctt ctcgcaaagt attttagat	540
tttccttgt tgcgtactct ccctacagac caagtacgta acgggatggc ggaattgga	600
aaaatcgctg tagtagcgca tcaagaagtt ttgaattgt tggagaagta cggcgaagaa	660
ttactacgta ctcatTTTgg caatatagat gcaactccag agattaaaga aatagcccat	720
cgTTtgactt acaaagctat ccataagatg ttggaattgg aagttccaa cctgcatgag	780
ttagacctag atagggtgat tgcttacggt cacacttggg gtccacactt ggaactgcg	840
cctcgtctac ccatgttcca cggacacgcc gttaatgtag atatggcttt ctcggcaacg	900
atcgccgccc gtagaggata tattacaatt gcagaacgcg atcgatTTT aggattaatg	960
agtcgcttg gtctatccct cgaccatccc atgttgata tagatTTTT gtggcgtggt	1020

actgaatcta tcacattaac tcgtgatggt ttgttaagag ctgctatgcc aaaaccatt	1080
ggtgattgtg tcttcgtcaa tgacctgaca agagaagaat tagcagccgc attagctgac	1140
cacaaagaac ttgtaccag ttatccccgt ggtggtgaag gtgtggatgt gtatccgtt	1200
tatcaaaaag aattaatcgg gagtgtaaa taa	1233
<210> 103	
<211> 840	
<212> DNA	
<213> Anabaena variabilis ATCC29413	
<400> 103	
ttgacaaatg tgattgtcca accaacagct agacctgtta caccattggg aattttaacc	60
aagcagttag aagccatagt ccaagaggtt aagcaacatc cagatttacc tggggaattg	120
atagcaaaca tccatcaggc ttggcgttta gccgcaggta tagaccctta ttggaagaa	180
tgaccactc cagaatctcc tgaactcgct gcattggcaa aaaccacagc caccgaagcc	240
tggggagaac acttcacgg aggtacaacc gtccgtctc tagaacaaga gatgcttct	300
ggtcatatcg aaggacaaac cttaaagatg ttgttcaca tgaccaaagc taaaaaagtc	360

ttagaaattg ggatgtttac cggttattcg gcgctggcga tggcggaagc attaccagag	420
gatggactgc ttgtggcttg tgaagttgac ccttacgcgg cggaaattgg acagaaagcc	480
ttcaacaat cccccacgg tggaagatt cgtgtggaat tggatgcagc ctagcaact	540
cttgataagt tagcagaagc tggggagtct ttgacttg tatttatcga cgcagataaa	600
aaagagtatg tagcctattt tcacaagttg ctaggtagca gttgttagc accagatggc	660
tttattgtg tagataacac cttattaca ggggaagttt atctaccagc agaggaaagt	720
agcgtcaatg gtgaagcgaat cgcgcaattt aatcatacag tagctataga cccccgtgta	780
gaacagggtt tgttgccgtt gcgagatggt ttaacaatta tccgcagaat acaaccttaa	840
	840

<210> 104
 <211> 1377
 <212> DNA
 <213> Anabaena variabilis ATCC29413

<400> 104	
atggcacaat ccctcccct ttctccgca cctgctacac cgtctctcc ttcccagacg	60
aaaatagccg caattatcca aaatatctgc actttggctt tgttattact agcattgccc	120

attaatgcc a cattgttt tatatccttg ttagtctcc gaccgcaaaa ggtcaaagca	180
gcaaaccccc aaaccattct tatcagtggc ggtaagatga ccaaagcttt acaactagca	240
aggcattcc acgcggctgg acatagagtt gtcttggtgg aaaccataa atactggtg	300
actggtcatc gttttccca agcagtggat aagttttaca cagtccccgc accccaggac	360
aatccccaag ctacattca ggcttggta gatatcgtca aacaagaaaa catcgatgtt	420
tatattcccg tcaccagtcc agtgggtagc tactacgact cattagccaa accagagtta	480
tcccattatt gcgaagtgtt tcacttgac gcagatatta cccaaatgtt ggatgataaa	540
tttgcgtga cacaaaaagc gcgatcgctt ggtttatcag tacccaaatc cttaaaatt	600
acctcaccag aacaagtcac caacttcgat tttctggag agacacgtaa atacatcctc	660
aaaagcattc cctacgactc agtgcggcgg ttggacttaa ccaaactccc ctgtgctact	720
ccagaggaaa cagcagcatt cgtcagaagt ttgccaatta ctcccgaaaa accgtggatt	780
atgcaggaat ttatccccgg taaggaattc tgcaccata gcaccgttcg gaatggggaa	840
ctcagactgc attgctgttg cgaatttca gccttccaag ttaattatga gaatgtaaat	900
aaccgcgaaa ttaccgaatg ggtacagcat ttgtcaagg aactgaaact gacaggacag	960

atttccttg actttatcca agccgaagac ggaacagttt acgccatcga gtgtaacccc	1020
cgcacacatt cagcaattac cacattttac gaccaccccc aggtagcaga agcgtacttg	1080
agtcaagcac cgacgactga aaccatacaa ccactaacga caagcaagcc tacctattgg	1140
acttatcacg aagtttggcg tttaactggg atccgttctt tcaccagtt gcaaagatgg	1200
ctggggaata ttggcgcg gactgatgcg atttatcagc cagatgaccc cttaccgttt	1260
ttgatggtac atcattggca aattccccta ctgtattga ataatttgcg tcgtcttaa	1320
ggttgacgc ggatagattt caatattggg aagtgggtgg aattgggggg agattag	1377
<210>	105
<211>	2358
<212>	DNA
<213>	Anabaena variabilis ATCC29413
<400>	105
gttcctattg accctgaata tcctcaagaa cgcatagctt atatgctaga agattctcag	60
gtgaaggtag tactaactca agaaaaatta ctcaatcaaa ttccccacca tcaagcacia	120
actatctgtg tagatagggg atgggagaaa attccacac aagctaatac caatcccaa	180

agtaatataa aaacggataa tcttgcttat gtaatttaca cctctgggtc cactggtaaa	240
ccaaaagggtg caatgaacac ccacaaaggt atctgtaatc gcttattgtg gatgcaggaa	300
gcttatcaaa tcgattccac agatagcatt ttacaaaaaa cccccttag tttgatgtt	360
tccgtttggg agttctttg gactttatta actggcgcac gtttggtaat agccaaacca	420
ggcggacata aagatagtcg ttacctatc gatttaatta ctcaagaaca aatcactacg	480
ttgcatttg tcccccaat gctgcaagtg ttttataaa atcgccatgt aagcaaatgc	540
agctctctaa aaagagttat ttgtagcggg gaagctttat ctatagattt acaaaataga	600
ttttccagc atttgcaatg tgaattacat aacctctatg gcccgacaga agcagcaatt	660
gatgtcacat ttggcaatg tagaaaagat agtaatttaa agagtgtacc tattggtcgt	720
cccattgcta atactcaaat ttatattctt gatgccgatt tacaaccagt aaatattggt	780
gtcactgggtg aaatttatat tgggtgtgta ggggttgctc gtggttattt gaataaagaa	840
gaattgacca aagaaaaatt tattattaat cccttccca attctgagtt taagcgactt	900
tataaaacag gtgatttagc tcgtatttta ccgatggaa atattgaata tcttggtaga	960
acagattatc aagtaaaaaat tcgggggttat agaattgaaa ttggcgagat tgaaaatgtt	1020

ttatcttcac acccacaagt cagagaagct gtagcatag cgcgggatga taacgctcaa	1080
gaaaaacaaa tcatcgctta tattacctat aactccatca aacctcagct tgataatctg	1140
cgtgattcc taaaagcaag gctacctgat ttatgattc cagccgctt tgtgatgctg	1200
gagcatcttc cttaactcc cagtggtaaa gtagaccgta aggcattacc taagcctgat	1260
ttatttaatt atagtgaaca taattcctat gtagcgctc ggaatgaagt tgaagaaaa	1320
ttagtacaaa tctggtcgaa tattctgcat ttacctaaag taggtgtgac agaaaactt	1380
ttcgctattg gtggaattc cctcaaagct ctacatttaa ttctcaaat tgaagagtta	1440
tttgctaaag agatatcctt agcaacactt ttaacaaatc cagtaattgc agatttagcc	1500
aaggttattc aagcaaacaa ccaaatccat aattcacccc tagttccaat tcaaccacaa	1560
ggtaagcagc agccttctt ttgtatacat cctgctggtg gtcattgtt atgctattt	1620
aaactcgcac aatatatagg aactgaccaa ccatttatg gcttacaagc tcaaggattt	1680
tatggagatg aagcaccctt gacgcgagtt gaagatatgg ctagtctcta cgtcaaaact	1740
attagagaat ttcaaccca agggccttat cgtgtcgggg ggtggtcatt tggaggagtc	1800
gtagcttatg aagtagcaca gcagttacat agacaaggac aagaagtatc ttactagca	1860

atattagatt ctacgtacc gattctgctg gataaacaaa aaccattga tgacgttat	1920
ttagtgtg ttctctccag agttttggc ggtatgttg gtcaagataa tctagtcaca	1980
cctgaagaaa tagaaaattt aactgtagaa gaaaaaatta attacatcat tgataaagca	2040
cggagcgcta gaattattccc gcctgggtga gaacgtcaaa ataatcgccg tattcttgat	2100
gtttgggtgg gaactttaa agcaacttat tcctatataa gacaaccata tccaggaaaa	2160
gtcactgtat ttcgagccag ggaaaaacat attatggctc ctgacccgac ctagtttg	2220
gtagaattat ttctgtaat ggcggctcaa gaaattaaga ttattgatgt ccctggaaac	2280
cattattcgt ttgtctaga accccatgta caggtttag cacagcggtt acaagattgt	2340
ctggaaaata attcataa	2358

<210> 106

<211> 1233

<212> DNA

<213> Nostoc punctiforme ATCC29133

<400> 106	
atgagtaatg tcaagcatc gttgaagca acggaagctg aattccgcgt ggaaggttac	60
gaaaaaattg agtttagtct tgtctatgta aatgggtgcat ttgatcag taacagagaa	120

attgcagaca gctatgagaa gttggccgt tgtctgactg tgattgatgc taatgtcaac	180
agattatatg gcaagcaaat caagtcatat ttagacact atggtattga tctgaccgta	240
gttccattg tgattactga gcctactaaa acccttgcaa ccttgagaa aattgtgat	300
gcttttctg actttggtt aatccgcaag gaaccagtat tagtagtggg tgggtgtta	360
accactgatg tagctgggtt tgcgtgtgct gcttaccgtc gtaagagtaa ctatattcgg	420
gttccgacaa cgctgattgg tctgattgat gcagggttag cgattaaggt tgcagtcaac	480
catcgcaagt taaaaaatcg cttgggtgca tatcatgctc cttgaaagt catcctcgat	540
tttccttct tgcaaacatt accaacggct caagttcgta atgggatggc agagttggc	600
aaaattgctg ttgtggcgaa ctctgaagtc ttgaattgt tgtatgaata tggcgaagag	660
ttgctttcca ctactttgg atatgtgaat ggtacaaagg aactgaaagc gatcgacat	720
aaactcaatt acgaggcaat aaaaactatg ctggagttgg aaactccaaa ctgcatgag	780
ttagacctcg atcgcgtcat tgcctacggt cacacttggg gtccgacctt agaattagct	840
ccgatgatac cgttgttca cggtcatgcc gtcaatatag acatggcttt gtctgcaact	900
attgcggaac gacgtggcta cattacatca ggagaacgcg atcgcathtt gagcttgatg	960

agtcgtatag gtttatcaat cgatcatcct ctactagatg gcgatttgct ctggtatgct	1020
acccaatcta ttagcttgac gcgagacggg aaacaacgcg cagctatgcc taaaccatt	1080
ggtgagtgct tctttgcaa cgatttcacc cgtgaagaac tagatgcagc ttagctgaa	1140
cacaaacgct tgtgtgtac ataccctcgt ggtggagatg gcattgacgc ttacatagaa	1200
actcaagaag aatccaaact attgggagtg tga	1233
<210> 107	
<211> 834	
<212> DNA	
<213> Nostoc punctiforme ATCC29133	
<400> 107	
atgaccagta ttttaggacg agataccgca agaccaataa cgccacatag cattctgga	60
gcacagctac aaaaaaccct cagaatggca gaggaaagta atattccttc agagatactg	120
acttctctgc gccaaggggt gcaattagca gcaggtttag atccctatct ggatgattgc	180
actaccctg aatcgaccgc attgacagca ctagcgcaga agacaagcat tgaagactgg	240
agtaaacgct tcagtgatgg tgaacagtg cgtcaattag agcaagaaat gctctcagga	300

catcttgaag gacaaacact aaagatgttt gtgcatatca ctaaggctaa aagcatccta 360

gaagtgggaa tgttcacagg atattcagct ttggcaatgg cagaggcggt accagatgat 420

gggcgactga ttgcttgta agtagactcc tatgtggccg agtttgctca aacttgcttt 480

caagagtctc cccacggccg caagattgtt gtagaagtgg cacctgcact agagacgctg 540

cacaagctgg tggctaaaaa agaatccttt gatctgatct tcattgatgc ggataaaaag 600

gagtatatag aatactcca aattatcttg gatagccatt tactagctcc cgacggatta 660

atctgtgtag ataatacttt gttgcaagga caagtttacc tgccatcaga acagcgta 720

gccaatgggtg aagcgatcgc tcaattcaac cgcattgtcg ccgcagatcc tcgtgtagag 780

caagttctgt tacccatacg agatgggtata accctgatta gacgcttgggt ataa 834

<210> 108

<211> 1086

<212> DNA

<213> Nostoc punctiforme ATCC29133

<400> 108

tactgggtat cagggcatag attctcaaat tctgtgagtc gttttatac agttcctgca 60

ccacaagacg acccagaagg ctatacccaa gcgctattgg aaattgtcaa acgagagaag 120

attgacgttt atgtacccgt atgcagccct gtagctagtt attacgactc ttggcaaag	180
tctgcactat cagaatattg tgagggtttt cactttgatg ctgatataac caagatgctg	240
gatgataaat ttgcctttac cgatcgggcg cgatcgcttg gttatcagc cccgaaatct	300
tttaaaatta ccgatcctga acaagttatc aacttcgatt ttagtaaaga gacgcgcaaa	360
tatattctta agagtatttc ttacgactca gttcgccgct taaatttaac caaacttct	420
tgtgatacc cagaagagac agcagcggtt gtcaagagtt taccatcag cccagaaaaa	480
ccttgatta tgcaagaatt tattcctggg aaagaattat gcacccatag cacagtccga	540
gacggcgaat taaggttgca ttgctgttca aattcttcag cgtttcagat taactatgaa	600
aatgtcgaaa atccccaaat tcaagaatgg gtacaacatt tcgtcaaaag ttacggctg	660
actggacaaa tatctcttga ctttatccaa gctgaagatg gtacagctta tgccattgaa	720
tgtaatcttc gcacccattc ggcgatcaca atgttctaca atcaccagg tggtgcagaa	780
gcctatcttg gtaaaactcc tctagctgca cctttggaac ctcttcaga tagcaagccc	840
acttactgga tatatcacga aatctggcga ttgactggga ttcgctctgg acaacaatta	900
caaacttggg ttgggagatt agtcagaggt acagatgcca ttatcgctt ggacgatccg	960

ggagaattgc ttcgccaagg agatattcca acaattacac ctccagcagt cgtcaaacct	480
gtaagttctg acaactcttt aggagtagtc ttagttaaag atgtgactga atatgatgct	540
gccttaaaga aagcatttga atatgcttcg gaggtcatcg tagaagcatt catcgaactt	600
ggtcgagaag tcagatgcgg catcattgta aaagacgggt agctaataagg ttaccctt	660
gaagagtatc tggtagaccc acacgataaa cctatccgta actatgctga taaactcaa	720
caaactgacg atggcgactt gcatttgact gctaaagata atatcaaggc ttggatttta	780
gaccctaacg acccaatcac ccaaaagggt cagcaagtgg ctaaaagggt tcatcaggct	840
ttgggtgtgc gccactacag ttatttgac ttccgaatcg atccaaaggg acaaccttgg	900
ttctagaag ctggattata ttgtctttt gccccaaaa gtgtgatttc ttctatggcg	960
aaagcagccg gaatccctct aaatgattta ttaataaccg ctattaatga aacattgggt	1020
agtaataaaa aggtgttaca aaattga	1047

<210> 110

<211> 1626

<212> DNA

<213> Saccharomyces cerevisiae CEN.PK-1D

<400> 110

aacaagccgg gctttacctt gtctgacaac tacacctatg tttcttggg tgacggtgt	60
ttgcaagaag gtatttctc agaagcttc tccttggtg gtcattgaa attgggtaac	120
ttgattgcca tctacgatga caacaagatc actatcgatg gtgctaccag tatctcattc	180
gatgaagatg ttgctaagag atacgaagcc tacggttggg aagttttgta cgtagaaaat	240
ggtaacgaag atctagccgg tattgccaag gctattgctc aagctaagtt atccaaggac	300
aaaccaactt tgatcaaaaat gaccacaacc attggttacg gttccttgca tgccggctct	360
cactctgtgc acggtgcccc attgaaagca gatgatgta aacaactaaa gagcaaattc	420
ggtttcaacc cagacaagtc cttgttgtt ccacaagaag ttacgacca ctacaaaag	480
acaattttaa agccaggtgt cgaagccaac aacaagtga acaagttgt cagcgaatac	540
caaaagaaat tcccagaatt aggtgctgaa ttggctagaa gattgagcgg ccaactacc	600
gcaaattggg aatctaagtt gccaacttac accgccaagg actctgccgt ggccactaga	660
aaattatcag aaactgttct tgaggatgt tacaatcaat tgccagagtt gattggtggt	720
tctgccgatt taacaccttc taactgacc agatggaagg aagcccttga ctccaacct	780
ccttctccg gttcaggtaa ctactctggt agatacatta ggtacggtat tagagaacac	840

gctatgggtg ccataatgaa cgggtattca gcttcgggtg ccaactacaa accatacggg	900
ggactttct tgaactcgt ttctatgct gctgggtccg ttagattgtc cgcttgtct	960
ggccaccag ttattgggt tgctacacat gactctatcg gtgtcggga agatggcca	1020
acacatcaac ctattgaaac tttagcacac ttcagatccc taccaaaca tcaagtttg	1080
agaccagctg atggtaacga agtttctgcc gcctacaaga actctttaga atccaagcat	1140
actccaagta tcattgctt gtccagacaa aacttgccac aattggaagg tagctctatt	1200
gaaagcgctt ctaagggtgg ttacgtacta caagatgtg ctaaccaga tattattta	1260
gtggctactg gtccgaagt gtcttgagt gttgaagctg ctaagactt ggccgcaaag	1320
aacatcaagg ctggtgtgt ttcttacca gatttctca ctttgacaa acaacccta	1380
gaatacagac tatcagtctt accagacaac gttccaatca tgtctgtga agtttggct	1440
accacatgtt ggggcaaata cgctcatcaa tcctcggta ttgacagatt tgggcctcc	1500
ggtaaggcac cagaagtctt caagttctc ggttcaccc cagaaggtgt tgctgaaaga	1560
gctcaaaaga ccattgcatt ctataagggt gacaagctaa ttctcctt gaaaaagct	1620
ttctaa	1626

<210> 111
 <211> 1113
 <212> DNA
 <213> *Saccharomyces cerevisiae* CEN.PK-1D

 <400> 111
 atgagtgaat ctccaatgtt cgctgccaac ggcatgccaa aggtaaatca aggtgctgaa 60

 gaagatgtca gaatttagg ttacgacca ttagcttctc cagctctcct tcaagtcaa 120

 atcccagcca caccaacttc ttggaaact gccaaagagag gtagaagaga agctatagat 180

 attattaccg gttaaagacga cagagtctt gtcattgtcg gtccttggtc catccatgat 240

 ctagaagccg ctcaagaata cgcttgaga ttaaagaaat tgcagatga attaaaaggt 300

 gatttatcca tcattatgag agcatacttg gagaagccaa gaacaaccgt cggctggaaa 360

 ggtctaatta atgaccctga tgtaacaac acttcaaca tcaacaaggg ttgcaatcc 420

 gctagacaat tgtttgtcaa ctgacaaat atcggttgc caattggtc tgaaatgctt 480

 gataccattt ctctcaata ctggctgat ttgtctcct tcggtgccat tgggtccaga 540

 accaccgaat ctcaactgca cagagaattg gcctccggtt tgtcttccc agttggttc 600

aagaacggta ccgatggtac cttaaagtgt gctgtggatg cttgtcaagc cgctgctcat	660
tctcaccatt tcatgggtgt tactaagcat ggtgttgctg ctatcaccac tactaagggt	720
aacgaacact gcttcgttat tctaagaggt ggtaaaaagg gtaccaacta cgacgctaag	780
tccgttgacag aagctaaggc tcaattgcct gccggttcca acggtctaata gattgactac	840
tctcacggta actccaataa ggatttcaga aaccaaccaa aggtcaatga cgttgttgt	900
gagcaaatcg ctaacggtga aaacgccatt accggtgtca tgattgaatc aaacatcaac	960
gaaggaacc aaggcatccc agccgaaggt aaagccggct tgaaatatgg tgttccatc	1020
actgatgctt gtataggttg ggaaactact gaagacgtct tgaggaaatt ggctgctgct	1080
gtcagacaaa gaagagaagt taacaagaaa tag	1113

<210> 112

<211> 1588

<212> PRT

<213> Saccharomyces cerevisiae

<400> 112

Met Val Gln Leu Ala Lys Val Pro Ile Leu Gly Asn Asp Ile Ile His

1

5

10

15

Val Gly Tyr Asn Ile His Asp His Leu Val Glu Thr Ile Ile Lys His

20

25

30

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

120

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

125

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> 113

<211> 820

<212> PRT

<213> *Anabaena variabilis* ATCC29413

<400> 113

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	
		130		

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> 114

<211> 1099

<212> PRT

<213> Anabaena variabilis ATCC29413

<400> 114

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 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
		140	

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> 115

<211> 410

<212> PRT

<213> *Anabaena variabilis* ATCC29413

<400> 115

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> 116

<211> 410

<212> PRT

<213> *Anabaena variabilis* ATCC29413

<400> 116

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> 117

<211> 279

<212> PRT

<213> *Anabaena variabilis* ATCC29413

<400> 117

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

149

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> 118

<211> 888

<212> PRT

<213> Anabaena variabilis ATCC29413

<400> 118

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 Leu Gly Val Gln Pro Glu Thr Leu Val Gly
65 70 75 80

Val Cys Leu Glu Arg Ser Leu Glu Met Val Ile Cys Leu Leu Gly Ile
85 90 95

Leu Lys Ala Gly Gly Ala Tyr Val Pro Ile Asp Pro Glu Tyr Pro Gln
100 105 110

Glu Arg Ile Ala Tyr Met Leu Glu Asp Ser Gln Val Lys Val Leu Leu
115 120 125

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

Ile Cys Val Asp Arg Glu Trp Glu Lys Ile Ser Thr Gln Ala Asn Thr
145 150 155 160

Asn Pro Lys Ser Asn Ile Lys Thr Asp Asn Leu Ala Tyr Val Ile Tyr
165 170 175

Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Ala Met Asn Thr His Lys
180 185 190

Gly Ile Cys Asn Arg Leu Leu Trp Met Gln Glu Ala Tyr Gln Ile Asp
195 200 205

Ser Thr Asp Ser Ile Leu Gln Lys Thr Pro Phe Ser Phe Asp Val Ser

210	215	220	
Val Trp Glu Phe Phe Trp Thr Leu Leu Thr Gly Ala Arg Leu Val Ile			
225	230	235	240
Ala Lys Pro Gly Gly His Lys Asp Ser Ala Tyr Leu Ile Asp Leu Ile			
	245	250	255
Thr Gln Glu Gln Ile Thr Thr Leu His Phe Val Pro Ser Met Leu Gln			
	260	265	270
Val Phe Leu Gln Asn Arg His Val Ser Lys Cys Ser Ser Leu Lys 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> 119

<211> 410

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 119

Met Ser Asn Val Gln Ala Ser Phe Glu Ala Thr Glu Ala Glu Phe Arg

1

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> 120

<211> 277

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 120

Met Thr Ser Ile Leu Gly Arg Asp Thr Ala Arg Pro Ile Thr Pro His

1	5	10	15
---	---	----	----

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	
161			

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> 121

<211> 461

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 121

Met Ala Gln Ser Ile Ser Leu Ser Leu Pro Gln Ser Thr Thr Pro Ser

1 5 10 15

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

163

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> 122

<211> 348

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 122

Met Pro Val Leu Asn Ile Leu His Leu Val Gly Ser Ala His Asp Lys

1

5

10

15

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

166

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

<210> 123

<211> 680

<212> PRT

<213> Saccharomyces cerevisiae CEN.PK-1D

<400> 123

Met Thr Gln Phe Thr Asp Ile Asp Lys Leu Ala Val Ser Thr Ile Arg

1 5 10 15

Ile Leu Ala Val Asp Thr Val Ser Lys Ala Asn Ser Gly His Pro Gly

20 25 30

Ala Pro Leu Gly Met Ala Pro Ala Ala His Val Leu Trp Ser Gln Met

35 40 45

Arg Met Asn Pro Thr Asn Pro Asp Trp Ile Asn Arg Asp Arg Phe Val

50 55 60

Leu Ser Asn Gly His Ala Val Ala Leu Leu Tyr Ser Met Leu His Leu

65 70 75 80

Thr Gly Tyr Asp Leu Ser Ile Glu Asp Leu Lys Gln Phe Arg Gln Leu

85 90 95

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

100 105 110

Val Thr Thr Gly Pro Leu Gly Gln Gly Ile Ser Asn Ala Val Gly Met

115 120 125

Ala Met Ala Gln Ala Asn Leu Ala Ala Thr Tyr Asn Lys Pro Gly Phe

130 135 140

Thr Leu Ser Asp Asn Tyr Thr Tyr Val Phe Leu Gly Asp Gly Cys Leu

145 150 155 160

Gln Glu Gly Ile Ser Ser Glu Ala Ser Ser Leu Ala Gly His Leu Lys

165 170 175

Leu Gly Asn Leu Ile Ala Ile Tyr Asp Asp Asn Lys Ile Thr Ile Asp

180 185 190

Gly Ala Thr Ser Ile Ser Phe Asp Glu Asp Val Ala Lys Arg Tyr Glu

195 200 205

Ala Tyr Gly Trp Glu Val Leu Tyr Val Glu Asn Gly Asn Glu Asp Leu

210 215 220

Ala Gly Ile Ala Lys Ala Ile Ala Gln Ala Lys Leu Ser Lys Asp Lys

225 230 235 240

Pro Thr Leu Ile Lys Met Thr Thr Thr Ile Gly Tyr Gly Ser Leu His

245 250 255

Ala Gly Ser His Ser Val His Gly Ala Pro Leu Lys Ala Asp Asp Val

260 265 270

Lys Gln Leu Lys Ser Lys Phe Gly Phe Asn Pro Asp Lys Ser Phe Val

275 280 285

Val Pro Gln Glu Val Tyr Asp His Tyr Gln Lys Thr Ile Leu Lys Pro

290 295 300

170

Gly Val Glu Ala Asn Asn Lys Trp Asn Lys Leu Phe Ser Glu Tyr Gln
305 310 315 320

Lys Lys Phe Pro Glu Leu Gly Ala Glu Leu Ala Arg Arg Leu Ser Gly
325 330 335

Gln Leu Pro Ala Asn Trp Glu Ser Lys Leu Pro Thr Tyr Thr Ala Lys
340 345 350

Asp Ser Ala Val Ala Thr Arg Lys Leu Ser Glu Thr Val Leu Glu Asp
355 360 365

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

Pro Ser Asn Leu Thr Arg Trp Lys Glu Ala Leu Asp Phe Gln Pro Pro
385 390 395 400

Ser Ser Gly Ser Gly Asn Tyr Ser Gly Arg Tyr Ile Arg Tyr Gly Ile
405 410 415

Arg Glu His Ala Met Gly Ala Ile Met Asn Gly Ile Ser Ala Phe Gly
420 425 430

Ala Asn Tyr Lys Pro Tyr Gly Gly Thr Phe Leu Asn Phe Val Ser Tyr
435 440 445

Ala Ala Gly Ala Val Arg Leu Ser Ala Leu Ser Gly His Pro Val Ile

450

455

460

Trp Val Ala Thr His Asp Ser Ile Gly Val Gly Glu Asp Gly Pro Thr

465

470

475

480

His Gln Pro Ile Glu Thr Leu Ala His Phe Arg Ser Leu Pro Asn Ile

485

490

495

Gln Val Trp Arg Pro Ala Asp Gly Asn Glu Val Ser Ala Ala Tyr Lys

500

505

510

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

515

520

525

Gln Asn Leu Pro Gln Leu Glu Gly Ser Ser Ile Glu Ser Ala Ser Lys

530

535

540

Gly Gly Tyr Val Leu Gln Asp Val Ala Asn Pro Asp Ile Ile Leu Val

545

550

555

560

Ala Thr Gly Ser Glu Val Ser Leu Ser Val Glu Ala Ala Lys Thr Leu

565

570

575

Ala Ala Lys Asn Ile Lys Ala Arg Val Val Ser Leu Pro Asp Phe Phe

580

585

590

Thr Phe Asp Lys Gln Pro Leu Glu Tyr Arg Leu Ser Val Leu Pro Asp

595	600	605	
Asn Val Pro Ile Met Ser Val Glu Val Leu Ala Thr Thr Cys Trp Gly			
610	615	620	
Lys Tyr Ala His Gln Ser Phe Gly Ile Asp Arg Phe Gly Ala Ser Gly			
625	630	635	640
Lys Ala Pro Glu Val Phe Lys Phe Phe Gly Phe Thr Pro Glu Gly Val			
	645	650	655
Ala Glu Arg Ala Gln Lys Thr Ile Ala Phe Tyr Lys Gly Asp Lys Leu			
	660	665	670
Ile Ser Pro Leu Lys Lys Ala Phe			
675	680		

<210> 124

<211> 370

<212> PRT

<213> Saccharomyces cerevisiae CEN.PK-1D

<400> 124

Met Ser Glu Ser Pro Met Phe Ala Ala Asn Gly Met Pro Lys Val Asn

1	5	10	15
---	---	----	----

Gln Gly Ala Glu Glu Asp Val Arg Ile Leu Gly Tyr Asp Pro Leu Ala

20	25	30	
Ser Pro Ala Leu Leu Gln Val Gln Ile Pro Ala Thr Pro Thr Ser Leu			
35	40	45	
Glu Thr Ala Lys Arg Gly Arg Arg Glu Ala Ile Asp Ile Ile Thr Gly			
50	55	60	
Lys Asp Asp Arg Val Leu Val Ile Val Gly Pro Cys Ser Ile His Asp			
65	70	75	80
Leu Glu Ala Ala Gln Glu Tyr Ala Leu Arg Leu Lys Lys Leu Ser Asp			
85	90	95	
Glu Leu Lys Gly Asp Leu Ser Ile Ile Met Arg Ala Tyr Leu Glu Lys			
100	105	110	
Pro Arg Thr Thr Val Gly Trp Lys Gly Leu Ile Asn Asp Pro Asp Val			
115	120	125	
Asn Asn Thr Phe Asn Ile Asn Lys Gly Leu Gln Ser Ala Arg Gln Leu			
130	135	140	
Phe Val Asn Leu Thr Asn Ile Gly Leu Pro Ile Gly Ser Glu Met Leu			
145	150	155	160
Asp Thr Ile Ser Pro Gln Tyr Leu Ala Asp Leu Val Ser Phe Gly Ala			
165	170	175	
174			

Ile Gly Ala Arg Thr Thr Glu Ser Gln Leu His Arg Glu Leu Ala Ser

180

185

190

Gly Leu Ser Phe Pro Val Gly Phe Lys Asn Gly Thr Asp Gly Thr Leu

195

200

205

Asn Val Ala Val Asp Ala Cys Gln Ala Ala Ala His Ser His His Phe

210

215

220

Met Gly Val Thr Lys His Gly Val Ala Ala Ile Thr Thr Thr Lys Gly

225

230

235

240

Asn Glu His Cys Phe Val Ile Leu Arg Gly Gly Lys Lys Gly Thr Asn

245

250

255

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

260

265

270

Ser Asn Gly Leu Met Ile Asp Tyr Ser His Gly Asn Ser Asn Lys Asp

275

280

285

Phe Arg Asn Gln Pro Lys Val Asn Asp Val Val Cys Glu Gln Ile Ala

290

295

300

Asn Gly Glu Asn Ala Ile Thr Gly Val Met Ile Glu Ser Asn Ile Asn

305

310

315

320

Glu Gly Asn Gln Gly Ile Pro Ala Glu Gly Lys Ala Gly Leu Lys Tyr
325 330 335

Gly Val Ser Ile Thr Asp Ala Cys Ile Gly Trp Glu Thr Thr Glu Asp
340 345 350

Val Leu Arg Lys Leu Ala Ala Ala Val Arg Gln Arg Arg Glu Val Asn
355 360 365

Lys Lys
370