

PF58891.ST25.txt
SEQUENCE LISTING

<110> Cropdesign N.V.
Crop Functional Genomics Center

<120> Plants having enhanced yield-related traits and a method for making the same

<130> PF58891

<160> 114

<170> PatentIn version 3.3

<210> 1
<211> 402
<212> DNA
<213> Xanthomonas axonopodis

<400> 1
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cagctgctga cccagctcat catggccttg cttcagcaga gcaacaatgc cgagcagggg 180
caggggtcaag gccaggggtg tgactctggc ggtcagggcg gcaatccgcg gcaggccggg 240
cagtcacaacg gctccccctc gcaatacacc caggcgctga tgaatatcgt cggagacatt 300
ctccaggcgc agaatgggtg cggttcggc ggcggctttg gtggtggctt cgggtggcatc 360
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<210> 2
<211> 133
<212> PRT
<213> Xanthomonas axonopodis

<400> 2
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1 5 10 15
Val Asp Pro Gly Gln Asn Thr Gln Ser Ser Pro Asn Gln Gly Asn Gln
20 25 30
Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Thr Gln Leu Ile Met
35 40 45
Ala Leu Leu Gln Gln Ser Asn Asn Ala Glu Gln Gly Gln Gly Gln Gly
50 55 60
Gln Gly Gly Asp Ser Gly Gly Gln Gly Gly Asn Pro Arg Gln Ala Gly
65 70 75 80
Gln Ser Asn Gly Ser Pro Ser Gln Tyr Thr Gln Ala Leu Met Asn Ile
85 90 95
Val Gly Asp Ile Leu Gln Ala Gln Asn Gly Gly Gly Phe Gly Gly Gly
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115 120 125
Thr Gly Ser Met Gln
130

<210> 3

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<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> conserved motif 1

<220>
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<223> /replace = "Glu" /replace = "Asp"

<220>
<221> VARIANT
<222> (3)..(3)
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<220>
<221> UNSURE
<222> (4)..(4)
<223> Xaa can e any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace = "Arg" /replace = "Pro"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace = "Ser"

<220>
<221> UNSURE
<222> (9)..(9)
<223> Xaa can e any naturally occurring amino acid

<220>
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<400> 3
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<210> 4
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> conserved motif 2

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<220>
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<220>
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<223> /replace = "Gln" /replace = "Ala"

<220>
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<222> (4)..(4)
<223> /replace = "Leu" /replace = "Tyr"

<220>
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<222> (7)..(7)
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<220>
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<222> (10)..(10)
<223> /replace = "Asn" /replace = "Gln"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace = "Met"

<220>
<221> VARIANT
<222> (14)..(14)
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<210> 5
<211> 2194
<212> DNA
<213> Oryza sativa

<400> 5
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catccaccta ctttagtggc aatcgggcta aataaaaaaag agtcgctaca ctagtttcgt      180
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tctgtcatga agttaaatga ttgcaggtag ccataattgt catcaaaactc ttcttgaata      300
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atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt      420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat      480
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<210> 6
 <211> 1179
 <212> DNA
 <213> Oryza sativa

<400> 6						
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cattaccact	ttacctgaca	ttttggacag	agattagaaa	tagtttcgta	ctacctgcaa	180
gttgcaactt	gaaaagtgaa	atltgttcct	tgtcaatata	ttggcgtgta	attcttttat	240
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cagacccaat	gggccttttc	tacgtgtctc	ggccacagcc	agtcgtttac	cgcacgttca	660
catgggcacg	aactcgcgtc	atcttcccac	gcaaaacgac	agatctgccc	tatctggtcc	720
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acgccccaac	acgcacacg	ggtcgcgata	gccacgacct	aatcacacaa	cgcacgtcca	840
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gtacacttga gctcactcca aactcaaaca ctcacacca 1179

<210> 7
 <211> 402
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic construct mutant elicitor of hypersensitive response
 HpaG_T44C gene

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 cagctgctgt gccagctcat catggccctg cttcagcaga gcaacaatgc cgagcagggg 180
 caggggtcaag gccaggggtg tgactctggc ggtcagggcg gcaatccgcg gcaggccggg 240
 cagtccaacg gctccccctc gcaatacacc caggcgctga tgaatatcgt cggagacatt 300
 ctccaggcgc agaatggtg cggtctcgcc ggcggtttg gtggtggctt cgggtggcatc 360
 ctcgtcacca gccttgcgag cgacaccgga tcgatgcagt aa 402

<210> 8
 <211> 133
 <212> PRT
 <213> Artificial sequence

<220>
 <223> mutant elicitor of hypersensitive response HpaG_T44C

<400> 8
 Met Asn Ser Leu Asn Thr Gln Leu Gly Ala Asn Ser Ser Phe Phe Gln
 1 5 10 15
 Val Asp Pro Gly Gln Asn Thr Gln Ser Ser Pro Asn Gln Gly Asn Gln
 20 25 30
 Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Cys Gln Leu Ile Met
 35 40 45
 Ala Leu Leu Gln Gln Ser Asn Asn Ala Glu Gln Gly Gln Gly Gln Gly
 50 55 60
 Gln Gly Gly Asp Ser Gly Gly Gln Gly Gly Asn Pro Arg Gln Ala Gly
 65 70 75 80
 Gln Ser Asn Gly Ser Pro Ser Gln Tyr Thr Gln Ala Leu Met Asn Ile
 85 90 95
 Val Gly Asp Ile Leu Gln Ala Gln Asn Gly Gly Gly Phe Gly Gly Gly
 100 105 110
 Phe Gly Gly Gly Phe Gly Gly Ile Leu Val Thr Ser Leu Ala Ser Asp
 115 120 125
 Thr Gly Ser Met Gln
 130

<210> 9
 <211> 378
 <212> DNA
 <213> Artificial sequence

<220>

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<223> synthetic construct mutant elicitor of hypersensitive response
HpaG-T gene

<400> 9
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cagctgctga cccagctcat catggccctg cttcagcaga gcaacaatgc cgagcagggg 180
caggggtcaag gccaggggtg tgactctggc ggtcagggcg gcaatccgcg gcaggccggg 240
cagccaacg gctccccctc gcaatacacc caggcgctga tgaatatcgt cggagacggc 300
ttcggcgcg gctttggtgg tggttcggg ggcacccctc tcaccagcct tgcgagcgac 360
accggtcga tgcagtaa 378

<210> 10
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> mutant elicitor of hypersensitive response HpaG-T

<400> 10
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1 5 10 15
Val Asp Pro Gly Gln Asn Thr Gln Ser Ser Pro Asn Gln Gly Asn Gln
20 25 30
Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Thr Gln Leu Ile Met
35 40 45
Ala Leu Leu Gln Gln Ser Asn Asn Ala Glu Gln Gly Gln Gly Gln Gly
50 55 60
Gln Gly Gly Asp Ser Gly Gly Gln Gly Gly Asn Pro Arg Gln Ala Gly
65 70 75 80
Gln Ser Asn Gly Ser Pro Ser Gln Tyr Thr Gln Ala Leu Met Asn Ile
85 90 95
Val Gly Asp Gly Phe Gly Gly Gly Phe Gly Gly Gly Phe Gly Gly Ile
100 105 110
Leu Val Thr Ser Leu Ala Ser Asp Thr Gly Ser Met Gln
115 120 125

<210> 11
<211> 414
<212> DNA
<213> Xanthomonas axonopodis pv. citri

<400> 11
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tccgacgata ttcacagca tctgggtgta ttgcgagggg gagccgttgg actgaccggc 180
ctgctgccga ttgccgccct gaccaccaga gtcaccaccc tggccttgac cctgaccctg 240
ctcggcattg ttgctctgct gaagcagggc catgatgagc tgggtcagca gctggtccag 300
ttgcttttcc gagatgccct gggtgccctg gttcgaacca gattgcgtgt tctggctggg 360
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<210> 12
<211> 137

PF58891.ST25.txt

<212> PRT

<213> Xanthomonas axonopodis pv. citri

<400> 12

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

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<210> 13

<211> 366

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic construct mutant elicitor of hypersensitive response
HpaG-N gene

<400> 13

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cagagcaaca atgccgagca gggtcagggc caaggccagg gtggtgactc tggcggtcag      180
ggcggcaatc cgcggcaggc cgggcagtc aacggctccc cctcgcaata caccagggcg      240
ctgatgaata tcgtcggaga cattctccag gcgcagaatg gtggcggcgtt cggcggcggc      300
tttggtggtg gcttcggtgg catcctcgtc accagccttg cgagcgacac cggatcgatg      360
cagtaa                                           366

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<210> 14

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> mutant elicitor of hypersensitive response HpaG-N

<400> 14

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Met Asn Ser Leu Asn Thr Gln Leu Gly Ala Asn Ser Ser Phe Phe Gln
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Val Asp Pro Gly Gln Asn Thr Gln Ser Ser Pro Asn Gln Gly Asn Thr
          20          25          30

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Gln	Leu	Ile	Met	Ala	Leu	Leu	Gln	Gln	Ser	Asn	Asn	Ala	Glu	Gln	Gly
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Gln	Gly	Gln	Gly	Gln	Gly	Gly	Asp	Ser	Gly	Gly	Gln	Gly	Gly	Asn	Pro
	50					55					60				
Arg	Gln	Ala	Gly	Gln	Ser	Asn	Gly	Ser	Pro	Ser	Gln	Tyr	Thr	Gln	Ala
65					70				75						80
Leu	Met	Asn	Ile	Val	Gly	Asp	Ile	Leu	Gln	Ala	Gln	Asn	Gly	Gly	Gly
			85					90					95		
Phe	Gly	Gly	Gly	Phe	Gly	Gly	Gly	Phe	Gly	Gly	Ile	Leu	Val	Thr	Ser
			100					105					110		
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		115					120								

<210> 15
 <211> 366
 <212> DNA
 <213> Xanthomonas axonopodis

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cagctgctga cccagctcat catggccctg cttcagcaga gcaacaatgc cgagcagggg	180
caggggtcaag gccaggggtg tgactctggc ggtcagggcg gcaatccgcg gcaggccggg	240
cagtccaacg gctccccctc gcaatacacc caggcgctga tgaatatcgt cggagacatt	300
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cagtaa	366

<210> 16
 <211> 121
 <212> PRT
 <213> Xanthomonas axonopodis

<400> 16	
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1	15
Val Asp Pro Gly Gln Asn Thr Gln Ser Ser Pro Asn Gln Gly Asn Gln	
	30
Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Thr Gln Leu Ile Met	
	45
Ala Leu Leu Gln Gln Ser Asn Asn Ala Glu Gln Gly Gln Gly Gln Gly	
50	60
Gln Gly Gly Asp Ser Gly Gly Gln Gly Gly Asn Pro Arg Gln Ala Gly	
65	80
Gln Ser Asn Gly Ser Pro Ser Gln Tyr Thr Gln Ala Leu Met Asn Ile	
	95
Val Gly Asp Ile Leu Gln Ala Gln Asn Gly Phe Ile Leu Val Thr Ser	
	110
Leu Ala Ser Asp Thr Gly Ser Met Gln	
	120

<210> 17
 <211> 402
 <212> DNA
 <213> Xanthomonas smithii subsp. smithii

PF58891.ST25.txt

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<400> 17
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cagctgctga cccagctcat catggccctg cttcagcaga gcaacaatgc cgaccagggc 180
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aatggtggg gcttcggcgg cgggttcggc ggtggccttg gtggcgggct cggcaccagc 360
ctcggcagca gccttgcgag cgacaccgga tcgatgcagt aa 402
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<210> 18
<211> 133
<212> PRT
<213> Xanthomonas smithii subsp. smithii
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<400> 18
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20 25 30
Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Thr Gln Leu Ile Met
35 40 45
Ala Leu Leu Gln Gln Ser Asn Asn Ala Asp Gln Gly Gln Gly Gly Asp
50 55 60
Ser Gly Gly Gln Gly Gly Asn Ser Arg Gln Ala Gly Gln Pro Asn Gly
65 70 75 80
Ser Pro Ser Ala Tyr Thr Gln Met Leu Met Asn Ile Val Gly Asp Ile
85 90 95
Leu Gln Ala Gln Asn Gly Gly Gly Phe Gly Gly Gly Phe Gly Gly Gly
100 105 110
Phe Gly Gly Gly Leu Gly Thr Ser Leu Gly Ser Ser Leu Ala Ser Asp
115 120 125
Thr Gly Ser Met Gln
130
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<210> 19
<211> 420
<212> DNA
<213> Xanthomonas oryzae pv. oryzae
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gaccagttgc tgtgccagct catctcggcc ctgcttcagt cgagcaaaaa tgctgaggag 180
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cagcagaatg gcccctcgcc attcaccagc atgctgatgc atatcgctcg agagattctc 300
caggcgcaga atggtgggtg tgctggtggc ggcgggttcg gcggcggggt cggcggcgac 360
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<210> 20
<211> 139
<212> PRT
<213> Xanthomonas oryzae pv. oryzae
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PF58891.ST25.txt

<400> 20

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

```

<210> 21

<211> 420

<212> DNA

<213> *Xanthomonas oryzae* pv. *oryzae*

<400> 21

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gaccagttgc tgtgccagct catctcggcc ctgcttcagt cgagcaaaaa tgctgaggag    180
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caggcgcaga atggtggtgg tgctggtggc ggcgggttcg gcggcgggtt cggcgggtgac   360
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<210> 22

<211> 139

<212> PRT

<213> *Xanthomonas oryzae* pv. *oryzae*

<400> 22

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20        25        30
Gln Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Cys Gln Leu Ile
35        40        45
Ser Ala Leu Leu Gln Ser Ser Lys Asn Ala Glu Glu Gly Lys Gly Gln
50        55        60
Gly Gly Asp Asn Gly Gly Gly Gln Gly Gly Asn Ser Gln Gln Ala Gly
65        70        75        80
Gln Gln Asn Gly Pro Ser Pro Phe Thr Gln Met Leu Met His Ile Val
85        90        95
Gly Glu Ile Leu Gln Ala Gln Asn Gly Gly Gly Ala Gly Gly Gly Gly
100       105       110

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Phe Gly Gly Gly Phe Gly Gly Asp Phe Ser Gly Asp Leu Gly Leu Gly
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 Thr Asn Leu Ser Ser Asp Ser Ala Ser Met Gln
 130 135

<210> 23
 <211> 420
 <212> DNA
 <213> Xanthomonas oryzae pv. oryzae

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 caggcgcaga atgggtggtg tgctggtggc ggcgggttcg gcggcgggtt cggcgggtgac 360
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<210> 24
 <211> 139
 <212> PRT
 <213> Xanthomonas oryzae pv. oryzae

<400> 24
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 Gln Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Cys Gln Leu Ile
 35 40 45
 Ser Ala Leu Leu Gln Ser Ser Lys Asn Ala Glu Glu Gly Lys Gly Gln
 50 55 60
 Gly Gly Asp Asn Gly Gly Gly Gln Gly Gly Asn Ser Gln Gln Ala Gly
 65 70 75 80
 Gln Gln Asn Gly Pro Ser Pro Phe Thr Gln Met Leu Met His Ile Val
 85 90 95
 Gly Glu Ile Leu Gln Ala Gln Asn Gly Gly Gly Ala Gly Gly Gly Gly
 100 105 110
 Phe Gly Gly Gly Phe Gly Gly Asp Phe Ser Gly Asp Leu Gly Leu Gly
 115 120 125
 Thr Asn Leu Ser Ser Asp Ser Ala Ser Met Gln
 130 135

<210> 25
 <211> 378
 <212> DNA
 <213> Xanthomonas oryzae pv. oryzicola

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 caactggacc agttgctgtg ccagctcatc caggccctgc ttcagccgaa caaaaatgct 180
 gaggaaggta agggtcagca ggggtggcgag aataatcagc aggcggggaa ggagaatggc 240

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gcccggcgca gcagcggcgg cgactttggg ggcagtttcg ccagcagctt ctcgaacgac 360
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<210> 26
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<212> PRT
<213> *Xanthomonas oryzae* pv. *oryzicola*

<400> 26
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Gly Ser Gln Gly Ile Ser Glu Lys Gln Leu Asp Gln Leu Leu Cys Gln
35 40 45
Leu Ile Gln Ala Leu Leu Gln Pro Asn Lys Asn Ala Glu Glu Gly Lys
50 55 60
Gly Gln Gln Gly Gly Glu Asn Asn Gln Gln Ala Gly Lys Glu Asn Gly
65 70 75 80
Ala Ser Pro Leu Thr Gln Met Leu Met Asn Ile Val Gly Glu Ile Leu
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Gln Ala Gln Asn Ala Gly Gly Ser Ser Gly Gly Asp Phe Gly Gly Ser
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Phe Ala Ser Ser Phe Ser Asn Asp Ser Gly Ser Met Gln
115 120 125

<210> 27
<211> 366
<212> DNA
<213> *Xanthomonas campestris* pv. *campestris*

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gtccat 366

<210> 28
<211> 121
<212> PRT
<213> *Xanthomonas campestris* pv. *campestris*

<400> 28
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20 25 30
Pro Ser Ala Asp Ser Glu Gln Gln Leu Asp Gln Leu Leu Ala Met Phe
35 40 45
Ile Met Met Met Leu Gln Gln Ser Gln Gly Ser Asp Ala Asp Gln Glu

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Cys Gly Asp Glu Gln Pro Gln Ser Gly Gln Gln Asp Gly Val Ser Pro				
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Leu Thr Gln Met Leu Met Gln Ile Val Met Gln Leu Met Gln Asn Gln				
	85		90	95
Gly Gly Ala Gly Met Gly Gly Thr Ser Leu Gly Gly Gly Phe Asn Ala				
	100		105	110
Asn Leu Ser Ser Ile Thr Gly Gln Ala				
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<210> 29
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 <212> DNA
 <213> Synechocystis sp.

<400> 29

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<210> 30
 <211> 1039
 <212> PRT
 <213> Synechocystis sp.

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Thr Ile Gly Asp Arg His Pro Phe Ala Leu Asp Leu Pro Asp Leu Leu
35     40     45
Gln Ala Trp Ser Asn Leu Pro Leu Ala Phe Pro Lys Ala Asp Gly Val
50     55     60
Thr Glu Ala Ala Leu Thr Leu His Leu Pro Ser His Arg Gln Gln Lys
65     70     75     80
Ile Pro Leu Pro Phe Val Thr Gly Gln Asp Pro Val Ala Met Asp Ala
85     90     95
Lys Tyr Leu His Trp Arg Ser Trp Gln Val Thr Gly Val Asn Leu Thr
100    105    110
Pro Ser Gln Thr Leu Thr Leu Gln Ser Ile Pro Leu Gly Gly Gln
115    120    125
Ala Leu Ala Asn Leu Gly Ser Glu Phe Tyr Phe Tyr Gly Gln Leu His
130    135    140
Arg Trp Cys Leu Asp Leu Val Leu Arg Gly Lys Phe Val Pro Gly Leu
145    150    155    160
Glu Gln Arg Gly Glu Asp Gly Asn Tyr Tyr Ala Gln Trp Ile Pro Ile
165    170    175
Leu Asp Ser Ile Gln Asp Gln Thr His Leu Ala Gln Phe Ser Gln Arg
180    185    190
Val Pro Ala Cys Ala Leu Ala Asn Leu Thr Asp Ser Gln Glu Pro Gln
195    200    205
Met Leu Val Val Asp Leu Leu Gln Lys Leu Leu Gln Ala Gln Ile Gly
210    215    220
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225    230    235    240

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Gln	Trp	Arg	Gly	Ala	Leu	Arg	Leu	Gln	Pro	Pro	Ala	Asp	Asp	Gly	Gly
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Val	Trp	Gln	Gly	Arg	Arg	Val	Asp	Gln	Gly	Ala	Glu	Ser	Leu	Leu	Arg
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Thr	Glu	Arg	Cys	Pro	Thr	Gly	Cys	Gly	Leu	Asp	Ala	Ile	Gln	Ala	Tyr
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Val	Ile	Leu	Pro	Pro	Gly	Leu	Glu	Arg	Gly	Gly	Thr	Ala	Lys	Arg	Leu
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Gly	Val	Lys	Val	Val	Gly	Glu	Val	Gln	Arg	Gln	Arg	Gly	Gln	Arg	Leu
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Gln	Ala	Arg	Gly	Val	Gly	Trp	Leu	Ala	Phe	Leu	Glu	Arg	Trp	Gly	Leu
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Arg	Arg	Lys	Lys	Gly	Gln	Pro	Leu	Val	Lys	Gln	Val	Lys	Asp	Gln	Gln
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Gly Phe Arg Ile Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Thr
705 710 715 720
Glu Leu Trp Ser Ile Leu Glu Phe Leu Asn Pro Gly Phe Leu Gly Asn
725 730 735
Gln Ser Phe Phe Gln Arg Arg Phe Ala Asn Pro Ile Glu Lys Phe Gly
740 745 750
Asp Arg Gln Ser Leu Leu Ile Leu Arg Asn Leu Val Arg Pro Phe Ile
755 760 765
Leu Arg Arg Leu Lys Thr Asp Gln Thr Ile Ile Gln Asp Leu Pro Glu
770 775 780
Lys Gln Glu Met Thr Val Phe Cys Asp Leu Ser Gln Glu Gln Ala Gly
785 790 795 800
Leu Tyr Gln Gln Leu Val Glu Glu Ser Leu Gln Ala Ile Ala Asp Ser
805 810 815
Glu Gly Ile Gln Arg His Gly Leu Val Leu Thr Leu Leu Thr Lys Leu
820 825 830
Lys Gln Val Cys Asn His Pro Asp Leu Leu Leu Lys Lys Pro Ala Ile
835 840 845
Thr His Gly His Gln Ser Gly Lys Leu Ile Arg Leu Ala Glu Met Leu
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900 905 910
Ala Leu Val Glu Arg Phe Gln Gln Asp Pro Asn Ser Pro Tyr Leu Phe
915 920 925
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930 935 940
Asn His Val Phe His Val Asp Arg Trp Trp Asn Pro Ala Val Glu Asn
945 950 955 960
Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Thr Arg Asn Val Gln
965 970 975
Val His Lys Phe Val Cys Thr Gly Thr Leu Glu Glu Lys Ile Asn Ala
980 985 990
Met Met Ala Asp Lys Gln Gln Leu Ala Glu Gln Thr Val Asp Ala Gly
995 1000 1005
Glu Asn Trp Leu Thr Arg Leu Asp Thr Asp Lys Leu Arg Gln Leu
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Asp

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<210> 31
 <211> 3237
 <212> DNA
 <213> *Anaebena variabilis*

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<400> 31

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tttgtttgca	atggtacctt	agaagaaaa	atccacgaca	tgattgaaag	taaaaacaa	3120
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3237

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 <212> PRT
 <213> *Anaebena variabilis*

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 Phe Glu Glu Ile Ala Leu Asn Pro Leu Ala Leu Ser Ala Ser Glu Leu
 35 40 45
 Ser Glu Trp Leu Gln Ser Gln His Gln Ala Ile Ala Gln Ile Leu Pro
 50 55 60
 Gln Gln Leu Ala Lys Lys Thr Ser Lys Ala Ala Ser Ser Pro Thr Thr
 65 70 75 80
 Asn Leu Pro Ile His Ser Gln Ile Ile Val Leu Pro Thr Glu Ile Ser
 85 90 95
 Gln Pro Arg Lys Lys Glu Thr Ile Phe Ile Ser Pro Val His Ser Ala
 100 105 110
 Ala Leu Glu Ser Asp Ala Asp Ser Glu Val Tyr Leu Gln Pro Trp Arg
 115 120 125
 Val Glu Gly Phe Cys Leu Pro Pro Ser Ala Ala Val Lys Phe Leu Thr
 130 135 140
 Ser Leu Pro Leu Asn Ile Thr Ser Thr Glu Asn Ala Phe Leu Gly Gly
 145 150 155 160
 Asp Leu Arg Phe Trp Ser Gln Ile Ala Arg Trp Ser Leu Asp Leu Ile
 165 170 175
 Ser Arg Ser Lys Phe Leu Pro Ile Ile Gln Arg Gln Pro Asn Asn Ser
 180 185 190
 Val Ser Ala Lys Trp Gln Val Leu Leu Asp Ser Ala Val Asp Gly Thr
 195 200 205
 Arg Leu Glu Lys Phe Ala Ala Lys Met Pro Leu Val Cys Arg Thr Tyr
 210 215 220
 Gln Arg Leu Gly Asn Glu Glu Leu Ser Pro Ser Pro Ile Tyr Ile Asp
 225 230 235 240
 Phe Pro Ser Gln Pro Gln Glu Leu Ile Leu Gly Phe Leu Asn Ser Ala
 245 250 255
 Ile Asp Thr Gln Leu Arg Glu Met Val Gly Asn Gln Pro Val Val Glu
 260 265 270
 Thr Arg Leu Met Ala Ser Leu Pro Ser Ala Val Arg Gln Trp Leu Gln
 275 280 285
 Gly Leu Ser Gly Ala Ser Asn Ser Val Asp Ala Asp Ala Val Gly Leu
 290 295 300
 Glu Arg Leu Glu Ala Ala Leu Lys Ala Trp Thr Met Pro Leu Gln Tyr
 305 310 315 320
 Gln Leu Ala Ser Lys Asn Gln Phe Arg Thr Cys Phe Glu Leu Arg Ser
 325 330 335
 Pro Glu Pro Gly Glu Thr Glu Trp Thr Leu Ala Tyr Phe Leu Gln Ala
 340 345 350
 Ala Asp Asn Pro Glu Phe Leu Val Asp Ala Gly Thr Ile Trp Gln His
 355 360 365

PF58891.ST25.txt

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Ile Ala Pro Thr Leu Asp Thr Glu Ser Pro Gln Phe Cys His Leu Asn
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Pro Met Gln Ala Tyr Glu Phe Ile Lys Ala Val Ala Trp Arg Phe Glu
          420          425          430
Asp Ser Gly Leu Gly Val Ile Leu Pro Pro Ser Leu Ala Asn Arg Glu
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Gly Trp Ala Asn Arg Leu Gly Leu Lys Ile Ser Ala Glu Thr Pro Lys
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Lys Lys Pro Gly Arg Leu Gly Leu Gln Ser Leu Leu Asn Phe Gln Trp
465          470          475          480
His Leu Ala Ile Gly Gly Gln Thr Ile Ser Lys Gly Glu Phe Asp Arg
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Leu Val Ala Leu Lys Ser Pro Leu Val Glu Ile Asn Gly Glu Trp Val
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Glu Leu Arg Pro Gln Asp Ile Lys Thr Ala Glu Ala Phe Phe Ala Ala
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Arg Lys Asp Gln Met Ala Leu Ser Leu Glu Asp Ala Leu Arg Leu Ser
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Ser Gly Asp Thr Gln Val Ile Glu Lys Leu Pro Val Val Ser Phe Glu
545          550          555          560
Ala Ser Gly Ala Leu Gln Glu Leu Ile Gly Ala Leu Thr Asn Asn Gln
          565          570          575
Ala Val Ala Pro Leu Pro Thr Pro Lys Asn Phe Gln Gly Lys Leu Arg
          580          585          590
Pro Tyr Gln Glu Arg Gly Ala Ala Trp Leu Ala Phe Leu Glu Arg Trp
          595          600          605
Gly Leu Gly Ala Cys Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Ile
          610          615          620
Gln Phe Ile Ala Phe Leu Leu His Leu Lys Glu Gln Asp Val Leu Glu
625          630          635          640
Lys Pro Thr Leu Leu Val Cys Pro Thr Ser Val Leu Gly Asn Trp Glu
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Arg Glu Val Lys Lys Phe Ala Pro Thr Leu Lys Val Leu Gln Tyr His
          660          665          670
Gly Asp Lys Arg Pro Lys Gly Lys Ala Phe Pro Glu Ala Val Lys Asn
          675          680          685
His Asp Leu Val Ile Thr Ser Tyr Ser Leu Ile His Arg Asp Ile Lys
          690          695          700
Ser Leu Gln Gly Leu Ser Trp Gln Ile Ile Val Leu Asp Glu Ala Gln
705          710          715          720
Asn Val Lys Asn Ala Glu Ala Lys Gln Ser Gln Ala Val Arg Gln Leu
          725          730          735
Asp Thr Thr Phe Arg Ile Ala Leu Thr Gly Thr Pro Val Glu Asn Arg
          740          745          750
Leu Gln Glu Leu Trp Ser Ile Leu Asp Phe Leu Asn Pro Gly Tyr Leu
          755          760          765
Gly Asn Lys Gln Phe Phe Gln Arg Arg Phe Ala Met Pro Ile Glu Lys
          770          775          780
Tyr Gly Asp Ala Ala Ser Leu Asn Gln Leu Arg Ala Leu Val Gln Pro
785          790          795          800

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PF58891.ST25.txt

Phe Ile Leu Arg Arg Leu Lys Thr Asp Arg Asp Ile Ile Gln Asp Leu
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Pro Asp Lys Gln Glu Met Thr Val Phe Cys Gly Leu Thr Gly Glu Gln
820 825 830
Ala Ala Leu Tyr Gln Lys Val Val Glu Thr Ser Leu Ala Glu Ile Glu
835 840 845
Ser Ala Glu Gly Leu Gln Arg Arg Gly Met Ile Leu Ala Leu Leu Ile
850 855 860
Lys Leu Lys Gln Ile Cys Asn His Pro Ala Gln Tyr Leu Lys Thr Asn
865 870 875 880
Thr Leu Glu Gln Tyr Ser Ser Gly Lys Leu Gln Arg Leu Glu Glu Met
885 890 895
Leu Glu Glu Val Leu Ala Glu Ser Asn Thr Tyr Gly Val Ala Gly Ala
900 905 910
Gly Arg Ala Leu Ile Phe Thr Gln Phe Ala Glu Trp Gly Lys Leu Leu
915 920 925
Lys Pro His Leu Glu Lys Gln Leu Gly Arg Glu Val Phe Phe Leu Tyr
930 935 940
Gly Ser Thr Ser Lys Lys Gln Arg Glu Glu Met Ile Asp Arg Phe Gln
945 950 955 960
His Asp Pro Gln Gly Pro Pro Ile Met Ile Leu Ser Leu Lys Ala Gly
965 970 975
Gly Val Gly Leu Asn Leu Thr Arg Ala Asn His Val Phe His Phe Asp
980 985 990
Arg Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Thr Asp Arg Val Phe
995 1000 1005
Arg Ile Gly Gln Thr Arg Asn Val Gln Val His Lys Phe Val Cys
1010 1015 1020
Asn Gly Thr Leu Glu Glu Lys Ile His Asp Met Ile Glu Ser Lys
1025 1030 1035
Lys Gln Leu Ala Glu Gln Val Val Gly Ala Gly Glu Glu Trp Leu
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<212> DNA
<213> uncultured methanogenic archaeon

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PF58891.ST25.txt

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gatggctaa 3129

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 <212> PRT
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 20 25 30
 Arg Gly Arg Pro Arg Lys Ser Ala Gly Glu Lys Gln His Pro Phe His

PF58891.ST25.txt

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Ile	Leu	Pro	Ser	Ala	Thr	Asp	Arg	Pro	Leu	Arg	Ser	Ala	Ser	Pro	Ser	
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Ala	Leu	Glu	Ser	Gly	Glu	Glu	Thr	Asn	Pro	Asp	Ser	Ser	Leu	Gln	Phe	
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Leu	Pro	Trp	Thr	Val	Thr	Gly	Ile	Asn	Ile	Lys	Pro	Gly	Asn	Ala	Leu	
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Thr	Asp	Arg	Lys	His	Tyr	Ala	Ser	Leu	Glu	Asn	Ser	Met	Pro	Leu	Ala	
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Glu	Met	Lys	Lys	Leu	Lys	Asp	Ser	Ala	Gly	Arg	Trp	Thr	Ser	Arg	Met	
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Lys	Thr	Glu	Ser	Lys	Gln	Ala	Leu	Lys	Thr	Cys	Phe	Ile	Leu	Glu	Pro	
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Pro	Ala	Pro	Asp	Thr	Glu	Tyr	Pro	Glu	Ala	Pro	Trp	Asn	Leu	Arg	Tyr	
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Cys	Leu	Gln	Ala	Ser	Asp	Asp	Pro	Ser	Leu	Val	Ile	Pro	Ala	Glu	Thr	
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	370					375					380					
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PF58891.ST25.txt

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Ser Gly Met Lys Ser Ser Gly Trp Leu Ala Glu Leu Phe Asp Arg Leu
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545          550          555          560
Gly Glu Leu Arg Asp Tyr Gln Val Lys Gly Tyr Ser Trp Leu Ala Phe
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Met Lys Lys Tyr Gly Leu Gly Ser Ile Leu Ala Asp Asp Met Gly Leu
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Asn Trp Gln Arg Glu Ala Lys Lys Phe Ala Pro Ala Leu Lys Val His
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Val Lys Ala His Asp Leu Ile Leu Ser Thr Tyr Ala His Ala Tyr Arg
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Asp Glu Glu Leu Leu Lys Glu Val Asn Trp Lys Leu Val Val Leu Asp
          675          680          685
Glu Ala Gln Asn Ile Lys Asn His His Thr Arg Gln Ala Arg Ala Ile
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705          710          715          720
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Ile Lys Pro Leu Val Leu Arg Arg Val Lys Thr Asp Pro Ala Ile Ile
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Lys Asp Leu Pro Asp Lys Ile Glu Ile Lys Glu Pro Cys Asn Leu Thr
785          790          795          800
Lys Glu Gln Ala Thr Leu Tyr Glu Ala Ile Val Glu Asn Met Leu Lys
          805          810          815
Ser Ile Asp Lys Ala Thr Ala Met Gln Arg Arg Gly Ile Val Leu Ala
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Ser Leu Met Lys Leu Lys Gln Val Cys Asp His Pro Ser Leu Tyr Ile
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Leu Lys Arg Leu Thr Glu Leu Leu Glu Glu Ala Leu Ala Glu Gly Asp
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[illegible]

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PF58891.ST25.txt

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 <212> PRT
 <213> *Bacillus cereus*

<400> 36

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Ser	Phe	Ala	Arg	Ile	Gln	Met	Asn	Gly	Pro	Ile	Thr	Ala	Leu	Thr	Glu
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Asp	Ala	Asn	Glu	Leu	Trp	Asp	Ala	Phe	Thr	Ser	Gly	Ser	Phe	Val	Pro
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Lys	Arg	Leu	Tyr	Glu	His	Tyr	Asp	Phe	Thr	Lys	Arg	Gln	Leu	Asp	Ala
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Ala	Leu	His	Glu	Asp	Trp	Leu	Arg	Lys	Ile	Gly	Tyr	Ile	Glu	Asp	
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Ile	Glu	Ile	Glu	Leu	Asp	Gly	Tyr	Tyr	Glu	Asp	Leu	Phe	Gln
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Leu	His	Ile	Gly	Asp	Ile	Pro	Lys	Val	Asp	Val	Pro	Ser	Ser
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 35 40 45
 Ile Ile Glu Gln Leu Asn Ser Asn Lys Ile Lys Ile Glu Lys Asn Lys
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Gly	Ile	Lys	Leu	Asn	Val	Asp	Asp	Thr	Ile	Asn	Ile	Leu	Ser	Gln	Leu		115	120	125
Pro	Leu	Gly	Leu	Thr	Asn	Asn	Asp	Glu	Asn	Tyr	Ile	Gly	Asp	Asn	Leu		130	135	140
Lys	Phe	Trp	Thr	His	Ile	Tyr	Arg	Trp	Ser	Leu	Asp	Leu	Leu	Thr	Arg		145	150	155
Gly	Lys	Tyr	Leu	Pro	Gln	Met	Glu	Glu	Gln	Asp	Asn	Asn	Cys	Tyr	Gly		165	170	175
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Lys	Phe	Ile	Gln	Thr	Met	Pro	Asn	Ser	Ser	Leu	Ala	Tyr	His	Asn	Leu		195	200	205
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Val	Ala	Ile	Thr	Pro	Ser	Ser	Phe	Ile	Gln	Lys	Trp	Leu	Tyr	Ser	Leu		245	250	255
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Phe	Lys	Leu	Glu	Asn	Pro	Ala	Lys	Ser	Gly	Lys	Lys	Leu	Glu	Gln	Ser		305	310	315
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Cys	Asn	Asn	Arg	Thr	Ile	Asn	His	Pro	Gln	Glu	Thr	Leu	Leu	Lys	Gly		355	360	365
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Asp	Asn	Lys	Pro	Ser	Phe	Ser	Glu	Leu	Asp	Pro	Ile	Gln	Val	Tyr	Glu		385	390	395
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Thr	Ile	Ser	Lys	Lys	Asp	Phe	Glu	Lys	Leu	Leu	Ala	Gln	Lys	Ser	Pro		465	470	475
Leu	Val	Glu	Val	Lys	Gly	Glu	Trp	Ile	Ala	Leu	Gln	Pro	Ala	Asp	Val		485	490	495

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Pro	Arg	Gly	Phe	Lys	Gly	Gln	Leu	Arg	Pro	Tyr	Gln	Gln	Arg	Gly	Val	565	570	575
Gly	Trp	Leu	Ser	Phe	Leu	Glu	Lys	Trp	Gly	Leu	Gly	Ala	Cys	Leu	Ala	580	585	590
Asp	Asp	Met	Gly	Leu	Gly	Lys	Thr	Pro	Gln	Leu	Ile	Gly	Phe	Leu	Leu	595	600	605
His	Leu	Arg	Ser	Glu	Gly	Met	Leu	Asp	Gln	Pro	Thr	Leu	Val	Ile	Cys	610	615	620
Pro	Thr	Ser	Val	Leu	Asn	Asn	Trp	Glu	Arg	Glu	Val	Gln	Lys	Phe	Ala	625	630	635
Pro	Thr	Leu	Ser	Thr	Leu	Ile	His	His	Gly	Asp	Lys	Arg	Ser	Lys	Gly	645	650	655
Lys	Ala	Phe	Val	Lys	Ala	Val	Ser	Lys	Lys	Asn	Val	Ile	Ile	Thr	Ser	660	665	670
Tyr	Ser	Leu	Ile	Tyr	Arg	Asp	Ile	Lys	Ser	Phe	Glu	Gln	Val	Glu	Trp	675	680	685
Gln	Gly	Ile	Val	Leu	Asp	Glu	Ala	Gln	Asn	Ile	Lys	Asn	Pro	Gln	Ala	690	695	700
Lys	Gln	Ser	Gln	Ala	Val	Arg	Gln	Ile	Ser	Thr	Gln	Phe	Arg	Ile	Ala	705	710	715
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Thr	Asp	Lys	Thr	Ile	Ile	Gln	Asp	Leu	Pro	Glu	Lys	Gln	Glu	Met	Thr	785	790	795
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Val	Asp	Asn	Ser	Leu	Val	Ala	Ile	Glu	Glu	Lys	Thr	Gly	Ile	Glu	Arg	820	825	830
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His	Pro	Ala	His	Phe	Leu	Lys	Gln	Lys	Ser	Leu	Lys	Thr	Ala	Glu	Gln	850	855	860
Ser	Gly	Lys	Leu	Leu	Arg	Leu	Glu	Glu	Met	Leu	Glu	Glu	Leu	Ile	Glu	865	870	875
Glu	Gly	Asp	His	Ala	Leu	Ile	Phe	Thr	Gln	Phe	Ser	Glu	Trp	Gly	Lys	885	890	895
Leu	Leu	Gln	Pro	Tyr	Leu	Gln	Lys	Lys	Phe	Gln	Gln	Asp	Val	Leu	Phe	900	905	910
Leu	Tyr	Gly	Ala	Thr	Arg	Arg	Val	Gln	Arg	Gln	Glu	Met	Ile	Asp	Arg	915	920	925

PF58891.ST25.txt

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 Ala Gly Gly Thr Gly Leu Asn Leu Thr Arg Ala Asn His Val Phe His
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 995 1000 1005
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 <212> DNA
 <213> Gloeobacter violaceus

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PF58891.ST25.txt

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<212> PRT
<213> Gloeobacter violaceus

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Arg Ser Glu Ala Pro Ala Pro His Pro Tyr Val Gln Gln Pro Ala Glu
35     40     45
Leu Ser Pro Arg Leu Ala Ala Gln Phe Pro Gln Ile Pro Leu Ser Leu
50     55     60
Leu Val Pro Glu Thr Leu Ala Leu Gln Leu Pro Ala Thr Val Glu Asn
65     70     75     80
Val Val Tyr Ser Ala Ser Ile Ala Pro Glu Gly Lys Leu Leu Glu Leu
85     90     95
Glu Pro Trp Leu Val Glu Gly Phe Trp Leu Asp Gly His Gln Ala Phe
100    105    110
Glu Leu Leu Leu Gly Val Pro Leu Gly Gly Gly Asp Ala Ser Ile Gly
115    120    125
Asp Asp Leu Arg Phe Trp Ser Gln Cys Ala Arg Trp Val Leu Asp Leu
130    135    140
Leu Val Arg Ala Lys Tyr Leu Pro Asp Leu Glu Ser Gly Asp Gly Gln
145    150    155    160
Glu Ile Pro Thr Ala Arg Trp Val Pro Leu Leu Asp Ser Ala Val Asp
165    170    175
Gln Ala Arg Leu Lys Glu Phe Ala Ala Arg Leu Pro Gly Ala Cys Arg
180    185    190
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Ser Ala Met Leu Asp Ala Arg Val Arg Thr Leu Leu Ala Cys Glu Pro

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PF58891.ST25.txt

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	260	265
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	275	280
Gln Gly Glu Trp Lys Leu His Phe Leu Leu Gln Thr Gly Asp Asp Pro		285
	290	300
Asp Ser Leu Met Ala Ala Gln Gln Val Trp Ser Ser Ala Gly Glu Leu		315
305	310	320
Gln Glu Val Phe Leu Ala Gly Leu Gly Leu Ala Ser Arg Ile Phe Val		335
	325	330
Pro Val Glu Arg Gly Leu Leu Val Pro Gln Pro Thr Cys Cys Thr Met		350
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Ser Thr Val Glu Ala Phe Gln Phe Leu Lys Ala Ala Thr Trp Arg Leu		365
	355	360
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385	390	400
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Trp Glu Leu Ser Leu Ala Gly Lys Thr Leu Ser Arg Ala Glu Phe Asp		430
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	500	505
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Arg Pro Tyr Gln Lys Ile Gly Val Gly Trp Leu Ala Phe Leu Gln Lys		540
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545	550	560
Val Glu Leu Ile Ala Phe Leu Leu Phe Leu Lys Ser Lys Asn Glu Leu		575
	565	570
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	595	600
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	610	615
Lys Lys Gln Ile Ile Val Ser Ser Tyr Ala Leu Val Gln Arg Asp Ser		635
625	630	640
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PF58891.ST25.txt

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Lys	Tyr	Gly	Asp	Arg	Ser	Ser	Ala	Asn	Ala	Leu	Lys	Ala	Leu	Val	Gln
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Leu	Pro	Glu	Lys	760				765	770				775		
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780				Gly	Ile	Gln	Arg	Arg	Gly	Thr	Val	Leu	Ala	Thr	Leu
Glu	Gln	Ser	Thr	790				795	800				805		
Val	Lys	Leu	Lys	Gln	Ile	Cys	Asn	His	Pro	Ser	His	Tyr	Leu	Gly	Asp
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935				940	945				950				955		
Arg	Ala	Asn	His	Val	Phe	His	Phe	Asp	Arg	Trp	Trp	Asn	Pro	Ala	Val
960				965	970				975				980		
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Val	Gln	Val	Tyr	Lys	Tyr	Val	Cys	Thr	Gly	Thr	Leu	Glu	Glu	Arg	Ile
985				990	995				1000				1005		
Asn	Ala	Leu	Ile	Glu	Ser	Lys	Lys	Ala	Leu	Ala	Glu	Gln	Val	Val	Ser
1010				1015	1020				1025				1030		
Ala	Gly	Glu	Asn	Trp	Leu	Ser	Asp	Leu	Asn	Thr	Asp	Gln	Leu	Arg	Gln
1035				1040	1045				1050				1055		
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<212>	DNA
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PF58891.ST25.txt

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<211> 1061

<212> PRT

<213> Lyngbya sp.

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35          40          45
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65          70          75          80
Gly Leu Tyr Pro Leu Gln Ser Thr Pro Gln Thr Asp Ser Glu Thr Asp
85          90          95
Ser Glu Ser Ile Cys Leu Tyr Pro Trp Lys Ile Glu Gly Ile Cys Leu
100          105          110
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PF58891.ST25.txt

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<210> 46
 <211> 1048
 <212> PRT
 <213> Methanospirillum hungatei

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

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Pro	Ala	Leu	Ser	Pro	Gln	Asp	Met	Glu	Trp	Val	Ser	Asp	Phe	Ser	Ser
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Arg	Met	Pro	Thr	Val	Cys	Lys	Tyr	Ala	Ile	Pro	Arg	Val	Ala	Lys	Asp
	210					215					220				
Pro	Tyr	Ile	Tyr	Lys	Pro	Glu	Thr	Arg	Leu	Glu	Lys	Phe	Ile	Val	Glu
225					230					235					240
Met	Met	Arg	Val	Ile	Ile	Arg	Thr	Ala	Leu	Gly	Gly	Tyr	Thr	Leu	Lys
				245					250					255	
Glu	Glu	Thr	Asp	Pro	Phe	Tyr	Glu	Pro	Ser	Glu	Asn	Glu	Met	Gln	Phe
			260					265					270		
Met	Thr	Asp	Leu	Leu	Gly	Val	Thr	Asp	Pro	Ile	Arg	Asn	Lys	Gly	Phe
		275					280					285			
Glu	Arg	Thr	Phe	Leu	Arg	Ala	Met	Gln	Asp	Trp	Leu	Thr	Phe	Ser	Ser
	290					295					300				
Ser	Gly	Arg	Phe	Ala	Pro	Phe	Glu	Phe	Cys	Met	Ile	Ile	Lys	Asp	Pro
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Pro	Glu	Gly	Gln	Thr	Glu	Pro	Trp	Asp	Phe	Thr	Leu	Ala	Val	Arg	Ser
				325					330					335	
Glu	Ala	Glu	Pro	Ser	Leu	Leu	Ile	Pro	Ala	Glu	Ile	Ile	Trp	Glu	Leu
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Pro	Asp	His	Gln	Ser	Gly	Leu	Phe	Pro	Gln	Ala	Ala	Tyr	Leu	Lys	His
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Ile	Leu	Leu	Ala	Gly	Ile	Gly	Leu	Leu	Thr	Ser	Ser	Ser	Ser	Ala	Leu
	370					375					380				
Trp	Arg	Pro	Leu	Ser	Gly	Ser	Lys	Pro	Thr	Gly	Gly	Ser	Met	Thr	Leu
385					390					395					400
Lys	Glu	Ala	Ala	Thr	Phe	Leu	Gly	Ser	Asp	Leu	Ala	Arg	Ala	Arg	Arg
				405					410					415	
Lys	Gly	Val	Thr	Val	Leu	Leu	Pro	Asp	Trp	Trp	Thr	Asp	Thr	Thr	Tyr
			420					425					430		
Thr	Pro	Arg	Val	Glu	Ile	His	Ala	Arg	Arg	Arg	Asp	Pro	Thr	His	Thr
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Gln	Thr	Arg	Ile	Gly	Leu	Gln	Glu	Leu	Leu	Ser	Phe	Asp	Tyr	Arg	Ile
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Ala	Ile	Gly	Asp	Glu	Ser	Phe	Ser	Pro	Asp	Glu	Phe	Trp	Glu	Lys	Val
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Lys	Glu	Lys	Ala	Pro	Phe	Ile	Trp	Leu	Gly	Asn	Arg	Trp	Ile	Ser	Phe
				485					490					495	
His	Pro	Asp	Ala	Ile	Gln	His	Ala	Leu	Asp	Ser	Phe	Ser	Arg	His	Gln
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Ser	Lys	Gly	Gly	Asp	Thr	Ile	Gly	Asp	Leu	Leu	Arg	Leu	Ser	Leu	Lys
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Lys	Met	Glu	Asp	Ser	Ala	Val	Pro	Val	Ser	Ile	His	Ala	Lys	Asp	Asp
	530					535					540				
Trp	Val	Ala	Asp	Leu	Leu	Asp	Phe	Phe	Arg	Thr	Glu	Thr	Asn	Gln	Ala
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Val	Pro	Val	Pro	Lys	Phe	Lys	Gly	Ile	Leu	Arg	Pro	Tyr	Gln	Glu	
				565				570					575		
Glu	Gly	Phe	Ser	Phe	Leu	Cys	Gln	Cys	Thr	Arg	Arg	Gly	Phe	Gly	Ala
			580					585					590		
Cys	Leu	Ala	Asp	Asp	Met	Gly	Leu	Gly	Lys	Thr	Pro	Gln	Thr	Leu	Ala
		595					600						605		

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Trp	Leu	Val	Tyr	Leu	Lys	Glu	Lys	Glu	Lys	Pro	Thr	Thr	Pro	Ser	Leu
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Leu	Ile	Cys	Pro	Met	Ser	Val	Val	Gly	Asn	Trp	Glu	Arg	Glu	Ile	Gln
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Arg	Phe	Ala	Pro	Ser	Leu	Arg	Ser	Trp	Val	His	His	Gly	Thr	Asp	Arg
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Cys	Lys	Gly	Asp	Asp	Phe	Val	Arg	His	Val	Gly	Ser	Tyr	Asp	Leu	Val
			660					665					670		
Leu	Thr	Thr	Tyr	His	Leu	Ala	Ala	Arg	Asp	Val	Asp	His	Leu	Lys	Thr
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Val	Pro	Trp	Ser	Ala	Ile	Ile	Leu	Asp	Glu	Ala	Gln	Asn	Ile	Lys	Asn
	690					695					700				
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Arg	Val	Ala	Leu	Thr	Gly	Thr	Pro	Val	Glu	Asn	Arg	Leu	Leu	Glu	Leu
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Trp	Ser	Ile	Met	Asp	Phe	Leu	Asn	Pro	Gly	Tyr	Leu	Gly	Ser	Gln	Ser
			740					745					750		
Ala	Phe	Thr	Asn	Arg	Tyr	Ser	Arg	Pro	Ile	Glu	Gln	Glu	Lys	Asn	Thr
		755					760					765			
Glu	Leu	Ile	Gln	Glu	Leu	Arg	Ser	Leu	Ile	Arg	Pro	Phe	Leu	Leu	Arg
	770					775					780				
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785					790					795					800
Glu	Asn	Arg	Val	Tyr	Cys	Thr	Leu	Thr	Pro	Glu	Gln	Ala	Thr	Leu	Tyr
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Gln	Ala	Val	Val	Leu	Asp	Met	Ala	Lys	Asn	Leu	Asp	Lys	Val	Glu	Gly
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Ile	Ala	Arg	Lys	Gly	Ala	Ile	Leu	Ala	Ala	Ile	Thr	Arg	Leu	Lys	Gln
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Ile	Cys	Asn	His	Pro	Gly	Arg	Val	Gly	Arg	Asp	Lys	Thr	Ile	Lys	Ala
	850					855					860				
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Thr	Ser	Glu	Gly	Asp	Ser	Ala	Leu	Ile	Phe	Ser	Gln	Tyr	Ala	Thr	Phe
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Ala	Glu	Glu	Leu	Ala	Gly	Met	Ile	Glu	Lys	Gln	Gly	Asp	Thr	Pro	Val
		900						905					910		
Leu	Leu	Leu	Thr	Gly	Ser	Thr	Pro	Arg	Lys	Lys	Arg	Glu	Gln	Met	Ile
		915					920					925			
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Lys	Ala	Gly	Gly	Thr	Gly	Leu	Asn	Leu	Thr	Lys	Ala	Thr	His	Val	Phe
945					950					955					960
His	Val	Asp	Arg	Trp	Trp	Asn	Pro	Ala	Val	Glu	Asp	Gln	Ala	Thr	Asp
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Ile	Thr	Ala	Gly	Thr	Leu	Glu	Glu	Arg	Ile	Asp	Leu	Ile	Asn	Gln	Glu
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Lys	Arg	Thr	Leu	Ala	Lys	Glu	Val	Leu	Ala	Gln	Ser	Asp	Glu	Tyr	
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Leu	Thr	Asn	Leu	Ser	Thr	Lys	Glu	Leu	Leu	Glu	Ile	Val	Ser	Leu	
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<210> 47
<211> 3270
<212> DNA
<213> Methanosarcina mazei

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PF58891.ST25.txt

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<210> 48
 <211> 1089
 <212> PRT
 <213> Methanosarcina mazei

<400> 48

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Lys	Pro	Lys	Thr	Pro	Ile	Val	Lys	Pro	Tyr	Pro	Tyr	Asp	Ser	Gly	Phe
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Glu	Asn	Leu	Ser	Ser	Ala	Leu	Glu	Leu	Leu	Leu	Gly	Ser	Thr	Asp	Arg
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Lys	Lys	Ala	Glu	Lys	Ile	Asn	Val	Trp	Thr	Pro	Thr	Ile	Gly	Gly	Asn
65					70					75					80
Pro	Val	Pro	Ser	Ser	Pro	Leu	Val	Ala	Glu	Ile	Ser	Asp	Ser	Lys	Ala
			85						90					95	
Glu	Pro	Ala	Leu	Ala	Pro	Cys	Thr	Val	His	Ala	Tyr	Pro	Leu	Glu	Ala
			100					105					110		
Glu	Glu	Ala	Ile	Val	Leu	Leu	Cys	Thr	Cys	Met	Glu	Lys	Lys	Val	Leu
		115					120					125			
Ala	Pro	Gly	Ile	Ile	Ser	Gly	Asn	Asp	Leu	Leu	Trp	Trp	Ala	Asp	Ala
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Leu	Lys	Phe	Ala	Gly	Ser	Leu	Val	Ala	Gly	Gln	Lys	Tyr	Leu	Pro	Gly
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Val	Arg	Gly	Gly	Glu	Gly	Glu	Tyr	Arg	Ala	Phe	Trp	Glu	Pro	Val	Phe
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Ser	Gly	Glu	Asp	Ala	Gly	Lys	Leu	Ala	Lys	Leu	Ala	Lys	Gln	Met	Pro
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Met	Pro	Ala	Ala	Leu	Ala	Ala	Lys	Gln	Phe	Ile	Glu	Asp	Ser	Leu	Asp
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Trp	Ile	Val	Arg	Ser	Glu	Ile	Gly	Glu	Lys	Lys	Leu	Ala	Lys	Glu	Thr
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Arg	Lys	Arg	Lys	Ser	Phe	Asp	Ser	Val	His	Asp	Ala	Trp	Val	Ser	Ala
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Leu	Arg	Ser	Pro	Glu	Gly	Leu	Ile	Tyr	Gly	Asp	Glu	Asn	Glu	Leu	Leu
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Gln	Leu	Ala	Ala	Arg	Thr	Arg	Glu	Trp	Gln	Arg	Pro	Leu	Thr	Ile	Leu
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PF58891.ST25.txt

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Glu Ala Gly Lys Arg Asp Thr Lys Lys Gly Arg Glu Gly Ile Ala Asp				
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Ile Glu Val Pro Glu Gly Leu Trp Tyr Val Arg Tyr Met Leu Gln Ser				
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Tyr Glu Asp Pro Ser Leu Leu Ile Pro Val Lys Glu Ala Trp Lys Pro				
	355		360	365
Lys Lys Gly Ser Pro Leu Lys Lys Tyr Asp Val Lys Asn Ile Arg Gln				
	370		375	380
Phe Leu Leu Ser Ser Leu Gly Gln Ala Ser Ser Ile Ser Ala Gly Ile				
385		390		395
Ala Ser Ser Leu Glu Ala Pro Asn Pro Ser Gly Tyr Ser Leu Asp Thr				
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Lys Glu Ala Tyr Arg Phe Leu Thr Glu Ser Ala Ala Asn Leu Ser Gln				
	420		425	430
Ala Gly Phe Gly Val Leu Leu Pro Gly Trp Trp Thr Arg Lys Gly Thr				
	435		440	445
Lys Thr His Leu Lys Ala Gln Ala Asn Val Lys Gly Lys Lys Lys Leu				
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Gln Ala Gly Tyr Gly Leu Thr Leu Asp Glu Ile Val Ser Phe Asp Trp				
465		470		475
Glu Ile Ala Leu Gly Asp Arg Val Leu Thr Val Arg Glu Leu Gln Ala				
	485		490	495
Leu Ala Lys Leu Lys Ala Pro Leu Val Lys Phe Arg Gly Gln Trp Val				
	500		505	510
Glu Val Asn Asp Ala Glu Ile Arg Ala Ala Leu Glu Phe Trp Lys Lys				
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Asn Pro Asn Gly Glu Ala Ser Leu Arg Glu Val Leu Lys Leu Ala Val				
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Gly Val Ser Glu Lys Ala Asp Gly Val Asn Val Glu Gly Leu Asn Ala				
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Phe Glu Glu Leu Pro Ala Pro Asn Gly Phe Ser Gly Thr Leu Arg Pro				
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PF58891.ST25.txt

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Thr Pro Val Glu Asn Asn Val Gly Asp Leu Trp Ser Ile Met Glu Phe
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PF58891.ST25.txt

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<211> 1013

PF58891.ST25.txt

<212> PRT

<213> Mycobacterium bovis

<400> 50

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PF58891.ST25.txt

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Phe	Thr	Ala	Thr	Leu	Arg	Pro	Tyr	Gln	Gln	Arg	Gly	Leu	Ala	Trp	Leu		
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PF58891.ST25.txt

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Lys Lys Ala Leu Ala Asp Leu Val Val Thr Asp Gly Glu Gly Trp Leu
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<213> Mycobacterium tuberculosis

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PF58891.ST25.txt

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 <211> 1013
 <212> PRT
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Val Val Asp Leu Asp Pro Thr Ala Ala Leu Ala Ala Phe Asp Gln Pro
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PF58891.ST25.txt

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Thr	Ser	Ala	Leu	Asp	Ala	Met	Val	Asp	Ala	Ala	Val	Arg	Ala	Ala
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Ser	Pro	Met	Asp	Leu	Leu	Pro	Pro	Arg	Arg	Gly	Arg	Ser	Lys	Arg
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Pro	Trp	Asp	Asp	Val	Gly	Ile	Gly	Thr	Val	Gly	Pro	Ala	Arg	Ala
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<210> 56
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 <212> PRT
 <213> Nocardia farcinica

<400> 56

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      20      25      30
Trp Thr Glu Gly Glu Val Pro Pro Ala Leu Pro Asp Pro Ala Gly Ala
      35      40      45
Leu Leu Arg Ala Ser Arg Phe Arg His Arg Ala Gln Val Leu Val Pro
      50      55      60
Gly Pro Ala Gly Pro Gln Leu Thr Gln Val Arg Ala His Ala Leu Val
65      70      75      80
Pro Gln Ala Ala Val Asp Val Leu Arg Gln Arg Leu Pro Val Glu Ser
      85      90      95
Val Ala Gly Asp Leu Arg Phe Leu Ala His Val Ala Asp Gly Ile Asp
      100     105     110
Arg Trp Val Arg Ala Gly Arg Val Val Pro Asp Leu His Arg Ala Asp
      115     120     125
Gly Gln Trp Trp Ala Arg Trp Arg Leu Val Gly Gly Ala Arg Gln Arg
130     135     140
Ala Trp Leu Ala Glu Leu Ala Val Ala Met Pro Ala Ala Leu Arg Val
145     150     155     160
Ala Gly Gln Pro Ala Ala Val Leu Asp Asp Leu Val Thr Glu Leu Thr
      165     170     175
Asp Pro Ile Val Arg Thr Arg Leu Ala Asp Ala Pro Val Thr His Pro
      180     185     190
Leu Val Arg Ala Leu Val Arg Asp Gln Pro Leu Glu Thr Gly Ser His
195     200     205
Gln Leu Ala Glu Val Leu Arg Arg Trp Arg Glu Ser Leu Thr Val Asp
210     215     220
Glu Pro Glu Leu Val Leu Arg Leu Leu Glu Pro Asp Gly Glu Thr Gly
225     230     235     240
Ile Asp Gly Asp Gly Gly Asp Asp Arg Asp Asp Thr Val Ala Leu Trp
      245     250     255
Arg Leu Glu Val Cys Leu Arg Thr Glu Gly Glu Ala Pro Ala Pro Val
      260     265     270
Pro Ala Thr Ala Asp Pro Asn Leu Leu Arg Ile Ala Val Glu Gln Leu
      275     280     285
Gly Arg Ala Gln Arg Ala Tyr Pro Arg Leu Arg Asp Leu Pro Gly Asp
290     295     300
Pro His Ser Leu Asp Leu Leu Leu Pro Thr Glu Val Val Ala Asp Leu
305     310     315     320
Val Ala His Gly Ala Gln Ala Leu Arg Glu Ala Gly Val Arg Leu Leu
      325     330     335
Leu Pro Arg Ala Trp Thr Ile Ala Glu Pro Thr Leu Arg Leu Ala Val
      340     345     350
Ser Ser Ala Ala Pro Ala Ala Glu Ser Thr Val Gly Met Gln Gly Leu
      355     360     365
Leu Ser Tyr Arg Trp Glu Leu Ala Val Gly Asp Lys Val Leu Thr Arg
370     375     380
Ala Glu Met Glu Arg Leu Val Arg Ala Lys Ser Asp Leu Val Gln Leu
385     390     395     400
Arg Gly Glu Trp Val Gln Ala Asp His Lys Val Leu Ala Ala Ala Ala
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Arg Tyr Val Ala Ala His Leu Asp Thr Ser Pro Val Thr Leu Ala Asp
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Leu Leu Gly Glu Ile Ala Ala Thr Arg Val Asp Lys Val Pro Leu Thr
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Glu Val Thr Ala Thr Gly Trp Ala Gly Glu Leu Phe Asp Gly Gly Arg
    450          455          460
Glu Pro Val Ala Thr Pro Gly Gly Leu Lys Ala Gln Leu Arg Pro Tyr
    465          470          475          480
Gln Leu Arg Gly Leu Ser Trp Leu Ala Thr Met Ser Arg Met Gly Cys
    485          490          495
Gly Gly Ile Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Val Gln Val
    500          505          510
Leu Ala Leu Leu Val His Glu Arg Glu Thr Ser Thr Ala Pro Pro Gly
    515          520          525
Pro Thr Leu Leu Val Cys Pro Met Ser Val Val Gly Asn Trp Gln Arg
    530          535          540
Glu Ala Gln Arg Phe Ala Pro Gly Leu Arg Val Leu Val His His Gly
    545          550          555          560
Ala Asp Arg Arg Arg Asp Ala Glu Leu Asp Ala Ala Val Ala Asp Ser
    565          570          575
Asp Leu Val Leu Thr Thr Tyr Ala Ile Leu Ala Arg Asp Ala Ala Glu
    580          585          590
Leu Ser Arg Gln Ser Trp Asp Arg Val Val Leu Asp Glu Ala Gln His
    595          600          605
Ile Lys Asn Ala Ala Thr Arg Gln Ala Arg Ala Ala Arg Ala Leu Pro
    610          615          620
Ala Arg His Arg Leu Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu
    625          630          635          640
Glu Glu Leu Arg Ser Ile Met Asp Phe Ala Val Pro Lys Leu Leu Gly
    645          650          655
Thr Ala Pro Thr Phe Arg Ala Arg Phe Ala Val Pro Ile Glu Arg Gly
    660          665          670
Gln Asp Pro Asn Ala Leu Ser Arg Leu Arg Phe Leu Thr Gln Pro Phe
    675          680          685
Val Leu Arg Arg Val Lys Ala Asp Pro Ala Val Ile Gly Asp Leu Pro
    690          695          700
Asp Lys Leu Glu Met Thr Val Arg Ala Asn Leu Thr Val Glu Gln Ala
    705          710          715          720
Ala Leu Tyr Gln Ala Val Val Asp Asp Met Leu Val Lys Leu Arg Ser
    725          730          735
Ala Lys Gly Met Ala Arg Lys Gly Ala Val Leu Gly Ala Leu Thr Arg
    740          745          750
Leu Lys Gln Val Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser
    755          760          765
Pro Val Leu His Arg Gly Arg His Arg Ser Gly Lys Leu Ala Leu Val
    770          775          780
Glu Asp Val Leu Asp Thr Val Val Ala Asp Gly Glu Lys Ala Leu Leu
    785          790          795          800
Phe Thr Gln Phe Arg Glu Phe Gly Asp Leu Leu Ala Pro Tyr Leu Ser
    805          810          815
Glu Arg Phe Gly Ala Pro Ile Pro Phe Leu His Gly Gly Val Thr Lys
    820          825          830
Lys Asn Arg Asp Thr Met Val Glu Arg Phe Gln Ser Gly Asp Gly Pro
    835          840          845
Pro Val Met Leu Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Thr Leu
    850          855          860

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Thr	Ala	Ala	Asn	His	Val	Val	His	Leu	Asp	Arg	Trp	Trp	Asn	Pro	Ala
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Val	Glu	Asn	Gln	Ala	Thr	Asp	Arg	Ala	Phe	Arg	Ile	Gly	Gln	Arg	Arg
				885					890					895	
Asp	Val	Gln	Val	Arg	Lys	Leu	Val	Cys	Val	Asp	Thr	Ile	Glu	Glu	Arg
			900					905					910		
Ile	Asp	Glu	Met	Ile	Thr	Gly	Lys	Ser	Arg	Leu	Ala	Asp	Leu	Ala	Val
	915					920					925				
Asp	Ala	Gly	Glu	Asn	Trp	Ile	Thr	Glu	Leu	Gly	Thr	Glu	Glu	Leu	Arg
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 <212> DNA
 <213> Nodularia spumigena

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<210> 58
 <211> 1087
 <212> PRT
 <213> Nodularia spumigena

<400> 58

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Leu	Asn	Val	Ser	Gln	Asp	Ile	Pro	Leu	His	Pro	Leu	Val	Met	Ser	Pro
		35					40					45			
Ile	Asp	Leu	Ser	Glu	Leu	Leu	Ser	Tyr	His	Asn	Ile	Lys	Ile	Pro	Ser
	50				55					60					
Leu	Ile	Gln	Gln	Ser	Gln	Val	Ala	Leu	Ser	Gly	Thr	Gly	Arg	Thr	Arg
65				70					75					80	
Lys	Ser	Thr	Ser	Thr	Thr	Lys	Phe	Ser	Trp	Thr	Thr	His	Ser	Leu	Ile
			85					90					95		
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		100					105					110			
Phe	Ile	Ser	Pro	Leu	His	Ser	Ala	Thr	Leu	Gly	Ser	Glu	Ile	Asn	Ser
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Pro	Gln	Tyr	Leu	Gln	Pro	Trp	Arg	Val	Glu	Gly	Phe	Cys	Leu	Asn	Pro
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Thr	Glu	Ala	Ile	Lys	Phe	Leu	Ala	Ala	Val	Pro	Leu	Asn	Ala	Ala	Arg
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Thr Ile Asp Ala Gln Val Arg Glu Met Leu Ala Ser Gln Pro Leu Leu		
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Glu Thr Arg Val Met Ala Ser Leu Pro Ser Ala Val Arg Gln Trp Leu		
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Gln Gly Leu Thr Ser Ala Ser His Thr Val Asn Ala Asp Ala Met Glu		
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Val Glu Arg Leu Glu Ala Ala Leu Lys Ser Trp Thr Met Pro Leu Gln		
	325	330
Tyr Gln Leu Val Gly Lys Pro Ser Phe Arg Ala Cys Phe Gln Leu Leu		
	340	345
Pro Pro Ala Ser Gly Ala Thr Asp Trp Ile Leu Ala Tyr Phe Leu Gln		
	355	360
Ala Ala Asp Asp Glu Asn Leu Val Asp Ala Ala Thr Ile Trp His		
	370	375
His Pro Val Glu Gln Leu Val Tyr Gln Asn Arg Thr Ile Asp Gln Pro		
385	390	395
Gln Glu Thr Leu Leu Arg Gly Leu Gly Leu Ala Ser Arg Leu Tyr Pro		
	405	410
Val Leu Thr Pro Ser Leu Glu Thr Glu Tyr Pro Gln Cys Cys Arg Leu		
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Asn Pro Leu Gln Ala Tyr Glu Phe Ile Lys Ser Val Ala Trp Arg Phe		
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Glu Asp Ser Gly Leu Gly Val Ile Leu Pro Pro Ser Leu Thr Asn Arg		
	450	455
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Lys Lys Lys Gln Gly Arg Leu Gly Leu Gln Ser Leu Leu Asn Phe Gln		
	485	490
Trp Gln Leu Ala Ile Gly Gly Gln Thr Ile Ser Lys Thr Glu Phe Asn		
	500	505
Lys Leu Val Ala Leu Asn Ser Pro Leu Val Glu Ile Asn Gly Glu Trp		
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Val Glu Leu Arg Pro Gln Asp Ile Lys Thr Ala Gln Thr Phe Phe Ala		
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Ser Arg Lys Asp Glu Met Thr Leu Ser Leu Glu Asp Ala Leu Arg Leu		
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Ser Ser Gly Asp Thr Gln Ala Ile Glu Lys Leu Pro Val Val Ser Phe		
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Gln Ala Ile Ser Pro Leu Pro Thr Pro Ala Asn Phe Gln Gly Gln Leu		
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Arg Pro Tyr Gln Glu Arg Gly Ala Ala Trp Leu Ala Phe Leu Glu Arg		
	610	615
Trp Gly Leu Gly Ala Cys Leu Ala Asp Asp Met Gly Leu Gly Lys Thr		
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Ile Gln Leu Ile Ala Phe Leu Leu His Leu Lys Glu Gln Asp Ala Leu		

PF58891.ST25.txt

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675																680																685															
His	Gly	Asp	Lys	Arg	Leu	Lys	Gly	Lys	Ala	Phe	Val	Glu	Ala	Val	Lys	His	Gly	Asp	Lys	Arg	Leu	Lys	Gly	Lys	Ala	Phe	Val	Glu	Ala	Val	Lys	His	Gly	Asp	Lys	Arg	Leu	Lys	Gly	Lys	Ala	Phe	Val	Glu	Ala	Val	Lys
690																695																700															
Lys	His	Asp	Val	Ile	Ile	Thr	Ser	Tyr	Ser	Leu	Val	His	Arg	Asp	Ile	Lys	His	Asp	Val	Ile	Ile	Thr	Ser	Tyr	Ser	Leu	Val	His	Arg	Asp	Ile	Lys	His	Asp	Val	Ile	Ile	Thr	Ser	Tyr	Ser	Leu	Val	His	Arg	Asp	Ile
705																710																715															
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755																760																765															
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Lys	Tyr	Gly	Asp	Thr	Ala	Ser	Leu	Asn	Gln	Leu	Arg	Gly	Leu	Val	Gln	Lys	Tyr	Gly	Asp	Thr	Ala	Ser	Leu	Asn	Gln	Leu	Arg	Gly	Leu	Val	Gln	Lys	Tyr	Gly	Asp	Thr	Ala	Ser	Leu	Asn	Gln	Leu	Arg	Gly	Leu	Val	Gln
805																810																815															
Pro	Phe	Ile	Leu	Arg	Arg	Leu	Lys	Thr	Asp	Arg	Asp	Ile	Ile	Gln	Asp	Pro	Phe	Ile	Leu	Arg	Arg	Leu	Lys	Thr	Asp	Arg	Asp	Ile	Ile	Gln	Asp	Pro	Phe	Ile	Leu	Arg	Arg	Leu	Lys	Thr	Asp	Arg	Asp	Ile	Ile	Gln	Asp
820																825																830															
Leu	Pro	Glu	Lys	Gln	Glu	Met	Thr	Val	Phe	Cys	Gly	Leu	Ala	Ala	Glu	Leu	Pro	Glu	Lys	Gln	Glu	Met	Thr	Val	Phe	Cys	Gly	Leu	Ala	Ala	Glu	Leu	Pro	Glu													

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1070
Glu Asp Glu Val
1085

1075

1080

<210> 59
<211> 3228
<212> DNA
<213> Nostoc sp.

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ttggcgctgt ctgcactgga attaagttag ttggttgagc ctcaacatca ggcgatcgct      180
aagttgtttac cgcaacaatt ggaaaaacga acctccaaag cagcaagttc tgtaaaaata      240
aatttattaa ctcatcaca aataattgcc ctgccaacgg aaatttccca acctcgtaaa      300
aaagaaacca ttttaatttc tctgtgcat tctgccgctt tagcatctga gtcagactct      360
gaagtttatt tacaaacttg gcgtgtagaa ggtttttgtc ttctctctag tgcagcaatt      420
aaattgctaa cttctttacc tttaaatata actagtgggg agaatgcttt tttaggtgga      480
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tttctcccaa ttatccaacg acaacctaat aattctgtaa gtgctaaatg gcaagtactt      600
ttagatagtg ccgtagatgg aactcgttta gaaaagtttg ctgcgaagat gcccttggtt      660
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cgacagtggg tgcaagcggt aattgctgca tctaattcaa ttgatgcaga tgctgttggt      900
ttagaaaggc tggaagcggc gctcaaggct tggacgatgc cgctacaata tcaactagca      960
agtaaaaaatc aatttcgcac ttgttttgaa ttacgttctc cagaaccaga cgaaactgaa     1020
tggacgctgg cgtatttccct gcaagcagcc gatgatccag aatttttagt agatgcggcg      1080
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caggaaacgt ttttgcgagg tttggggtta gcttctcgat tgtatccggt cattgcccc      1200
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aaatcattgc agggatttcc ttggcaaata attgttttag atgaagccca aaatgtgaag      2160
aatgcggaag ccaaacaatc acaagcagtc agacaattag aaacaacatt tcgtattgct      2220
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aatcctgggt acttaggtaa taagcaattc ttccaagac gttttgctat gccaaattgaa      2340
aagtatggtg atgcagcatc tttaaatcaa ttgcgtgctt tagtgcaacc atttattctg      2400
cgtcggctga aaacagaccg tgatattatt caagacttgc ccgataagca agaaatgaca      2460
gtattttgtg gtttgactgg agaacaagct gcactttatc aaaaagcggg agaaacatct      2520
ttagcagaaa ttgaatcagc cgaaggattg caacgccgag ggatgatttt agctttatta      2580
attaaactca aacaaatctg caatcatcca gcccaatatc tgaaaataaa tacattagaa      2640

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caacacagtt ctggaaaact gcaaagatta gaagaaatgt tagaagaggt gttagcagag 2700
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caagggccac caattatgat tctctccctc aaagcagggtg gtgtaggggtt gaacttaacc 2940
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<210> 60
 <211> 1075
 <212> PRT
 <213> Nostoc sp.

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20     25     30
Phe Ala Glu Ile Ser Leu Asn Pro Leu Ala Leu Ser Ala Leu Glu Leu
35     40     45
Ser Glu Trp Leu Gln Ser Gln His Gln Ala Ile Ala Lys Leu Leu Pro
50     55     60
Gln Gln Leu Glu Lys Arg Thr Ser Lys Ala Ala Ser Ser Val Lys Ile
65     70     75     80
Asn Leu Leu Thr His Ser Gln Ile Ile Ala Leu Pro Thr Glu Ile Ser
85     90     95
Gln Pro Arg Lys Lys Glu Thr Ile Leu Ile Ser Pro Val His Ser Ala
100    105    110
Ala Leu Ala Ser Glu Ser Asp Ser Glu Val Tyr Leu Gln Thr Trp Arg
115    120    125
Val Glu Gly Phe Cys Leu Pro Pro Ser Ala Ala Ile Lys Leu Leu Thr
130    135    140
Ser Leu Pro Leu Asn Ile Thr Ser Gly Glu Asn Ala Phe Leu Gly Gly
145    150    155    160
Asp Leu Arg Phe Trp Ser Gln Ile Ala Arg Trp Ser Leu Asp Leu Ile
165    170    175
Ser Arg Ser Lys Phe Leu Pro Ile Ile Gln Arg Gln Pro Asn Asn Ser
180    185    190
Val Ser Ala Lys Trp Gln Val Leu Leu Asp Ser Ala Val Asp Gly Thr
195    200    205
Arg Leu Glu Lys Phe Ala Ala Lys Met Pro Leu Val Cys Arg Thr Tyr
210    215    220
Gln Glu Ile Gly Ser Gly Glu Ser Pro Ile Tyr Ile Asp Phe Pro Ser
225    230    235    240
Gln Pro Gln Asp Leu Ile Leu Gly Phe Leu Asn Ser Ala Ile Asp Thr
245    250    255
Gln Leu Arg Glu Met Val Gly Asn Gln Pro Val Val Glu Thr Arg Leu
260    265    270
Met Ala Ser Leu Pro Ser Ala Val Arg Gln Trp Leu Gln Ala Leu Ile
275    280    285
Ala Ala Ser Asn Ser Ile Asp Ala Asp Ala Val Gly Leu Glu Arg Leu

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290		295		300
Glu Ala Ala Leu Lys	Ala Trp Thr Met Pro Leu Gln Tyr Gln Leu Ala			
305		310		320
Ser Lys Asn Gln Phe Arg Thr Cys Phe Glu Leu Arg Ser Pro Glu Pro				
		325		335
Asp Glu Thr Glu Trp Thr Leu Ala Tyr Phe Leu Gln Ala Ala Asp Asp				
		340		350
Pro Glu Phe Leu Val Asp Ala Ala Thr Ile Trp Gln Asn Pro Val Glu				
		355		365
Gln Leu Ile Tyr Gln Gln Arg Thr Ile Glu Glu Pro Gln Glu Thr Phe				
		370		380
Leu Arg Gly Leu Gly Leu Ala Ser Arg Leu Tyr Pro Val Ile Ala Pro				
385		390		400
Thr Leu Asp Thr Glu Ser Pro Gln Phe Cys His Leu Lys Pro Met Gln				
		405		415
Ala Tyr Glu Phe Ile Lys Ala Val Ala Trp Arg Phe Glu Asp Ser Gly				
		420		430
Leu Gly Val Ile Leu Pro Pro Ser Leu Ala Asn Arg Glu Gly Trp Ala				
		435		445
Asn Arg Leu Gly Leu Lys Ile Ser Ala Glu Thr Pro Lys Lys Lys Pro				
		450		460
Gly Arg Leu Gly Leu Gln Ser Leu Leu Asn Phe Gln Trp His Leu Ala				
465		470		480
Ile Gly Gly Gln Thr Ile Ser Lys Ala Glu Phe Asp Arg Leu Val Ala				
		485		495
Leu Lys Ser Pro Leu Val Glu Ile Asn Gly Glu Trp Val Glu Leu Arg				
		500		510
Pro Gln Asp Ile Lys Thr Ala Glu Ala Phe Phe Thr Ala Arg Lys Asp				
		515		525
Gln Met Ala Leu Ser Leu Glu Asp Ala Leu Arg Leu Ser Ser Gly Asp				
		530		540
Thr Gln Val Ile Glu Lys Leu Pro Val Val Ser Phe Glu Ala Ser Gly				
545		550		560
Ala Leu Gln Glu Leu Ile Gly Ala Leu Thr Asn Asn Gln Ala Val Ala				
		565		575
Pro Leu Pro Thr Pro Lys Asn Phe Gln Gly Gln Leu Arg Pro Tyr Gln				
		580		590
Glu Arg Gly Ala Ala Trp Leu Ala Phe Leu Glu Arg Trp Gly Leu Gly				
		595		605
Ala Cys Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Ile Gln Phe Ile				
		610		620
Ala Phe Leu Leu His Leu Lys Glu Gln Asp Val Leu Glu Lys Pro Thr				
625		630		640
Leu Leu Val Cys Pro Thr Ser Val Leu Gly Asn Trp Glu Arg Glu Val				
		645		655
Arg Lys Phe Ala Pro Thr Leu Lys Val Leu Gln Tyr His Gly Asp Lys				
		660		670
Arg Pro Lys Gly Lys Ala Phe Gln Glu Ala Val Lys Lys His Asp Leu				
		675		685
Val Ile Thr Ser Tyr Ser Leu Ile His Arg Asp Ile Lys Ser Leu Gln				
		690		700
Gly Ile Pro Trp Gln Ile Ile Val Leu Asp Glu Ala Gln Asn Val Lys				
705		710		720
Asn Ala Glu Ala Lys Gln Ser Gln Ala Val Arg Gln Leu Glu Thr Thr				

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              725              730              735
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              740              745              750
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              755              760              765
Gln Phe Phe Gln Arg Arg Phe Ala Met Pro Ile Glu Lys Tyr Gly Asp
              770              775              780
Ala Ala Ser Leu Asn Gln Leu Arg Ala Leu Val Gln Pro Phe Ile Leu
785              790              795              800
Arg Arg Leu Lys Thr Asp Arg Asp Ile Ile Gln Asp Leu Pro Asp Lys
              805              810              815
Gln Glu Met Thr Val Phe Cys Gly Leu Thr Gly Glu Gln Ala Ala Leu
              820              825              830
Tyr Gln Lys Ala Val Glu Thr Ser Leu Ala Glu Ile Glu Ser Ala Glu
              835              840              845
Gly Leu Gln Arg Arg Gly Met Ile Leu Ala Leu Leu Ile Lys Leu Lys
              850              855              860
Gln Ile Cys Asn His Pro Ala Gln Tyr Leu Lys Ile Asn Thr Leu Glu
865              870              875              880
Gln His Ser Ser Gly Lys Leu Gln Arg Leu Glu Glu Met Leu Glu Glu
              885              890              895
Val Leu Ala Glu Ser Asn Thr Tyr Gly Val Ala Gly Ala Gly Arg Ala
              900              905              910
Leu Ile Phe Thr Gln Phe Ala Glu Trp Gly Lys Leu Leu Lys Pro His
              915              920              925
Leu Glu Lys Gln Leu Gly Arg Glu Ile Phe Phe Leu Tyr Gly Gly Thr
              930              935              940
Ser Lys Lys Gln Arg Glu Glu Met Ile Asp Arg Phe Gln His Asp Pro
945              950              955              960
Gln Gly Pro Pro Ile Met Ile Leu Ser Leu Lys Ala Gly Gly Val Gly
              965              970              975
Leu Asn Leu Thr Arg Ala Asn His Val Phe His Phe Asp Arg Trp Trp
              980              985              990
Asn Pro Ala Val Glu Asn Gln Ala Thr Asp Arg Val Phe Arg Ile Gly
              995              1000              1005
Gln Thr Arg Asn Val Gln Val His Lys Phe Val Cys Asn Gly Thr
              1010              1015              1020
Leu Glu Glu Lys Ile His Asp Met Ile Glu Ser Lys Lys Gln Leu
              1025              1030              1035
Ala Glu Gln Val Val Gly Ala Gly Glu Glu Trp Leu Thr Glu Leu
              1040              1045              1050
Asp Thr Asp Gln Leu Arg Asn Leu Leu Ile Leu Asp Arg Ser Thr
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Val Ile Asp Glu Glu Ala Asp
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<210> 61
 <211> 3168
 <212> DNA
 <213> Nostoc sp.

<400> 61
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PF58891.ST25.txt

catcccggac	atctatcttc	tcttgaatta	ctcaattttc	tgactcaaac	tttggggatt	180
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gctaataatg	agccattacc	ttcaccagag	ttagtcaa	atttagaagt	agaagttcct	300
gaagagtatg	aaaattttca	atattggcag	gtaacttggt	atgaaactgt	tacttctgtg	360
aaagcagtga	tagcaattaa	tattattaaa	ttactcaaag	atattcattt	tttagccctg	420
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<210> 62
<211> 1055

PF58891.ST25.txt

<212> PRT

<213> Nostoc sp.

<400> 62

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          20          25          30
Lys Lys Arg Thr His Thr Gln Val His Pro Gly His Leu Ser Ser Leu
          35          40          45
Glu Leu Leu Asn Phe Leu Thr Gln Thr Leu Gly Ile Lys Glu Thr Glu
          50          55          60
Ala Gln Leu Lys Gln Arg Ile Cys Ser Lys Tyr Phe Ala Leu Pro Thr
65          70          75          80
Ala Asn Asn Glu Pro Leu Pro Ser Pro Glu Leu Val Lys Tyr Leu Glu
          85          90          95
Val Glu Val Pro Glu Glu Tyr Glu Asn Phe Gln Tyr Trp Gln Val Thr
          100          105          110
Cys Tyr Glu Thr Val Thr Ser Val Lys Ala Val Ile Ala Ile Asn Ile
          115          120          125
Ile Lys Leu Leu Lys Asp Ile His Phe Leu Ala Leu Tyr Asn Ala Ser
          130          135          140
Glu Phe Gln Leu Gly Ser Asp Leu Leu Phe Trp Tyr His Tyr Thr Gln
145          150          155          160
Ser Phe Arg Gln Ile Ile Thr Lys Asp Gln Tyr Ile Pro Ser Leu Lys
          165          170          175
Tyr Arg Ala Asn Ala Ala Thr Thr Lys Lys Lys Pro Lys Gln Pro Pro
          180          185          190
Pro Gly Phe Glu Ile Tyr Ala Gly Trp Glu Ile Ile Ser Glu Gln Tyr
          195          200          205
Glu Ala Asn Ile Gln Lys Tyr Ile Glu Tyr Met Pro Leu Ile Cys Val
          210          215          220
Ala Gly Asn Ser Thr Gln Thr Asp Lys Leu Glu Phe Phe Ala Pro Glu
225          230          235          240
Thr Leu Leu Arg His Phe Ser Glu Tyr Leu Leu Asn Asn Leu Val Ser
          245          250          255
Lys Thr Pro Leu Thr Ala Ala Phe Glu Lys Gln Ile Asp Asp Ser Leu
          260          265          270
Ile His Tyr Cys Leu Tyr Pro Gln Lys His Asn Pro Leu Lys Thr His
          275          280          285
Thr Ala Leu Gln Glu Tyr Gln Gln Trp Leu Gly Trp Lys Asn Arg Ile
          290          295          300
Ile Arg Thr Gln Ala Glu Ser Pro Phe His Leu Cys Phe Gln Leu His
305          310          315          320
Ser Pro Asp Ala Glu Gln Ile Asp Asn Trp Gln Met Gln Phe Leu Val
          325          330          335
Ser Ser Lys Lys Asp Pro Ser Leu Lys Leu Ala Leu Ala Asp Tyr Trp
          340          345          350
Ile Met Asn Ser Lys Thr Lys Ala Gly Val His Lys Glu Phe Gly Lys
          355          360          365
Asp Phe Asp Thr Asn Leu Leu Leu Asn Leu Gly Tyr Ala Ala Arg Met
          370          375          380
Tyr Pro Lys Leu Trp Gln Gly Leu Glu Thr Asp Ser Pro Thr Gly Met
385          390          395          400

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PF58891.ST25.txt

Gln	Leu	Ser	Leu	Asp	Glu	Ala	Phe	Asp	Phe	Leu	Lys	Asp	Ser	Ala	Trp
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Pro	Ala	Gly	Arg	Arg	Arg	Ala	Lys	Ile	Arg	Leu	Lys	Ala	Ser	Ser	Gly
		435					440					445			
Arg	Lys	Val	Ala	Ala	Thr	Val	Gly	Glu	Ser	Lys	Ser	Tyr	Phe	Gly	Leu
	450					455					460				
Asp	Ser	Leu	Val	Gln	Tyr	Gln	Tyr	Glu	Leu	Ala	Ile	Gly	Glu	Gln	Thr
465				470						475					480
Leu	Thr	Pro	Gln	Glu	Trp	Glu	Gln	Leu	Ile	Asn	Thr	Lys	Ala	Pro	Leu
			485						490					495	
Val	His	Phe	Arg	Gly	Gln	Trp	Met	Glu	Leu	Asp	Arg	Asp	Lys	Met	Gln
			500					505					510		
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<213> Nostoc punctiforme

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PF58891.ST25.txt

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Phe Ile Gln Gln Pro Gln Ile Ala Ile Ala Thr Thr Gly Arg Thr Arg
65        70        75        80
Lys Ala Ala Thr Ala Thr Glu Ile Asn Leu Pro Thr His Ser Gln Ile
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PF58891.ST25.txt

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Val Gly Phe Lys Gly Gln Leu Arg Pro Tyr Gln Glu Arg Gly Ala Ala
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Trp Leu Ser Phe Leu Glu Arg Trp Gly Leu Gly Ala Cys Leu Ala Asp
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Ala Phe Leu Glu Ala Val Lys Asn His Asp Leu Ile Val Thr Ser Tyr
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<213>	<i>Prochlorococcus marinus</i>

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Lys Leu His Lys Lys Glu Gly Asn Glu Tyr Arg Ala Ser Trp Ile Pro		
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		355					360					365		Asn
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	370					375					380			Pro
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Pro	Ile	Glu	Arg	Gly	Leu	Glu	Asn	Ala	Thr	Pro	Asn	Asn	Met	Gln
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Thr	Pro	Ala	Glu	Ala	Phe	Val	Leu	Val	Arg	Thr	Ala	Ser	Lys	Gln
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Arg	Asp	Ile	Gly	Ile	Gly	Val	Ile	Leu	Pro	Arg	Ser	Leu	Ser	Gly
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Ser	Lys	Arg	Ser	Pro	Leu	Val	Arg	Tyr	Lys	Asp	Ser	Trp	Leu	Glu
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Ala Arg Ser Pro Ile Gly Gln Arg His Ala Lys Thr Leu Gly Leu Leu
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<211> 3300

<212> DNA

<213> *Prochlorococcus marinus*

<400> 71

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 <213> Prochlorococcus marinus

<400> 72

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<210> 73
 <211> 3300
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 <213> *Prochlorococcus marinus*

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<212> PRT

<213> Prochlorococcus marinus

<400> 74

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755          760          765
Asp Lys Asn Asn Arg Phe Arg Ile Ala Leu Thr Gly Thr Pro Val Glu
770          775          780
Asn Arg Val Ser Glu Leu Trp Ala Leu Met Asp Phe Leu Asn Pro Arg
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<212>	DNA
<213>	Rhodococcus sp.

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gacgggggtg	ggttggtatg	cctggctcgc	taccgctggg	aggtgtccct	cggcgaccag	1440
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cgtgggcgct	gggtggagct	ggacccgaaa	cgtctcgcgc	ccggcctgcg	gctgctccgt	1560
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gctgtggagc	ggcaactcac	cccgggtggc	gcggttcctg	cgttccaggg	cgttctccgc	1740
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gtgctcgtcg	acgacatggg	tctcggcaag	acggtacagc	tactcgcgtt	gctcgtggtt	1860
gacccgcccg	gcgtcggtcc	gacctgttg	gtctgtccga	tgtcactggt	cggttaactg	1920
cagcgggagg	cgccgacctt	caccccgggc	gtacgggtcc	atgtgcatca	cggcgccgag	1980
cgggccccgc	gggcggcggt	caccgcggcg	gtggaggcag	cggacctggt	cctcaccacc	2040
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cggatcaccg	gcccgttcgt	gctgcgtcgc	ctcaagaccg	actcttcggt	tatctccgac	2400
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PF58891.ST25.txt

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ggcacggtgg aggagaaggc cgccgcgctc atcgccgaca agcgctcggc cgctcgcacg 3060
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<210> 78
 <211> 1050
 <212> PRT
 <213> *Salinispora tropica*

<400> 78
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 20 25 30
 Arg Ala Pro Arg Glu Arg Pro His Pro Phe Ala Ala Gly His Pro Val
 35 40 45
 Leu Ala Ala Ala Leu Ala Glu Val Ala Glu Pro Thr Glu Pro Gly Thr
 50 55 60
 Ala Leu Leu Thr Leu Pro Thr Arg Ala Gly Ser Pro Leu Asp Ser Pro
 65 70 75 80
 Glu Leu Val Arg Thr Ala Ser Val Glu Pro Leu Arg Gly Pro Val Thr
 85 90 95
 Leu Ala Gly Trp Arg Val Pro Ala Leu Val Tyr Ala Pro Asp Ala Ala
 100 105 110
 Leu Ser Leu Leu Ser Gln Ile Thr Ala Ala Gly Ala Leu Pro Asp Ala
 115 120 125
 Val Pro Gly Ala Thr Leu Arg His Leu Ala Glu Leu Ala Ala Phe Ala
 130 135 140
 Val Asp Leu Ala Ala Arg Gly Arg Val Leu Pro Gly Val Arg Pro Pro
 145 150 155 160
 Lys Glu Arg Ala Ser Ala Ala Trp Ala Val Trp Gln Pro Leu Leu Thr
 165 170 175
 Gly Val Asp Ala Gly Trp Ala Arg Ala Leu Ala Leu Ala Leu Pro Pro
 180 185 190
 Ala Val Arg Ala Ala Val Glu Ile Asp Pro Ala Pro Leu Ala Val Pro
 195 200 205
 Gly Gly Pro Glu Thr Pro Ala Asn Gly Gly Val Pro Pro Gln Ala Arg
 210 215 220
 Thr Arg Arg Pro Thr Ala Ala Ala Gly Glu Pro Gly Glu Leu Val Val
 225 230 235 240
 Glu Ala Leu Asp Ala Leu Thr Asp Ala Ala Val Arg Ala Ala Leu Ala
 245 250 255
 Glu Thr Ser Leu Thr Arg Gly Ala Arg Pro Arg Gly Ala Val Ala Ala
 260 265 270
 Trp Leu Ala Ala Leu Thr Gly Pro Arg Arg Asp Phe Thr Ala Asp Ser

PF58891.ST25.txt

275	280	285
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Ala Val Gly Gly Ser Val Arg Ala Ser Phe Arg	Leu Val Glu Pro Pro	
305	310	315
Thr Asp Gly Leu Phe Glu Ala Ala Ala Gly Gly	Leu Ala Ala Ala Glu	
	325	330
		335
Gly Ser Trp Arg Val Glu Phe Gly Leu Gln Pro	Ala Asp Gln Pro Gly	
	340	345
		350
Leu His Val Asp Ala Val Arg Ile Trp His Glu	Ser Ala Ala Leu Pro	
	355	360
		365
Gly Pro Ala Ala Pro Gln Glu Ala Leu Leu Thr	Glu Leu Gly Arg Ala	
370	375	380
Ser Arg Leu Trp Pro Glu Leu Asn Ser Ala Leu	Arg Thr Ala Thr Pro	
385	390	395
Glu Ala Leu Glu Leu Asp Ala Ala Gly Ala His	Arg Phe Leu Arg Asp	
	405	410
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Gly Ala Pro Val Leu His Ala Ala Gly Phe Ala	Val Leu Leu Pro Ser	
	420	425
		430
Trp Trp Gln Arg Pro Ser Ser Arg Leu Gly Ala	Arg Leu Gln Ala Gln	
	435	440
		445
Ser Arg Thr Ala Pro Gly Thr Val Ala Gly Ala	Gly Asp Gly Val Gly	
450	455	460
Leu Asp Ala Leu Val Asp Tyr Arg Trp Glu Val	Ser Leu Gly Asp Gln	
465	470	475
Pro Leu Thr Ala Glu Glu Leu Glu Ser Leu Ala	Ala Leu Lys Ser Pro	
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Leu Val Arg Leu Arg Gly Arg Trp Val Glu Leu	Asp Pro Lys Arg Leu	
	500	505
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Ala Ala Gly Leu Arg Leu Leu Arg Ser Ala Gly	Glu Leu Thr Val Gly	
	515	520
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Asp Leu Leu Arg Leu Gly Leu Ser Asp Pro Ala	Thr Asp Ala Leu Pro	
530	535	540
Val Leu Glu Val Ala Ala Asp Gly Ala Leu Gly	Asp Leu Leu Ala Gly	
545	550	555
Ala Val Glu Arg Gln Leu Thr Pro Val Asp Ala	Val Pro Ser Phe Gln	
	565	570
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Gly Val Leu Arg Pro Tyr Gln Arg Arg Gly Leu	Ala Trp Leu Ser Phe	
	580	585
		590
Leu Gln Ser Leu Gly Leu Gly Gly Val Leu Ala	Asp Asp Met Gly Leu	
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Gly Lys Thr Val Gln Leu Leu Ala Leu Leu Ala	Gly Asp Pro Pro Gly	
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625	630	635
Gln Arg Glu Ala Ala Thr Phe Thr Pro Gly Val	Arg Val His Val His	
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His Gly Ala Glu Arg Ala Arg Gly Ala Ala Phe	Thr Ala Ala Val Glu	
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Ala Ala Asp Leu Val Leu Thr Thr Tyr Thr Val	Ala Ala Arg Asp Ala	
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Gly Glu Leu Ala Gly Val Asp Trp His Arg Val	Val Val Asp Glu Ala	
690	695	700
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PF58891.ST25.txt

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              740              745              750
Leu Gly Pro Ala Ala Glu Phe Lys Lys Arg Tyr Ala Glu Pro Ile Glu
              755              760              765
Arg His Gly Asp Ala Glu Ala Ala Glu Arg Leu Arg Arg Ile Thr Gly
770              775              780
Pro Phe Val Leu Arg Arg Leu Lys Thr Asp Ser Ser Val Ile Ser Asp
785              790              795              800
Leu Pro Glu Lys Leu Glu Met Glu Val Val Cys Asn Leu Thr Ala Glu
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Gln Ala Ala Leu Tyr Arg Ala Val Val Asp Asp Met Met Ala Gln Ile
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Glu Ser Ser Glu Gly Ile Glu Arg Arg Gly Leu Val Leu Ala Ala Met
              835              840              845
Thr Arg Leu Lys Gln Val Cys Asn His Pro Ala His Leu Leu Arg Asp
850              855              860
Asn Ser Ala Leu Val Gly Arg Ser Gly Lys Leu Ala Arg Leu Glu Glu
865              870              875              880
Ile Leu Asp Glu Val Leu Val Ala Gly Glu Lys Ala Leu Leu Phe Thr
              885              890              895
Gln Tyr Ala Glu Phe Gly Gly Met Leu Arg Gly His Leu Ser Ala Arg
              900              905              910
Phe Gly Gln Glu Thr Leu Phe Leu His Gly Gly Val Gly Lys Ala Asp
915              920              925
Arg Asp Ala Met Val Thr Arg Phe Gln Ser Pro Asp Gly Pro Ala Leu
930              935              940
Phe Val Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Thr Leu Thr Ala
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Ala Asn His Val Val His Val Asp Arg Trp Trp Asn Pro Ala Val Glu
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Asp Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Arg Arg Val
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Gln Val Arg Lys Phe Val Cys Ala Gly Thr Val Glu Glu Lys Val Ala
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Ala Leu Ile Ala Asp Lys Arg Arg Leu Ala Ser Thr Val Val Gly
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<210> 79
 <211> 2970
 <212> DNA
 <213> Symbiobacterium thermophilum

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ccgcgccacc catgcgcaac cgagccggaa gcgctctacc ccgccctgag aggattgccc      180
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PF58891.ST25.txt

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<210> 80
 <211> 989
 <212> PRT
 <213> Symbiobacterium thermophilum

<400> 80
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PF58891.ST25.txt

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Pro	Glu	Ala	Leu	Tyr	Pro	Ala	Leu	Arg	Gly	Leu	Pro	Tyr	Leu	Asn	Thr
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Leu	Ser	Leu	Val	Gln	Trp	Gln	Pro	Gly	Pro	Asp	Gly	Val	Ser	Pro	Ala
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Arg	Val	Pro	Gly	Ile	Ala	Leu	Ser	Val	Pro	Asn	Ala	Val	Gln	Trp	Leu
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Leu	Asp	Leu	Pro	Asp	His	Phe	Arg	Gly	Thr	Pro	Leu	Arg	Pro	Gly	His
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Ser	Leu	Gln	Leu	Trp	Cys	Val	Ala	Ser	Lys	Leu	Leu	Leu	Glu	Phe	Leu
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Gly	Arg	Gly	Leu	Met	Leu	Pro	Val	Leu	Gln	Ala	Glu	Ala	Gly	Val	Leu
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Ser	Ala	Gly	Trp	Ala	Leu	His	Leu	Thr	Asp	Ala	Asp	Asp	Val	Arg	Arg
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Leu	Thr	Arg	Leu	Ala	Gly	Leu	Pro	Glu	Ala	Cys	Arg	Ala	Leu	Val	
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Pro	Pro	Asp	Arg	Thr	Pro	Asn	Thr	Tyr	Pro	Leu	Pro	Val	Ala	Asp	Gly
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Leu	Val	His	Gln	Phe	Met	Arg	Thr	Ala	Ala	Ala	Gly	Val	Ile	Arg	Leu
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Leu	Pro	Pro	Gly	Leu	Pro	Gly	Ala	Gln	Glu	Leu	Tyr	Ala	Ala	Leu	Asp
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Thr	Gly	Val	Arg	Leu	His	Leu	Pro	Gly	Pro	Glu	Thr	Asp	Gly	Glu	Trp
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Thr	Ala	Asp	Ala	Val	Trp	Ala	Ser	Leu	Gly	Ala	Glu	Val	Glu	Ile	Gly
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Gly	Gln	Arg	Tyr	Gln	Gly	Ala	Glu	Gln	Arg	Leu	Leu	Ala	Asp	Leu	Pro
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Ser	Pro	Ala	Gly	Gly	Ser	Pro	Ser	Met	Phe	Gly	Leu	His	Gln	Ile	Val
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Ala	Trp	Leu	Ala	Phe	Leu	Arg	Arg	Trp	Gly	Leu	Gly	Ala	Cys	Leu	Ala		
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Asp	Asp	Met	Gly	Leu	Gly	Lys	Thr	Val	Gln	Leu	Ile	Ala	Leu	Leu	Leu		
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His	Glu	Arg	Glu	Ala	Gly	Trp	Ala	Ala	Gly	Pro	Thr	Leu	Leu	Val	Cys		
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Pro	Val	Ser	Val	Leu	Gly	Asn	Trp	Cys	Arg	Glu	Leu	Ala	Arg	Phe	Ala		
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Pro	Gly	Leu	Arg	Val	Leu	Val	His	His	Gly	Pro	Gly	Arg	Leu	Gly	Glu		
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Tyr	Ser	Leu	Leu	Ala	Arg	Asp	Ala	Ala	Leu	Leu	Gly	Gln	Val	Thr	Trp		
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Gln	His	Ala	Arg	Ala	Leu	Arg	Ser	Leu	Ser	Gly	Gly	Tyr	Arg	Ile	Ala		
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Leu	Thr	Gly	Thr	Pro	Val	Glu	Asn	His	Leu	Gly	Asp	Leu	Trp	Ser	Leu		
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Phe	Gln	Phe	Leu	Asn	Pro	Gly	Leu	Leu	Gly	Ser	Arg	Glu	Glu	Phe	Glu		
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Arg	Arg	Tyr	Ala	Val	Pro	Ile	Gln	Arg	Tyr	Gln	Asp	Glu	Glu	Ala	Ala		
705					710					715					720		
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				725					730					735			
Asn	Asp	Pro	Ala	Ile	Ala	Pro	Asp	Leu	Pro	Asp	Lys	Leu	Glu	Asn	Thr		
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Glu	Leu	Val	Thr	Leu	Ser	Val	Glu	Gln	Ala	Ala	Leu	Tyr	Glu	Ala	Ile		
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PF58891.ST25.txt

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Ala Gly Glu Ala Pro	Leu Phe Ile Leu Ser Leu Lys Ala Gly Gly Leu					
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Trp Asn Pro Ala Val	Glu Asp Gln Ala Thr Asp Arg Ala Tyr Arg Ile					
	915		920		925	
Gly Gln Thr Arg Arg	Val Leu Val His Arg Leu Ile Thr Ala Gly Thr					
	930		935		940	
Leu Glu Glu Arg Ile	Asp Arg Leu Leu Ala Glu Lys Arg Ala Leu Ala					
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Gly Gln Val Ile Ile	Ser Gly Glu Ser Trp Leu Gly Gln Leu Ser Thr					
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 <212> DNA
 <213> *Synechococcus* sp.

<400> 81

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<210> 82
 <211> 1037
 <212> PRT
 <213> Synechococcus sp.

<400> 82

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

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His Trp Arg Glu Ala	Val Ala Gly Arg Val Glu	Pro Ala Arg Ala Cys			
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Leu Glu Leu Asp Thr	Pro Asp Glu Gly Glu Asp	Leu Trp Pro Leu Arg			
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	355	360	365		
Gln Val Phe Glu Pro	Ile Glu Arg Gly Leu Asp	Thr Ala Thr Pro Glu			
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Arg Met Ala Leu Thr	Pro Ala Glu Ala Phe Val	Leu Val Arg Thr Ala			
385	390	395	400		
Ala Leu Lys Leu Arg	Asp Val Gly Val Gly Val	Leu Pro Pro Ser			
	405	410	415		
Leu Ser Gly Gly Leu	Ala Ser Arg Leu Gly	Leu Ser Ile Glu Ala Asp			
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Ser Trp Glu Leu Met	Ile Gly Gly Val Thr	Leu Thr Leu Arg Asp Leu			
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Glu Arg Leu Ala Gly	Lys Arg Ser Pro Leu Val	Gln His Lys Gly Ala			
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Gly Pro Arg Leu Lys	Ala Val Leu Glu Gln Tyr	His Gln Gln Lys Ala			
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Pro Asp Pro Leu Pro	Ala Pro Glu Gly Phe Ala	Gly Gln Leu Arg Pro			
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Tyr Gln Glu Arg Gly	Leu Gly Trp Leu Ala Phe	Leu His Arg Phe Asp			
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Pro Val Leu Leu Val	Ala Pro Thr Ser Val Leu	Thr Asn Trp Leu Arg			
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Ala Arg Pro Leu Lys Gln Ser Arg Phe Arg Ile Ala Leu Thr Gly Thr
705                710                715                720
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Asn Pro Lys Val Leu Gly Glu Glu Glu Phe Phe Arg Gln Arg Tyr Arg
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Leu Ser Pro Glu Gln Val Lys Leu Tyr Arg Arg Thr Val Glu Asp Thr
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Gln Thr His Leu Gln Gln Arg Phe His Gln Glu Val Pro Phe Leu Tyr
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Gly Ser Thr Ser Lys Gly Glu Arg Gln Ala Met Val Asp Arg Phe Gln
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Gly Val Gly Leu Asn Leu Thr Arg Ala Ser His Val Phe His Ile Asp
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Arg Ile Gly Gln Thr Asn Arg Val Met Val His Lys Phe Ile Thr Ser
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PF58891.ST25.txt

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 <213> Synechococcus sp.

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 Glu Gly Pro Ala Trp Thr Gly Leu Pro Met Gln Ala Gly Glu Pro Ile
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 Pro Lys Gln Met Glu Trp Trp Pro Trp Gln Val Gln Gly Leu Ala Val
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 130 135 140
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 Arg Trp Ser Leu Ser Leu Val Ala Arg Gly Arg Trp Ile Pro Gln Met
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 Glu Leu Ser Lys Gly Glu Gly Tyr Pro His Arg Ala Arg Trp Val Pro
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 Gly Arg Arg Ser Asn Arg Thr Thr Arg Leu Arg Pro Glu Ala Met Arg
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 Phe Glu Pro Ser Thr Glu Gly Leu Asp Pro Leu Leu Thr Leu Trp Gln
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 Ala Glu Arg Leu Thr Ala Ala Ser Leu His Trp Arg Glu Gly Ile Ala
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 Gly Gly Phe Ala Ala Arg Thr Cys Leu Glu Leu Asn Thr Pro Asn
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PF58891.ST25.txt

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515      520      525
Leu Asp Asp Ala Leu Arg Leu Thr Gly Thr Glu Gly Glu Leu Leu Met
530      535      540
Arg Met Pro Val His Arg Phe Asp Ala Gly Pro Arg Leu Gln Ser Val
545      550      555      560
Leu Gln Gln Tyr His Gln Gln Lys Ala Pro Asp Pro Leu Pro Ala Pro
565      570      575
Glu Gly Phe Ser Gly Gln Leu Arg Pro Tyr Gln Glu Arg Gly Leu Gly
580      585      590
Trp Leu Ala Phe Leu His Arg Phe Asp Gln Gly Ala Cys Leu Ala Asp
595      600      605
Asp Met Gly Leu Gly Lys Thr Ile Gln Leu Leu Ala Phe Leu Gln His
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Ser Asn Arg Phe Arg Ile Ala Leu Thr Gly Thr Pro Val Glu Asn Arg
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Phe Thr Gln Phe Ala Glu Trp Gly His Leu Leu Arg Ala Trp Met Gln
915          920          925
Gln Arg Trp Lys Ser Glu Val Pro Phe Leu His Gly Gly Thr Arg Lys
930          935          940
Asn Glu Arg Gln Ala Met Val Asp Arg Phe Gln Glu Asp Pro Arg Gly
945          950          955          960
Pro Gln Leu Phe Leu Leu Ser Leu Lys Ala Gly Gly Val Gly Leu Asn
          965          970          975
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980          985          990
Ala Val Glu Asn Gln Ala Thr Asp Arg Ala Tyr Arg Ile Gly Gln Thr
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<400> 90

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Arg	Gly	Leu	Glu	Ser	Ala	Thr	Pro	Glu	Thr	Met	Gln	Leu	Thr	Pro Ala
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Glu	Ala	Phe	Val	Leu	Val	Arg	Thr	Ala	Thr	His	Gln	Leu	Arg	Asn Ala
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Thr	Ser	Val	Leu	Thr	Asn	Trp	Arg	Arg	Glu	Ala	Glu	Ala	Phe	Thr Pro
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		675					680					685		
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Gln	Gly	Val	Val	Ile	Asp	Glu	Ala	Gln	Ala	Ile	Lys	Asn	Pro	Gly Ala
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Lys	Gln	Ser	Gln	Ala	Ala	Arg	Asp	Leu	Ala	Arg	Ala	Gly	Lys	Ser Ser
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Asp Met Ser Ser Leu Arg Asp Leu Lys Ala Arg Val Gly Pro Phe Ile
785          790          795          800
Leu Arg Arg Leu Lys Thr Asp Lys Ser Ile Ile Ser Asp Leu Pro Glu
805          810          815
Lys Val Glu Leu Ser Glu Trp Val Gly Leu Ser Lys Glu Gln Lys Ser
820          825          830
Leu Tyr Asn Lys Thr Val Glu Asp Thr Leu Asp Ala Ile Ala Thr Ala
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Pro Arg Gly Gln Arg His Gly Gln Val Leu Ala Leu Leu Thr Arg Leu
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Lys Gln Ile Cys Asn His Pro Ala Leu Ala Gln Arg Glu Gly Ala Val
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Ile Leu Glu Glu Val Ile Glu Ala Gly Asp Arg Ala Leu Leu Phe Thr
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Gln Phe Ala Glu Trp Gly His Leu Leu Gln Ala Trp Met Gln Gln Arg
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980          985          990
Glu Asn Gln Ala Thr Asp Arg Ala Tyr Arg Ile Gly Gln Thr Asn Arg
995          1000          1005
Val Met Val His Lys Phe Val Thr Arg Gly Ser Val Glu Glu Lys
1010          1015          1020
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Thr Val Lys Pro Lys Arg Lys Arg Gly Glu Thr Ala Pro Val Asp Glu
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Thr Glu Trp Trp Pro Trp Gln Val Gln Gly Leu Ala Val Glu Pro Gly
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Ala Ala Thr Ala Trp Leu Ala Arg Leu Pro Leu Ser Gly Arg His Pro
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Asp Leu Ala Asp Glu Leu Arg Trp Trp Ser His Met Gln Arg Trp Ala
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Leu Ser Leu Ile Ala Arg Ser Arg Trp Ile Pro Gln Val Glu Leu Ser
165    170    175
Lys Gly Glu Gly Tyr Pro His Arg Ala Arg Trp Val Pro Leu Leu Asn
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Arg Glu Asp Asp Arg Arg Arg Leu Glu Asp Met Ala Ala Arg Leu Pro
195    200    205
Leu Val Ala Thr Cys Ala Leu Pro Trp Arg Glu Pro Thr Gly Lys Arg
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Ser Asn Arg Thr Thr Arg Leu Arg Pro Glu Ala Met Arg Ala Ala Asn
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Gln Thr Asp Gly Leu Asp Pro Leu Leu Ala Ala Trp Glu Glu Ala Leu
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Gly Ser Asp Thr Gly Val Ile His Leu Gly Asp Glu Asp Ala Glu Arg
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Gln Leu Gly Glu Ile Ala Val Glu His Pro Gly Glu Leu Leu Leu Glu
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Gly Met Gly Arg Ala Leu Thr Val Phe Pro Pro Ile Glu Arg Gly Leu
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 35 40 45
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 50 55 60
 Pro Asp Gly Ile Ile Asp Ala Thr Ala Cys Leu Thr Leu Pro Ser Arg
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 Ser Glu Glu Gln Pro Pro Trp Cys Gly Leu Pro Leu Gln Ala Gly Glu

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Ser Ala Lys Gln Ser Gln Ala Ala Arg Asp Leu Ala Arg Thr Arg Lys					
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Gly Ser Arg Phe Arg Ile Ala Leu Thr Gly Thr Pro Val Glu Asn Arg					
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Val Ser Glu Leu Trp Ala Leu Met Asp Phe Leu Asn Pro Asn Val Leu					
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Phe Ile Leu Arg Arg Leu Lys Thr Asp Lys Ala Ile Ile Ser Asp Leu					
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Pro Glu Lys Val Glu Leu Ser Glu Trp Val Gly Leu Ser Lys Glu Gln					
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Lys Ser Leu Tyr Ala Lys Thr Val Glu Asn Thr Leu Asp Ala Ile Ala					
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Arg Leu Lys Gln Ile Cys Asn His Pro Ala Leu Ala Leu Lys Glu Glu					
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Glu Glu Ile Leu Glu Glu Val Ile Ala Ala Gly Asp Arg Ala Leu Leu					
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Phe Thr Gln Phe Ala Glu Trp Gly His Leu Leu Gln Gly Tyr Leu Gln					
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<210> 96
 <211> 1063
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 <213> *Synechococcus* sp.

<400> 96

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Glu	Glu	Pro	Ile	Trp	Thr	Gly	Leu	Pro	Met	Gln	Ala	Gly	Glu	Pro	Ile
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245      250      255
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Phe Glu Pro Ser Thr Asp Gly Leu Asp Pro Leu Leu Thr Leu Trp Gln
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Asp Pro Ser Leu Lys Leu Pro Ala Ala Ala Trp Ala Ser Gly Ala
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385      390      395      400
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Glu Ala Phe Val Leu Val Arg Thr Ala Ala Arg Gln Leu Arg Asp Ala
420      425      430
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485      490      495
Ser Pro Leu Val Arg His Lys Gly Ala Trp Ile Glu Leu Arg Pro Asn
500      505      510
Asp Leu Arg Asn Ala Glu Arg Phe Cys Gly Ala Asn Pro Glu Leu Ser
515      520      525
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530      535      540
Arg Leu Pro Val His Arg Phe Glu Ala Gly Pro Arg Leu Gln Ala Val
545      550      555      560
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565      570      575
Glu Gly Phe Cys Gly Gln Leu Arg Pro Tyr Gln Glu Arg Gly Leu Gly
580      585      590
Trp Leu Ala Phe Leu Asn Arg Phe Asp Gln Gly Ala Cys Leu Ala Asp
595      600      605
Asp Met Gly Leu Gly Lys Thr Ile Gln Leu Leu Ala Phe Leu Gln His
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Leu Lys Ala Glu Gln Glu Leu Lys Arg Pro Val Leu Leu Val Ala Pro

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Tyr Gly Leu Leu Gln Arg Asp Ser Glu Leu Leu Glu Ser Gln Asp Trp
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Gln Gly Val Val Ile Asp Glu Ala Gln Ala Ile Lys Asn Pro Ser Ala
705          710          715          720
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Trp Lys Ala Asp Val Pro Phe Leu His Gly Gly Thr Arg Lys Asn Glu
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Ile Asp Arg Met Ile Arg Glu Lys Ser Arg Leu Ala Glu Asp Val
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1055

1060

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 <212> DNA
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<400> 98

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	50					55					60				
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Pro	Leu	Gly	Ser	Ala	Glu	Asp	His	Pro	Trp	Leu	Gly	Pro	Asp	Leu	Arg
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Gly	Asn	Trp	Glu	Arg	Glu	Val	Gln	Lys	Phe	Ala	Pro	Glu	Leu	Arg	Trp
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Lys	Leu	His	Tyr	Gly	Pro	Asp	Arg	Ala	Gln	Gly	Lys	Ala	Leu	Ala	Thr
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Arg	Asp	Gln	Lys	Ala	Ile	Ala	Ala	Ile	Asp	Trp	Gln	Gly	Ile	Val	Leu
			645						650					655	
Asp	Glu	Ala	Gln	Asn	Ile	Lys	Asn	Asp	Gln	Ala	Lys	Gln	Thr	Gln	Ala
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Arg Arg Gly Gln Ile Leu Ala Leu Leu Thr Arg Leu Lys Gln Leu Cys
805          810          815
Asn His Pro Ser Leu Leu Leu Glu Lys Pro Lys Leu Asp Pro Asn Phe
820          825          830
Gly Asp Arg Ser Ala Lys Leu Gln Arg Leu Leu Glu Met Leu Ala Glu
835          840          845
Leu Thr Asp Ala Gly Asp Arg Ala Leu Val Phe Thr Gln Phe Ala Gly
850          855          860
Trp Gly Ser Leu Leu Gln Gln Phe Leu Gln Glu Gln Leu Gly Arg Glu
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980          985          990
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 <212> DNA
 <213> *Synechococcus elongatus*

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 <212> PRT
 <213> *Synechococcus elongatus*

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 20 25 30
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 35 40 45
 Lys Tyr Arg Leu Gly Ser Leu Thr Gly Thr Pro Thr Glu Val Leu Leu
 50 55 60
 Ser Ile Pro Ser Asp Leu Lys Lys Glu Ala Val Leu Pro Phe Leu Ser
 65 70 75 80
 Gly Gln Glu Ile Pro Asp Gly Ala Leu Leu Trp Ser Trp Gln Ile Pro

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Phe	Trp	Ser	His	Ile	Tyr	Arg	Trp	Ala	Gln	Ser	Leu	Leu	Ala	Arg	Gly
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Trp	Leu	Pro	Leu	Phe	Asn	Gln	Ala	Gly	Asp	Arg	Gln	Arg	Phe	Asp	Arg
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Tyr	Ser	Gln	Gln	Leu	Pro	Phe	Ser	Gln	Phe	Cys	Tyr	Gln	Ala	Ile	Glu
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Thr	Ala	Ala	Ala	Cys	Pro	Trp	Gln	Pro	Gln	Pro	Gln	Asp	Leu	Leu	Leu
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225					230					235					240
Leu	Ala	Asn	Gly	Lys	Pro	Leu	Lys	Leu	Glu	Asp	Ser	Glu	Ala	Ser	Arg
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Glu	Gln	Pro	Trp	Gln	Leu	Glu	Phe	Gly	Leu	Gln	Ala	Ala	Thr	Asp	Pro
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Gly	Leu	Pro	Asp	Gln	Ser	Gln	Glu	Leu	Leu	Leu	Arg	Gly	Leu	Gly	Gln
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Ala	Thr	Leu	Pro	Ser	Asp	Arg	Pro	Ser	Val	Gly	Leu	Glu	Ala	Leu	Leu
				405					410					415	
Gln	Phe	Arg	Trp	Glu	Leu	Ser	Leu	Gly	Gly	Gln	Arg	Leu	Thr	Lys	Ala
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Glu	Val	Glu	Arg	Leu	Ala	Ala	Leu	Glu	Thr	Pro	Leu	Val	Glu	Ile</	

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625					630					635					640
Arg	Asp	Gln	Lys	Ala	Ile	Ala	Ala	Ile	Asp	Trp	Gln	Gly	Ile	Val	Leu
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Asp	Glu	Ala	Gln	Asn	Ile	Lys	Asn	Asp	Gln	Ala	Lys	Gln	Thr	Gln	Ala
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Ile	Val	Glu	Phe	Leu	Gln	Pro	Gly	His	Leu	Gly	Thr	Lys	Pro	Phe	Phe
705					710					715					720
Gln	Lys	Arg	Phe	Val	Thr	Pro	Ile	Glu	Arg	Phe	Gly	Asp	Ala	Asp	Ser
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Val	Leu	Phe	Leu	Ser	Gly	Ser	Thr	Lys	Lys	Gly	Asp	Arg	Gln	Gln	Met
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Val	Phe	His	Tyr	Asp	Arg	Trp	Trp	Asn	Pro	Ala	Val	Glu	Asn	Gln	Ala
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 980 985 990
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 <213> Thermosynechococcus elongatus

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<211> 999

<212> PRT

<213> Thermosynechococcus elongatus

<400> 102

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35        40        45
Thr Pro Leu Arg Lys Thr Ala Arg Pro Ser Ala Thr Tyr Val Ala Leu
50        55        60
Pro Ala Gln Ile Gln Gly His Gln Leu Leu Pro Pro Leu Ala Glu
65        70        75        80
Val Gln Gly Glu Leu Phe Leu Trp Gln Val Pro Gly Trp Ser Ile
85        90        95
Pro Ala Ser Glu Val Leu Glu Gln Leu His Gln Leu Ser Leu His Gly
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Gln Asp Ser Gly Ser Ile Gly Asp Asp Leu Arg Tyr Trp Leu His Val
115       120       125
Ser Arg Trp Leu Leu Asp Leu Ile Val Arg Gly Gln Tyr Leu Pro Thr
130       135       140
Pro Glu Gly Trp Arg Ile Leu Leu Thr His Gly Gly Asp Arg Asp Arg
145       150       155       160
Leu Arg His Phe Ser Gln Leu Met Pro Asp Leu Cys Arg Cys Tyr Gln
165       170       175
Ala Asp Gly Thr Ala Leu Gln Leu Pro Pro His Ala Ala Asp Leu Leu
180       185       190
Ala Asp Phe Leu Gln His Thr Leu Gln Gly Tyr Leu His Thr Ala Leu
195       200       205
Ala Asp Leu Glu Leu Pro Lys Val Gly Leu Ala Lys Glu His Gly His
210       215       220
Trp Leu Ala Phe Leu Lys Thr Gly Gln Thr Pro Glu Leu Pro Pro Pro
225       230       235       240
Leu Ile Glu Arg Leu His Arg Trp Gln Glu Pro Tyr Arg Glu Gln Leu
245       250       255
His Leu Arg Pro Gln Trp Arg Leu Ala Leu Gln Leu Val Pro Pro Asp
260       265       270
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		335
Arg Ser Leu Gln Glu Arg Ser Pro Val Ala Leu Thr Leu His Thr Thr		
	340	345
		350
Glu Val Tyr Ala Phe Leu Gln Ser Ala Ile Ala Pro Leu Glu Gln Gln		
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Gly Val Ala Ile Ile Leu Pro Pro Ser Leu Arg Arg Asn Ser Ala Gln		
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		380
His Arg Leu Gly Leu Lys Ile Ile Ala Thr Leu Pro Pro Pro Ala Thr		
385	390	395
Asn Gly Leu Thr Ile Asp Ser Leu Met Gln Phe Gln Trp Gln Leu Gln		
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		415
Leu Gly Gln His Pro Leu Ser Glu Ala Asp Phe Asp Gln Leu Arg Arg		
	420	425
		430
Gln Gly Thr Pro Leu Val Tyr Leu Asn Gly Glu Trp Val Leu Leu Arg		
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		445
Pro Gln Glu Val Lys Ala Ala Gln Glu Phe Leu Gln Ser Pro Pro Lys		
	450	455
		460
Thr Gln Leu Ser Leu Ala Glu Thr Leu Arg Ile Ala Thr Gly Asp Thr		
465	470	475
Val Thr Val Ala Lys Leu Pro Ile Leu Gly Leu Asp Thr Asn Asp Ala		
	485	490
		495
Leu Gln Thr Leu Leu Asp Gly Leu Thr Gly Lys Gln Ser Leu Asp Pro		
	500	505
		510
Val Pro Thr Pro Gln Glu Phe Cys Gly Glu Leu Arg Pro Tyr Gln Ala		
	515	520
		525
Arg Gly Val Ala Trp Leu Ser Phe Leu Glu Arg Trp Arg Leu Gly Ala		
	530	535
		540
Cys Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Ile Gln Leu Leu Ala		
545	550	555
		560
Phe Leu Leu His Leu Lys Glu Thr Gly Arg Ala Tyr Arg Pro Thr Leu		
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		575
Leu Ile Cys Pro Thr Ser Val Leu Gly Asn Trp Leu Arg Glu Cys Gln		
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		590
Lys Phe Ala Pro Thr Leu Arg Ala Tyr Val His His Gly Ser Asp Arg		
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Pro Lys Gly Lys Ala Phe Leu Lys Lys Val Glu Thr His Asp Leu Ile		
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Leu Thr Ser Tyr Ala Leu Leu Gln Arg Asp Arg Thr Thr Leu Gln Gln		
625	630	635
Val Leu Trp Gln His Leu Val Leu Asp Glu Ala Gln Asn Ile Lys Asn		
	645	650
		655
Ala Asn Thr Gln Gln Ser Gln Ala Ala Arg Glu Leu Ser Ala Gln Phe		
	660	665
		670
Arg Ile Ala Leu Thr Gly Thr Pro Leu Glu Asn Arg Leu Leu Glu Leu		
	675	680
		685
Trp Ser Ile Met Asp Phe Leu His Pro Gly Tyr Leu Gly His Arg Thr		
	690	695
		700
Tyr Phe Gln His Arg Tyr Val Arg Pro Ile Glu Arg Tyr Gly Asp Thr		

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```

705              710              715              720
Thr Ser Leu Asn Ala Leu Arg Thr Tyr Val Gln Pro Phe Ile Leu Arg
              725              730              735
Arg Leu Lys Thr Asp Arg Ser Ile Ile Gln Asp Leu Pro Glu Lys Gln
              740              745              750
Glu Met Leu Val Tyr Cys Gly Leu Thr Leu Glu Gln Met Gln Leu Tyr
              755              760              765
Thr Ala Val Val Glu Asp Ser Leu Ala Ala Ile Glu Asn Ser Gln Gly
              770              775              780
Ile Gln Arg Arg Gly Asn Ile Leu Ala Thr Leu Thr Lys Leu Lys Gln
785              790              795              800
Ile Cys Asn His Pro Ala Gln Tyr Leu Lys Gln Glu Asp Tyr Ala Pro
              805              810              815
Asp Arg Ser Gly Lys Leu Gln Arg Leu Ile Glu Met Leu Gln Ala Leu
              820              825              830
Gln Glu Val Gly Asp Arg Ala Leu Val Phe Thr Gln Phe Ala Glu Phe
              835              840              845
Gly Thr His Leu Lys Thr Tyr Leu Glu Lys Ala Leu Gln Gln Glu Val
              850              855              860
Phe Phe Leu Ser Gly Arg Thr Pro Lys Ala Gln Arg Glu Leu Met Val
865              870              875              880
Glu Arg Phe Gln His Asp Pro Glu Ala Pro Arg Val Phe Ile Leu Ser
              885              890              895
Leu Lys Ala Gly Gly Val Gly Leu Asn Leu Thr Arg Ala Asn His Val
              900              905              910
Phe His Tyr Asp Arg Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Ser
              915              920              925
Asp Arg Val Phe Arg Ile Gly Gln Ala Arg Asn Val Gln Ile His Lys
930              935              940
Phe Ile Cys Thr Gly Thr Leu Glu Glu Lys Ile His Glu Gln Ile Glu
945              950              955              960
Gln Lys Lys Ala Leu Ala Glu Met Ile Val Gly Ser Gly Glu His Trp
              965              970              975
Leu Thr Glu Leu Asn Leu Asp Gln Leu Arg Gln Leu Leu Thr Leu Asp
              980              985              990
Lys Glu Arg Leu Ile Thr Leu
              995

```

```

<210> 103
<211> 10
<212> PRT
<213> Artificial sequence

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<220>
<223> motif 1

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<220>
<221> VARIANT
<222> (10)..(10)
<223> /replace = "Ser"

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```

<400> 103
Leu Ala Asp Asp Met Gly Leu Gly Lys Thr
1              5              10

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<210> 104
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> motif 1a

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace = "Val" /replace = "Ile"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace = "Ile" /replace = "Leu"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace = "Cys"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace = "Met" /replace = "Val"

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace = "Ile" /replace = "Leu"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace = "Ile" /replace = "Leu"

<220>
<221> UNSURE
<222> (10)..(10)

<400> 104
Leu Leu Val Ala Pro Thr Ser Val Val Xaa Asn Trp
1          5          10

<210> 105
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> motif 2

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<220>
 <221> VARIANT
 <222> (5)..(5)
 <223> /replace = "Ala" /replace = "His"

<220>
 <221> VARIANT
 <222> (6)..(6)
 <223> /replace = "Ile" /replace = "Leu"

<400> 105
 Asp Glu Ala Gln Asn Val Lys Asn
 1 5

<210> 106
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 3

<220>
 <221> VARIANT
 <222> (2)..(2)
 <223> /replace = "Met"

<220>
 <221> UNSURE
 <222> (7)..(7)

<400> 106
 Ala Leu Thr Gly Thr Pro Xaa Glu Asn
 1 5

<210> 107
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 4

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> /replace = "Ile"

<220>
 <221> UNSURE
 <222> (2)..(2)

<220>

<221> VARIANT
 <222> (4)..(4)
 <223> /replace = "Ser"

<220>
 <221> VARIANT
 <222> (6)..(6)
 <223> /replace = "Tyr"

<400> 107
 Leu Xaa Phe Thr Gln Phe
 1 5

<210> 108
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motif 5

<220>
 <221> VARIANT
 <222> (2)..(2)
 <223> /replace = "Val"

<220>
 <221> VARIANT
 <222> (7)..(7)
 <223> /replace = "Thr" /replace = "Leu"

<220>
 <221> VARIANT
 <222> (9)..(9)
 <223> /replace = "Ile"

<220>
 <221> VARIANT
 <222> (10)..(10)
 <223> /replace = "Ile"

<220>
 <221> UNSURE
 <222> (13)..(13)

<220>
 <221> UNSURE
 <222> (13)..(13)

<400> 108
 Ser Leu Lys Ala Gly Gly Val Gly Leu Asn Leu Thr Xaa Ala Asn His
 1 5 10 15
 Val

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<210> 109
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> motif 5a

<400> 109
Asp Arg Trp Trp Asn Pro Ala Val Glu
1             5

<210> 110
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> motif 6

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace = "Ser"

<220>
<221> VARIANT
<222> (6)..(6)
<223> /replace = "Thr" /replace = "Val"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace = "Tyr"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace = "Leu"

<400> 110
Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln
1             5             10

<210> 111
<211> 460
<212> PRT
<213> Artificial sequence

<220>
<223> ATPase domain of SEQ ID NO: 2

<400> 111

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Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Pro Gln Leu Leu Ala Phe
1      5      10      15
Leu Leu His Leu Ala Ala Glu Asp Met Leu Val Lys Pro Val Leu Ile
20      25      30
Val Cys Pro Thr Ser Val Leu Ser Asn Trp Gly His Glu Ile Asn Lys
35      40      45
Phe Ala Pro Gln Leu Lys Thr Leu Leu His His Gly Asp Arg Arg Lys
50      55      60
Lys Gly Gln Pro Leu Val Lys Gln Val Lys Asp Gln Gln Ile Val Leu
65      70      75      80
Thr Ser Tyr Ala Leu Leu Gln Arg Asp Phe Ser Ser Leu Lys Leu Val
85      90      95
Asp Trp Gln Gly Ile Val Leu Asp Glu Ala Gln Asn Ile Lys Asn Pro
100     105     110
Gln Ala Lys Gln Ser Gln Ala Ala Arg Gln Leu Pro Ala Gly Phe Arg
115     120     125
Ile Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Thr Glu Leu Trp
130     135     140
Ser Ile Leu Glu Phe Leu Asn Pro Gly Phe Leu Gly Asn Gln Ser Phe
145     150     155     160
Phe Gln Arg Arg Phe Ala Asn Pro Ile Glu Lys Phe Gly Asp Arg Gln
165     170     175
Ser Leu Leu Ile Leu Arg Asn Leu Val Arg Pro Phe Ile Leu Arg Arg
180     185     190
Leu Lys Thr Asp Gln Thr Ile Ile Gln Asp Leu Pro Glu Lys Gln Glu
195     200     205
Met Thr Val Phe Cys Asp Leu Ser Gln Glu Gln Ala Gly Leu Tyr Gln
210     215     220
Gln Leu Val Glu Glu Ser Leu Gln Ala Ile Ala Asp Ser Glu Gly Ile
225     230     235     240
Gln Arg His Gly Leu Val Leu Thr Leu Leu Thr Lys Leu Lys Gln Val
245     250     255
Cys Asn His Pro Asp Leu Leu Leu Lys Lys Pro Ala Ile Thr His Gly
260     265     270
His Gln Ser Gly Lys Leu Ile Arg Leu Ala Glu Met Leu Glu Glu Ile
275     280     285
Ile Ser Glu Gly Asp Arg Val Leu Ile Phe Thr Gln Phe Ala Ser Trp
290     295     300
Gly His Leu Leu Lys Pro Tyr Leu Glu Lys Tyr Phe Asn Gln Glu Val
305     310     315     320
Leu Tyr Leu His Gly Gly Thr Pro Ala Glu Gln Arg Gln Ala Leu Val
325     330     335
Glu Arg Phe Gln Gln Asp Pro Asn Ser Pro Tyr Leu Phe Ile Leu Ser
340     345     350
Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Arg Ala Asn His Val
355     360     365
Phe His Val Asp Arg Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Thr
370     375     380
Asp Arg Ala Phe Arg Ile Gly Gln Thr Arg Asn Val Gln Val His Lys
385     390     395     400
Phe Val Cys Thr Gly Thr Leu Glu Glu Lys Ile Asn Ala Met Met Ala
405     410     415
Asp Lys Gln Gln Leu Ala Glu Gln Thr Val Asp Ala Gly Glu Asn Trp
420     425     430

```

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Leu Thr Arg Leu Asp Thr Asp Lys Leu Arg Gln Leu Leu Thr Leu Ser
 435 440 445
 Ala Thr Pro Val Asp Tyr Gln Ala Glu Ala Ser Asp
 450 455 460

<210> 112
 <211> 1244
 <212> DNA
 <213> Oryza sativa

<400> 112
 aaaaccaccg agggacctga tctgcaccgg ttttgatagt tgagggaccc gttgtgtctg 60
 gttttccgat cgagggacga aaatcggatt cgggtgtaaag ttaagggacc tcagatgaac 120
 ttattccgga gcatgattgg gaaggaggga cataaggccc atgtcgcgatg tgtttggaag 180
 gtccagatct ccagatcact cagcaggatc ggccgcgttc gcgtagcacc cgcggtttga 240
 ttccgcttcc cgcaaggcgg cggccggtgg ccgtgccgcc gtagcttccg ccggaagcga 300
 gcacgccgcc gccgccgacc cggctctgcg tttgcaccgc cttgcacgcg atacatcggg 360
 atagatagct actactctct ccgtttcaca atgtaaatca ttctactatt ttccacattc 420
 atattgatgt taatgaatat agacatatat atctatattg attcattaac atcaatatga 480
 atgtaggaaa tgctagaatg acttacattg tgaattgtga aatggacgaa gtacctacga 540
 tggatggatg caggatcatg aaagaattaa tgcaagatcg tatctgccgc atgcaaaatc 600
 ttactaattg cgctgcatat atgcatgaca gcctgcatgc gggcgtgtaa gcgtgttcat 660
 ccattaggaa gtaaccttgt cattaacttat accagtacta cactactatat agtattgatt 720
 tcatgagcaa atctacaaaa ctggaaagca ataagaaata cgggactgga aaagactcaa 780
 cattaatcac caaatatttc gccttctcca gcagaatata tatctctcca tcttgatcac 840
 tgtacacact gacagtgtac gcataaacgc agcagccagc ttaactgtcg tctcaccgtc 900
 gcacactggc cttccatctc aggctagctt tctcagccac ccacgtgaca tgtcaactcg 960
 gcgcgcgcac aggcacaaat tacgtacaaa acgcatgacc aaatcaaaac caccggagaa 1020
 gaatcgctcc cgcgcgcggc ggcgacgcgc acgtacgaac gcacgcacgc acgccaacc 1080
 ccacgacacg atcgcgcgcg acgcgcgcga caccggccgt ccacccgcgc cctcacctcg 1140
 ccgactataa atacgtaggc atctgcttga tcttgctcat catctcacca ccaaaaaaaaa 1200
 aaggaaaaaa aaacaaaaca caccaagcca aataaaagcg acaa 1244

<210> 113
 <211> 59
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm08774

<400> 113
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatggc gactatccac ggtaattgg 59

<210> 114
 <211> 49
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm08779

<400> 114
 ggggaccact ttgtacaaga aagctgggtt caatcggacg cttcggctt 49