SEQUENCE LISTING

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<120> REGULATED GENE EXPRESSION SYSTEMS AND CONSTRUCTS THEREOF

<130> 80000229-0027

<150> U.S. Provisional Application Serial No. 61/467,873
<151> 2012-03-24

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Ser Val Val Val Ala Asn Arg His His Glu Glu Leu Ser Asn Leu Gly
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Thr Ala Val Gly Ser Glu Ile Tyr His Pro Glu Gly Leu Asp Gln His
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Trp Ala Asp Tyr Leu Ser Glu His Trp Gln Arg Asp Ile Leu Gln Ala
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Ile Ala Asp Gly Phe Glu Ala Leu Lys Pro Gln Ser Pro Leu Glu Gln
100 105 110

Asn Pro Trp Lys Ile Ser Tyr His Leu Asp Pro Gln Ala Cys Pro Thr
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Val Ile Asp Gln Leu Thr Glu Met Leu Lys Glu Thr Gly Ile Pro Val
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195 200 205

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35 40 45

Arg Tyr Trp Leu Pro Thr Val Asp Thr Glu Val Lys Thr Pro Leu Ala
50 55 60

Ile Ala Lys Ala Ser Leu Ile Asp Pro Gln Thr Pro Phe Val Ile Val
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Pro Ile Leu Arg Ala Gly Leu Ala Leu Val Glu Gly Ala Gln Gly Leu
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Leu Pro Leu Ala Lys Ile Tyr His Leu Gly Leu Val Arg Asn Glu Thr
100 105 110

Thr Leu Glu Pro Ser Leu Tyr Leu Asn Lys Leu Pro Glu Arg Phe Ala
115 120 125

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

145 150 155 160

Asn Leu Ile Arg Leu Val Ser Val Val Ala Ala Pro Thr Ala Leu Gln
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Lys Leu Ser Asn Ala His Pro Asn Leu Thr Ile Tyr Thr Ala Met Ile
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Arg Glu Trp Leu Pro Thr Ile Pro Ala Ala Val Gln Thr Pro Leu Ala
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Leu Pro Thr Ala Arg Ile Phe His Val Gly Leu Lys Arg Asp Glu Val
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Ser Leu Glu Pro Arg Cys Tyr Leu Asn His Leu Pro Glu Gln Leu Glu
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Val Asn Ser Arg Val Leu Val Leu Asp Pro Met Leu Ala Thr Gly Gly
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Ser Leu Leu Tyr Thr Leu Asp Leu Leu Arg Asp Arg Gly Val Ser Ala
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Glu Gln Val Arg Val Leu Ser Ile Val Ala Ala Pro Pro Ala Leu Gln
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Lys Leu Ser Gln Ala Tyr Pro Ala Leu Thr Ile Tyr Ser Ala Ile Ile
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<213> Synechocystis PCC6803

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35 40 45

Val Phe Ile Arg Asp Asn Val Pro Val Met Ile Phe Leu Leu Leu Gln
50 55 60

Asn Glu Thr Glu Ile Val Gln Asn Phe Leu Glu Ile Cys Leu Thr Leu
65 70 75 80

Gln Ser Lys Gly Phe Pro Thr Tyr Gly Ile Phe Pro Thr Ser Phe Val
85 90 95

Glu Thr Glu Asn His Glu Leu Lys Ala Asp Tyr Gly Gln Arg Ala Ile
100 105 110

Gly Arg Val Cys Ser Val Asp Ala Ser Leu Trp Trp Pro Ile Leu Ala
115 120 125

Tyr Tyr Tyr Val Gln Arg Thr Gly Asn Glu Ala Trp Ala Arg Gln Thr
130 135 140

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

Val Phe Arg Asp Ala Pro Thr Leu Phe Val Pro Asp Gly Ala Phe Met
165 170 175

Ile Asp Arg Pro Met Asp Val Trp Gly Ala Pro Leu Glu Ile Gln Thr
180 185 190

Leu Leu Tyr Gly Ala Leu Lys Ser Ala Ala Gly Leu Leu Leu Ile Asp
195 200 205

Leu Lys Ala Lys Gly Tyr Cys Ser Asn Lys Asp His Pro Phe Asp Ser
210 215 220

Phe Thr Met Glu Gln Ser His Gln Phe Asn Leu Ser Val Asp Trp Leu
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Lys Lys Leu Arg Thr Tyr Leu Leu Lys His Tyr Trp Ile Asn Cys Asn
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Ile Val Gln Ala Leu Arg Arg Arg Pro Thr Glu Gln Tyr Gly Glu Glu
            260                 265                 270

Ala Ser Asn Glu His Asn Val His Thr Glu Thr Ile Pro Asn Trp Leu
        275                 280                 285

Gln Asp Trp Leu Gly Asp Arg Gly Gly Tyr Leu Ile Gly Asn Ile Arg
    290                 295                 300

Thr Gly Arg Pro Asp Phe Arg Phe Phe Ser Leu Gly Asn Cys Leu Gly
305                 310                 315                 320

Ala Ile Phe Asp Val Thr Ser Leu Ala Gln Gln Arg Ser Phe Phe Arg
                325                 330                 335

Leu Val Leu Asn Asn Gln Arg Glu Leu Cys Ala Gln Met Pro Leu Arg
            340                 345                 350

Ile Cys His Pro Pro Leu Lys Asp Asp Asp Trp Arg Ser Lys Thr Gly
        355                 360                 365

Phe Asp Arg Lys Asn Leu Pro Trp Cys Tyr His Asn Ala Gly His Trp
    370                 375                 380

Pro Cys Leu Phe Trp Phe Leu Val Val Ala Val Leu Arg His Ser Cys
385                 390                 395                 400

His Ser Asn Tyr Gly Thr Val Glu Tyr Ala Glu Met Gly Asn Leu Ile
                405                 410                 415

Arg Asn Asn Tyr Glu Val Leu Leu Arg Arg Leu Pro Lys His Lys Trp
            420                 425                 430

Ala Glu Tyr Phe Asp Gly Pro Thr Gly Phe Trp Val Gly Gln Gln Ser
        435                 440                 445

Arg Ser Tyr Gln Thr Trp Thr Ile Val Gly Leu Leu Leu Val His His
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Phe Thr Glu Val Asn Pro Asp Asp Ala Leu Met Phe Asp Leu Pro Ser
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<213> Synechococcus PCC7942

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<213> Synechococcus PCC7942

<400> 73

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

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Ala Ala Asn Tyr Arg Glu Ile Phe Ile Arg Asp Asn Val Pro Val Met
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Leu Tyr Leu Leu Leu Gln Gly Lys Thr Asp Val Val Arg Asp Phe Leu
65                  70                  75                  80

Gln Leu Ser Leu Ser Leu Gln Ser Gln Ala Leu Gln Thr Tyr Gly Ile
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Leu Pro Thr Ser Phe Val Cys Glu Glu Thr His Cys Val Ala Asp Tyr
            100                 105                 110

Gly Gln Arg Ala Ile Gly Arg Val Val Ser Ala Asp Pro Ser Leu Trp
        115                 120                 125

Trp Pro Val Leu Leu Gln Ala Tyr Arg Arg Ala Ser His Asp Asp Ala
    130                 135                 140

Phe Val His Ser Pro Thr Val Gln Gln Gly Leu Gln Arg Leu Leu Ala
145                 150                 155                 160

Phe Leu Leu Arg Pro Val Phe Asn Gln Asn Pro Leu Leu Glu Val Pro
                165                 170                 175

Asp Gly Ala Phe Met Val Asp Arg Pro Leu Asp Val Ala Gly Ala Pro
            180                 185                 190

Leu Glu Ile Gln Val Leu Leu Tyr Gly Ala Leu Arg Ala Cys Gly Gln
        195                 200                 205

Leu Leu Gln Tyr Thr Glu Ala Ala Asn Ala Ala His Val Gln Ala Arg
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Arg Leu Arg Gln Tyr Leu Cys Trp His Tyr Trp Val Thr Pro Asp Arg
225                 230                 235                 240

Leu Arg Arg Trp Gln Gln Trp Pro Thr Glu Glu Phe Gly Asp Arg Ser
                245                 250                 255

His Asn Pro Tyr Asn Ile Gln Pro Ile Ala Ile Pro Asp Trp Val Glu
            260                 265                 270

Pro Trp Leu Gly Glu Ser Gly Gly Tyr Phe Leu Gly Asn Ile Arg Ala
        275                 280                 285

Gly Arg Pro Asp Phe Arg Phe Phe Ser Leu Gly Asn Leu Leu Ala Ile
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Val Phe Asp Val Leu Pro Leu Asn Gln Gln Gly Ala Ile Leu Arg Leu
305                 310                 315                 320
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Ile Leu Gln Asn Glu Ala Gln Ile Leu Gly Gln Val Pro Leu Arg Leu
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Cys Tyr Pro Ala Leu Thr Gly Ser Ala Trp Lys Ile Leu Thr Gly Cys
            340                 345                 350

Asp Pro Lys Asn Gln Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro
        355                 360                 365

Ser Leu Leu Trp Tyr Leu Ser Ala Ala Val Leu His Tyr Gln Gln Arg
    370                 375                 380

Gly Gly Asp Arg Asn Leu Cys Gln Val Trp Leu Asn Lys Leu Gln His
385                 390                 395                 400

Tyr His Thr Gln Gln Cys Glu Gln Leu Pro Gly Asp Glu Trp Pro Glu
                405                 410                 415

Tyr Tyr Glu Gly Gln Asp Ser Val Gln Ile Ala Thr Arg Ala Cys Arg
            420                 425                 430

Tyr Gln Thr Trp Thr Phe Thr Gly Leu Leu Leu Asn His Ala Leu Leu
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Ser Gln Pro Gln Gly Ile Gln Leu Leu Ser Leu Arg Gly Leu Pro
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<211> 966
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<213> Synechocystis PCC6803

<400> 74

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acagcaaatt caagtgatcg ttggttaatt atggaattac cccaaccttg gacagaggaa      120

cgctttcatc atgaccccat tcttaaacca attcatgatc tttttcatca actttctgat      180

caaggagtta aagtatctcc aatggcgatc gcctcagatc acgagtattc tcaatcagga      240

tttagtcgta ttattcacta ccaaaagttt aatttgctct tttccagttt tataaaagaa      300

gaatatttag ttcctgatga tcaaaggtgg gatcttatca aaaatttatg ttatcaatct      360

ccagagttag aaaattttcg taactataaa ctgtcagatg ttgttgatcg agatatgatg      420

gtatgtactc atggaaacat tgatgtggct tgttcgagat ttggttatcc tatttataaa      480

caattacgac aaaaatatgc atcaaaaaat ttaagaatat ggcgctgctc tcattttggg      540

ggacatcagt ttgctccgac tttaattgat tttccaaatg ggcaagtttg gggacatctt      600

gagtctgaag ttttagataa tctggtaagg caagaaggtc aagttaaaca actttataaa      660

ttttatcgag gttgggtagg cgtaacaaaa tttgcccaga ttgttgagcg tgaaatttgg      720

actcaacgag gttggcaatg gttaaattat caaaaatcag ctcaaatatt gaacatggat      780
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gataatcagc atgatcccaa ttgggtagag gttcaatttg attttatttc tcccgataaa 840

gttaaaggag cttattttgc aagagttgaa gtcaatgggt cagtgatgac tgctagaaat 900

tcaggagatg aacttatttc tgtcaagcag tatagtgtca gctacttaaa agaaattgat 960

aaataa 966

<210> 75
<211> 321
<212> PRT
<213> Synechocystis PCC6803

<400> 75

Met Ile Asn Cys Gln Phe Cys Ser Val Ile Ser Lys Ser Asn Gly Glu
1 5 10 15

Asp Pro Ile Gly Thr Ala Asn Ser Ser Asp Arg Trp Leu Ile Met Glu
20 25 30

Leu Pro Gln Pro Trp Thr Glu Glu Arg Phe His His Asp Pro Ile Leu
35 40 45

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

Val Ser Pro Met Ala Ile Ala Ser Asp His Glu Tyr Ser Gln Ser Gly
65 70 75 80

Phe Ser Arg Ile Ile His Tyr Gln Lys Phe Asn Leu Leu Phe Ser Ser
85 90 95

Phe Ile Lys Glu Glu Tyr Leu Val Pro Asp Asp Gln Arg Trp Asp Leu
100 105 110

Ile Lys Asn Leu Cys Tyr Gln Ser Pro Glu Leu Glu Asn Phe Arg Asn
115 120 125

Tyr Lys Leu Ser Asp Val Val Asp Arg Asp Met Met Val Cys Thr His
130 135 140

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

Gln Leu Arg Gln Lys Tyr Ala Ser Lys Asn Leu Arg Ile Trp Arg Cys
165 170 175

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

Asn Gly Gln Val Trp Gly His Leu Glu Ser Glu Val Leu Asp Asn Leu
195 200 205

Val Arg Gln Glu Gly Gln Val Lys Gln Leu Tyr Lys Phe Tyr Arg Gly

210 215 220

Trp Val Gly Val Thr Lys Phe Ala Gln Ile Val Glu Arg Glu Ile Trp
225 230 235 240

Thr Gln Arg Gly Trp Gln Trp Leu Asn Tyr Gln Lys Ser Ala Gln Ile
245 250 255

Leu Asn Met Asp Asp Asn Gln His Asp Pro Asn Trp Val Glu Val Gln
260 265 270

Phe Asp Phe Ile Ser Pro Asp Lys Val Lys Gly Ala Tyr Phe Ala Arg
275 280 285

Val Glu Val Asn Gly Ser Val Met Thr Ala Arg Asn Ser Gly Asp Glu
290 295 300

Leu Ile Ser Val Lys Gln Tyr Ser Val Ser Tyr Leu Lys Glu Ile Asp
305 310 315 320

Lys

<210> 76
<211> 1425
<212> DNA
<213> Escherichia coli

<400> 76
atgagtcgtt tagtcgtagt atctaaccgg attgcaccac cagacgagca cgccgccagt 60

gccggtggcc ttgccgttgg catactgggg gcactgaaag ccgcaggcgg actgtggttt 120

ggctggagtg gtgaaacagg gaatgaggat cagccgctaa aaaaggtgaa aaaaggtaac 180

attacgtggg cctcttttaa cctcagcgaa caggaccttg acgaatacta caaccaattc 240

tccaatgccg ttctctggcc cgcttttcat tatcggctcg atctggtgca atttcagcgt 300

cctgcctggg acggctatct acgcgtaaat gcgttgctgg cagataaatt actgccgctg 360

ttgcaagacg atgacattat ctggatccac gattatcacc tgttgccatt tgcgcatgaa 420

ttacgcaaac ggggagtgaa taatcgcatt ggtttctttc tgcatattcc tttcccgaca 480

ccggaaatct tcaacgcgct gccgacatat gacaccttgc ttgaacagct ttgtgattat 540

gatttgctgg gtttccagac agaaaacgat cgtctggcgt tcctggattg tctttctaac 600

ctgacccgcg tcacgacacg tagcgcaaaa agccatacag cctggggcaa agcatttcga 660

acagaagtct acccgatcgg cattgaaccg aaagaaatag ccaaacaggc tgccgggcca 720

ctgccgccaa aactggcgca acttaaagcg gaactgaaaa acgtacaaaa tatcttttct 780

gtcgaacggc tggattattc caaaggtttg ccagagcgtt ttctcgccta tgaagcgttg 840

ctggaaaaat atccgcagca tcatggtaaa attcgttata cccagattgc accaacgtcg 900

cgtggtgatg tgcaagccta tcaggatatt cgtcatcagc tcgaaaatga agctggacga 960

attaatggta aatacgggca attaggctgg acgccgcttt attatttgaa tcagcatttt 1020

gaccgtaaat tactgatgaa aatattccgc tactctgacg tgggcttagt gacgccactg 1080

cgtgacggga tgaacctggt agcaaaagag tatgttgctg ctcaggaccc agccaatccg 1140

ggcgttcttg ttctttcgca atttgcggga gcggcaaacg agttaacgtc ggcgttaatt 1200

gttaacccct acgatcgtga cgaagttgca gctgcgctgg atcgtgcatt gactatgtcg 1260

ctggcggaac gtatttcccg tcatgcagaa atgctggacg ttatcgtgaa aaacgatatt 1320

aaccactggc aggagtgctt cattagcgac ctaaagcaga tagttccgcg aagcgcggaa 1380

agccagcagc gcgataaagt tgctaccttt ccaaagcttg cgtag 1425

<210> 77
<211> 474
<212> PRT
<213> Escherichia coli

<400> 77

Met Ser Arg Leu Val Val Val Ser Asn Arg Ile Ala Pro Pro Asp Glu
1 5 10 15

His Ala Ala Ser Ala Gly Gly Leu Ala Val Gly Ile Leu Gly Ala Leu
20 25 30

Lys Ala Ala Gly Gly Leu Trp Phe Gly Trp Ser Gly Glu Thr Gly Asn
35 40 45

Glu Asp Gln Pro Leu Lys Lys Val Lys Lys Gly Asn Ile Thr Trp Ala
50 55 60

Ser Phe Asn Leu Ser Glu Gln Asp Leu Asp Glu Tyr Tyr Asn Gln Phe
65 70 75 80

Ser Asn Ala Val Leu Trp Pro Ala Phe His Tyr Arg Leu Asp Leu Val
85 90 95

Gln Phe Gln Arg Pro Ala Trp Asp Gly Tyr Leu Arg Val Asn Ala Leu
100 105 110

Leu Ala Asp Lys Leu Leu Pro Leu Leu Gln Asp Asp Asp Ile Ile Trp
115 120 125

Ile His Asp Tyr His Leu Leu Pro Phe Ala His Glu Leu Arg Lys Arg
130 135 140

Gly Val Asn Asn Arg Ile Gly Phe Phe Leu His Ile Pro Phe Pro Thr
145 150 155 160

Pro Glu Ile Phe Asn Ala Leu Pro Thr Tyr Asp Thr Leu Leu Glu Gln
165 170 175

Leu Cys Asp Tyr Asp Leu Leu Gly Phe Gln Thr Glu Asn Asp Arg Leu

```
            180                 185                 190

Ala Phe Leu Asp Cys Leu Ser Asn Leu Thr Arg Val Thr Thr Arg Ser
        195                 200                 205

Ala Lys Ser His Thr Ala Trp Gly Lys Ala Phe Arg Thr Glu Val Tyr
    210                 215                 220

Pro Ile Gly Ile Glu Pro Lys Glu Ile Ala Lys Gln Ala Ala Gly Pro
225                 230                 235                 240

Leu Pro Pro Lys Leu Ala Gln Leu Lys Ala Glu Leu Lys Asn Val Gln
                245                 250                 255

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

Arg Phe Leu Ala Tyr Glu Ala Leu Leu Glu Lys Tyr Pro Gln His His
        275                 280                 285

Gly Lys Ile Arg Tyr Thr Gln Ile Ala Pro Thr Ser Arg Gly Asp Val
    290                 295                 300

Gln Ala Tyr Gln Asp Ile Arg His Gln Leu Glu Asn Glu Ala Gly Arg
305                 310                 315                 320

Ile Asn Gly Lys Tyr Gly Gln Leu Gly Trp Thr Pro Leu Tyr Tyr Leu
                325                 330                 335

Asn Gln His Phe Asp Arg Lys Leu Leu Met Lys Ile Phe Arg Tyr Ser
            340                 345                 350

Asp Val Gly Leu Val Thr Pro Leu Arg Asp Gly Met Asn Leu Val Ala
        355                 360                 365

Lys Glu Tyr Val Ala Ala Gln Asp Pro Ala Asn Pro Gly Val Leu Val
    370                 375                 380

Leu Ser Gln Phe Ala Gly Ala Ala Asn Glu Leu Thr Ser Ala Leu Ile
385                 390                 395                 400

Val Asn Pro Tyr Asp Arg Asp Glu Val Ala Ala Ala Leu Asp Arg Ala
                405                 410                 415

Leu Thr Met Ser Leu Ala Glu Arg Ile Ser Arg His Ala Glu Met Leu
            420                 425                 430

Asp Val Ile Val Lys Asn Asp Ile Asn His Trp Gln Glu Cys Phe Ile
        435                 440                 445

Ser Asp Leu Lys Gln Ile Val Pro Arg Ser Ala Glu Ser Gln Gln Arg
    450                 455                 460
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```
Asp Lys Val Ala Thr Phe Pro Lys Leu Ala
465                 470
```

<210> 78
<211> 746
<212> DNA
<213> Escherichia coli

<400> 78

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acaatattct gcaaggacta cagctactgg caaccgcaag tgatggtgca ttggcattga      120

tatcagggcg ctcaatggtg gagcttgacg cactggcaaa accttatcgc ttcccgttag      180

cgggcgtgca tggggcggag cgccgtgaca tcaatggtaa aacacatatc gttcatctgc      240

cggatgcgat tgcgcgtgat attagcgtgc aactgcatac agtcatcgct cagtatcccg      300

gcgcggagct ggaggcgaaa gggatggctt ttgcgctgca ttatcgtcag gctccgcagc      360

atgaagacgc attaatgaca ttagcgcaac gtattactca gatctggcca caaatggcgt      420

tacagcaggg aaagtgtgtt gtcgagatca aaccgagagg taccagtaaa ggtgaggcaa      480

ttgcagcttt tatgcaggaa gctcccttta tcgggcgaac gcccgtattt ctgggcgatg      540

atttaaccga tgaatctggc ttcgcagtcg ttaaccgact gggcggaatg tcagtaaaaa      600

ttggcacagg tgcaactcag gcatcatggc gactggcggg tgtgccggat gtctggagct      660

ggcttgaaat gataaccacc gcattacaac aaaaaagaga aaataacagg agtgatgact      720

atgagtcgtt tagtcgtagt atctaa                                           746
```

<210> 79
<211> 266
<212> PRT
<213> Escherichia coli

<400> 79

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Met Thr Glu Pro Leu Thr Glu Thr Pro Glu Leu Ser Ala Lys Tyr Ala
1               5                  10                  15

Trp Phe Phe Asp Leu Asp Gly Thr Leu Ala Glu Ile Lys Pro His Pro
            20                  25                  30

Asp Gln Val Val Val Pro Asp Asn Ile Leu Gln Gly Leu Gln Leu Leu
        35                  40                  45

Ala Thr Ala Ser Asp Gly Ala Leu Ala Leu Ile Ser Gly Arg Ser Met
    50                  55                  60

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

Val His Gly Ala Glu Arg Arg Asp Ile Asn Gly Lys Thr His Ile Val
                85                  90                  95
```

```
His Leu Pro Asp Ala Ile Ala Arg Asp Ile Ser Val Gln Leu His Thr
            100                 105                 110

Val Ile Ala Gln Tyr Pro Gly Ala Glu Leu Glu Ala Lys Gly Met Ala
        115                 120                 125

Phe Ala Leu His Tyr Arg Gln Ala Pro Gln His Glu Asp Ala Leu Met
    130                 135                 140

Thr Leu Ala Gln Arg Ile Thr Gln Ile Trp Pro Gln Met Ala Leu Gln
145                 150                 155                 160

Gln Gly Lys Cys Val Val Glu Ile Lys Pro Arg Gly Thr Ser Lys Gly
                165                 170                 175

Glu Ala Ile Ala Ala Phe Met Gln Glu Ala Pro Phe Ile Gly Arg Thr
            180                 185                 190

Pro Val Phe Leu Gly Asp Asp Leu Thr Asp Glu Ser Gly Phe Ala Val
        195                 200                 205

Val Asn Arg Leu Gly Gly Met Ser Val Lys Ile Gly Thr Gly Ala Thr
    210                 215                 220

Gln Ala Ser Trp Arg Leu Ala Gly Val Pro Asp Val Trp Ser Trp Leu
225                 230                 235                 240

Glu Met Ile Thr Thr Ala Leu Gln Gln Lys Arg Glu Asn Asn Arg Ser
                245                 250                 255

Asp Asp Tyr Glu Ser Phe Ser Arg Ser Ile
            260                 265
```

<210> 80
<211> 1500
<212> DNA
<213> Synechocystis PCC6803

<400> 80

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ggcaaaacgg tgtatcgaga gaaaaagagt cccaacggga ttttgcccac cctcaaaagt      120

ttttttgccg atgcggaaca gagcacctgg gtcgcatgga aacaggtttc gccgaagcaa      180

aaggatgatt ttcaggcgga tatgtccatt gaaggccttg gcgatcgttg tacggtgcgc      240

cgggtgcccc tgacggcgga gcaggtaaaa aacttctatc acatcacttc caaggaagcc      300

ttttggccca ttctccactc tttcccctgg cagttcacct acgattcttc tgattgggat      360

aattttcagc acattaaccg cttatttgcc gaggcggcct gtgccgatgc cgatgacaat      420

gcattgtttt gggtccacga ctataacctc tggttagcgc ccctttacat tcgtcagctc      480

aagcccaacg ccaagattgc ctttttccac cacacccccc tccccagcgt tgatattttc      540
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aatattttgc cctggcggga ggcgatcgta gaaagcttgc tggcctgtga tctctgtggt 600

tttcatattc cccgctacgt agaaaatttt gtcgccgtgg cccgtagtct caagccggtg 660

gaaatcacca gacgggttgt ggtagaccaa gcctttaccc cctacggtac ggccctggcg 720

gaaccggaac tcaccaccca gttgcgttat ggcgatcgcc tcattaacct cgatgcgttt 780

cccgtgggca ccaatccggc aaatatccgg gcgatcgtgg ccaaagaaag tgtgcaacaa 840

aaagttgctg aaattaaaca agatttaggc ggtaagaggc taattgtttc cgctgggcgg 900

gtggattacg tgaagggcac caaggaaatg ttgatgtgct atgaacgtct actggagcgt 960

cgccccgaat tgcaggggga aattagcctg gtagtccccg tagccaaggc cgctgaggga 1020

atgcgtattt atcgcaacgc ccaaaacgaa attgaacgac tggcagggaa aattaacggt 1080

cgctttgcca aactgtcctg gacaccagtg atgctgttca cctctccttt agcctatgag 1140

gagctcattg ccctgttctg tgccgccgac attgcctgga tcactcccct gcgggatggg 1200

ctaaacctgg tggctaagga gtatgtggtg gctaaaaatg gcgaagaagg agttctgatc 1260

ctctcggaat ttgccggttg tgcggtggaa ctacccgatg cggtgttgac taacccctac 1320

gcttccagcc gtatggacga atccattgac caggccctgg ccatggacaa agacgaacag 1380

aaaaaacgca tggggagaat gtacgccgcc attaagcgtt acgacgttca acaatgggcc 1440

aatcacctac tgcgggaagc ctacgccgat gtggtactgg gagagccccc ccaaatgtag 1500

<210> 81
<211> 499
<212> PRT
<213> Synechocystis PCC6803

<400> 81

Met Asn Ser Ser Leu Val Ile Leu Tyr His Arg Glu Pro Tyr Asp Glu
1 5 10 15

Val Arg Glu Asn Gly Lys Thr Val Tyr Arg Glu Lys Lys Ser Pro Asn
20 25 30

Gly Ile Leu Pro Thr Leu Lys Ser Phe Phe Ala Asp Ala Glu Gln Ser
35 40 45

Thr Trp Val Ala Trp Lys Gln Val Ser Pro Lys Gln Lys Asp Asp Phe
50 55 60

Gln Ala Asp Met Ser Ile Glu Gly Leu Gly Asp Arg Cys Thr Val Arg
65 70 75 80

Arg Val Pro Leu Thr Ala Glu Gln Val Lys Asn Phe Tyr His Ile Thr
85 90 95

Ser Lys Glu Ala Phe Trp Pro Ile Leu His Ser Phe Pro Trp Gln Phe
100 105 110

Thr Tyr Asp Ser Ser Asp Trp Asp Asn Phe Gln His Ile Asn Arg Leu

```
        115                 120                 125

Phe Ala Glu Ala Ala Cys Ala Asp Ala Asp Asp Asn Ala Leu Phe Trp
    130                 135                 140

Val His Asp Tyr Asn Leu Trp Leu Ala Pro Leu Tyr Ile Arg Gln Leu
145                 150                 155                 160

Lys Pro Asn Ala Lys Ile Ala Phe Phe His His Thr Pro Phe Pro Ser
                165                 170                 175

Val Asp Ile Phe Asn Ile Leu Pro Trp Arg Glu Ala Ile Val Glu Ser
            180                 185                 190

Leu Leu Ala Cys Asp Leu Cys Gly Phe His Ile Pro Arg Tyr Val Glu
        195                 200                 205

Asn Phe Val Ala Val Ala Arg Ser Leu Lys Pro Val Glu Ile Thr Arg
    210                 215                 220

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

Glu Pro Glu Leu Thr Thr Gln Leu Arg Tyr Gly Asp Arg Leu Ile Asn
                245                 250                 255

Leu Asp Ala Phe Pro Val Gly Thr Asn Pro Ala Asn Ile Arg Ala Ile
            260                 265                 270

Val Ala Lys Glu Ser Val Gln Gln Lys Val Ala Glu Ile Lys Gln Asp
        275                 280                 285

Leu Gly Gly Lys Arg Leu Ile Val Ser Ala Gly Arg Val Asp Tyr Val
    290                 295                 300

Lys Gly Thr Lys Glu Met Leu Met Cys Tyr Glu Arg Leu Leu Glu Arg
305                 310                 315                 320

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

Ala Ala Glu Gly Met Arg Ile Tyr Arg Asn Ala Gln Asn Glu Ile Glu
            340                 345                 350

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

Pro Val Met Leu Phe Thr Ser Pro Leu Ala Tyr Glu Glu Leu Ile Ala
    370                 375                 380

Leu Phe Cys Ala Ala Asp Ile Ala Trp Ile Thr Pro Leu Arg Asp Gly
385                 390                 395                 400
```

Leu Asn Leu Val Ala Lys Glu Tyr Val Val Ala Lys Asn Gly Glu Glu
405 410 415

Gly Val Leu Ile Leu Ser Glu Phe Ala Gly Cys Ala Val Glu Leu Pro
420 425 430

Asp Ala Val Leu Thr Asn Pro Tyr Ala Ser Ser Arg Met Asp Glu Ser
435 440 445

Ile Asp Gln Ala Leu Ala Met Asp Lys Asp Glu Gln Lys Lys Arg Met
450 455 460

Gly Arg Met Tyr Ala Ala Ile Lys Arg Tyr Asp Val Gln Gln Trp Ala
465 470 475 480

Asn His Leu Leu Arg Glu Ala Tyr Ala Asp Val Val Leu Gly Glu Pro
485 490 495

Pro Gln Met

<210> 82
<211> 1269
<212> DNA
<213> Synechocystis PCC6803

<400> 82
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caaactgaaa atttactcat tgtccaagac ttggatgggg tctgcatgga attagtgcaa 120

gatcccctca gtcgccgcct ggatgccgat tatgtccggg ccaccaccct gtttgctgaa 180

catttttacg tgttgaccaa tggggagcac gtgggaaaaa gaggagtaca gggcattgtg 240

gaacaatcct ttggggatgc ttcctttgtg caacaggaag gcctatattt gcccggtttg 300

gcggccgggg gagtgcagtg gcaggatcgc catggcaaag taagtcatcc tggagtgggg 360

caaacggagc tggagttttt agcggcggtg cccgaaaaaa tcactaattg tttaaaaacc 420

ttttttggcg atcgccccca ttccctatcc ccagagcaat tacaaacggg cattgaagct 480

tcggttttag ataatgtggc ttcccccacc gccaatttaa ataccttggc caatctgtta 540

caagactttc cgcaaattta ccgagatttg caggaaacca tggctcaatt attggatcag 600

ttgatggcgg aagccgttgc ccagggtttg gggaatagtt tttttgtcca ctatgctccc 660

aatttaggta gggatgaacg aggtaaggaa attattcgtt gggccaaagc tggggattcc 720

ggcaccaccg attttcaatt tatgttgcgg ggtggggtca aagaagccgg ggttttggct 780

ttgctaaatc gttactatca caatcggaca gggcaatatc ctctgggaga aagttttagt 840

gctcgccaag cgcccccatc ccaccaggac ttgttgcatt tggtgaaagc gcaatttgat 900

ccggccttga tgccgctgat cattggagtt ggggatacgg tcaccagtca ggtggatgaa 960

gctaccgggg aaattcgacg tggcgggagc gatcgccaat ttttgcaatt aatccaagat 1020

ttgggggatt ggggaaatca cggtaactta gtggtgtatg tggacagttc ccaggggggag 1080

gtgaaaaatc gccaacctct acaactagaa accgtggcgg ggcaaaccca agtggtggct 1140

ggccctgggg atatgcggga cagggaagag ccattgaaga tcaatgtggc ttttcctggt 1200

ggccatgacc aatatgtagc ggcgtttaag caggcggccc agcgccgaag agtccatttt 1260

tcccagtag 1269

<210> 83
<211> 422
<212> PRT
<213> Synechocystis PCC6803

<400> 83

Met Val Leu His Gln Gln Arg Phe Ser Leu Asp His Gly Ala Phe Cys
1 5 10 15

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

Gly Val Cys Met Glu Leu Val Gln Asp Pro Leu Ser Arg Arg Leu Asp
35 40 45

Ala Asp Tyr Val Arg Ala Thr Thr Leu Phe Ala Glu His Phe Tyr Val
50 55 60

Leu Thr Asn Gly Glu His Val Gly Lys Arg Gly Val Gln Gly Ile Val
65 70 75 80

Glu Gln Ser Phe Gly Asp Ala Ser Phe Val Gln Gln Glu Gly Leu Tyr
85 90 95

Leu Pro Gly Leu Ala Ala Gly Gly Val Gln Trp Gln Asp Arg His Gly
100 105 110

Lys Val Ser His Pro Gly Val Gly Gln Thr Glu Leu Glu Phe Leu Ala
115 120 125

Ala Val Pro Glu Lys Ile Thr Asn Cys Leu Lys Thr Phe Phe Gly Asp
130 135 140

Arg Pro His Ser Leu Ser Pro Glu Gln Leu Gln Thr Gly Ile Glu Ala
145 150 155 160

Ser Val Leu Asp Asn Val Ala Ser Pro Thr Ala Asn Leu Asn Thr Leu
165 170 175

Ala Asn Leu Leu Gln Asp Phe Pro Gln Ile Tyr Arg Asp Leu Gln Glu
180 185 190

Thr Met Ala Gln Leu Leu Asp Gln Leu Met Ala Glu Ala Val Ala Gln
195 200 205

```
Gly Leu Gly Asn Ser Phe Phe Val His Tyr Ala Pro Asn Leu Gly Arg
    210                 215                 220

Asp Glu Arg Gly Lys Glu Ile Ile Arg Trp Ala Lys Ala Gly Asp Ser
225                 230                 235                 240

Gly Thr Thr Asp Phe Gln Phe Met Leu Arg Gly Gly Val Lys Glu Ala
                245                 250                 255

Gly Val Leu Ala Leu Leu Asn Arg Tyr Tyr His Asn Arg Thr Gly Gln
            260                 265                 270

Tyr Pro Leu Gly Glu Ser Phe Ser Ala Arg Gln Ala Pro Pro Ser His
        275                 280                 285

Gln Asp Leu Leu His Leu Val Lys Ala Gln Phe Asp Pro Ala Leu Met
    290                 295                 300

Pro Leu Ile Ile Gly Val Gly Asp Thr Val Thr Ser Gln Val Asp Glu
305                 310                 315                 320

Ala Thr Gly Glu Ile Arg Arg Gly Gly Ser Asp Arg Gln Phe Leu Gln
                325                 330                 335

Leu Ile Gln Asp Leu Gly Asp Trp Gly Asn His Gly Asn Leu Val Val
            340                 345                 350

Tyr Val Asp Ser Ser Gln Gly Glu Val Lys Asn Arg Gln Pro Leu Gln
        355                 360                 365

Leu Glu Thr Val Ala Gly Gln Thr Gln Val Val Ala Gly Pro Gly Asp
    370                 375                 380

Met Arg Asp Arg Glu Glu Pro Leu Lys Ile Asn Val Ala Phe Pro Gly
385                 390                 395                 400

Gly His Asp Gln Tyr Val Ala Ala Phe Lys Gln Ala Ala Gln Arg Arg
                405                 410                 415

Arg Val His Phe Ser Gln
            420
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<210> 84
<211> 1365
<212> DNA
<213> Agrobacterium tumefaciens

<400> 84
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gataccgggg ggcaggtggt ttatgtgctt gagcttgcac gaaaactcgg ccaactcggt 180

tataccgtcg atctttacac ccgacgcttc gaagaccagc cggaattcga cgaggtcgat 240

gagcgcgtcc gtgtggtgcg cattccctgc ggcgggcgcg atttcattcc caaggaatat 300

ctgcaccggc acctgatgga atggtgcgag aacgcgctac gcttcatcaa aaaaaacgac 360

ctcaattact ccttcatcaa cagccactac tgggatgccg gcgtggccgg gcagcggctc 420

tccgaagcac tgaaaatccc ccatctgcac acgccgcact cgctcggcat ctggaagaag 480

cgccagatgg agaccgatta tccggaaaag gccgatacgt tcgagcttga gttcaacttc 540

aaggagcgca tccagcacga gctgatcatc tatcgcagct gcgacatggt gatcgccacc 600

acgccggtgc agctggacgt gctgatcgaa gattatggcc tgaagcgcaa acatatccac 660

atgatcccgc cgggttatga cgacaaccgc ttcttccccg tctcggatgc gacgcgtcag 720

atgatccggc agcgtttcgg ttttgaaggc aaagtggtgc tggcactcgg tcggctcgcc 780

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<212> PRT
<213> Agrobacterium tumefaciens

<400> 85

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Ala His Pro Pro Leu Gly Ala Ala Asp Thr Gly Gly Gln Val Val Tyr
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Val Leu Glu Leu Ala Arg Lys Leu Gly Gln Leu Gly Tyr Thr Val Asp
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Leu Tyr Thr Arg Arg Phe Glu Asp Gln Pro Glu Phe Asp Glu Val Asp
65 70 75 80

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Glu Arg Val Arg Val Val Arg Ile Pro Cys Gly Gly Arg Asp Phe Ile
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Pro Lys Glu Tyr Leu His Arg His Leu Met Glu Trp Cys Glu Asn Ala
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Leu Arg Phe Ile Lys Lys Asn Asp Leu Asn Tyr Ser Phe Ile Asn Ser
        115                 120                 125

His Tyr Trp Asp Ala Gly Val Ala Gly Gln Arg Leu Ser Glu Ala Leu
    130                 135                 140

Lys Ile Pro His Leu His Thr Pro His Ser Leu Gly Ile Trp Lys Lys
145                 150                 155                 160

Arg Gln Met Glu Thr Asp Tyr Pro Glu Lys Ala Asp Thr Phe Glu Leu
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Glu Phe Asn Phe Lys Glu Arg Ile Gln His Glu Leu Ile Ile Tyr Arg
            180                 185                 190

Ser Cys Asp Met Val Ile Ala Thr Thr Pro Val Gln Leu Asp Val Leu
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Ile Glu Asp Tyr Gly Leu Lys Arg Lys His Ile His Met Ile Pro Pro
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Gly Tyr Asp Asp Asn Arg Phe Phe Pro Val Ser Asp Ala Thr Arg Gln
225                 230                 235                 240

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

Gly Arg Leu Ala Thr Asn Lys Gly Tyr Asp Leu Leu Ile Asp Gly Phe
            260                 265                 270

Ser Val Leu Ala Glu Arg Glu Pro Glu Ala Arg Leu His Leu Ala Val
        275                 280                 285

Gly Gly Glu Asn Met Asp Glu Gln Glu Thr Thr Ile Leu Asn Gln Leu
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Lys Glu Arg Val Lys Ser Leu Gly Leu Glu Asp Lys Val Ala Phe Ser
305                 310                 315                 320

Gly Tyr Val Ala Asp Glu Asp Leu Pro Asp Ile Tyr Arg Ala Ala Asp
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Leu Phe Val Leu Ser Ser Arg Tyr Glu Pro Phe Gly Met Thr Ala Ile
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Glu Ala Met Ala Ser Gly Thr Pro Thr Val Val Thr Ile His Gly Gly
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Leu Phe Arg Ala Ile Ser Tyr Gly Arg His Ala Leu Phe Ala Asp Pro
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Phe Asp Lys Glu Asp Leu Gly Ile Thr Met Met Lys Pro Phe Lys His
385                 390                 395                 400

Glu Arg Leu Tyr Gly Arg Leu Ser Arg Met Gly Ala His Lys Ala Arg
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Ser Leu Phe Thr Trp Thr Gly Ile Ala Gln Gln Leu Leu Ala Leu Val
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<400> 87

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Pro Asp Asp Leu Arg Pro Val Leu Val Phe Asn Ser Gly Arg Leu Ile
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Asp Asp Gln Leu Ala Leu Leu Glu Glu Val Pro Leu Pro Gln Pro Asp
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Tyr Ile Ile Gly Gly Val Gly Thr Met Leu His Ala Lys Lys Arg Ser
65 70 75 80

Glu Leu Glu Thr Ala Tyr Thr Gln Ser Leu Gly Thr Gly Phe Asp Pro
85 90 95

Arg Lys Ile Ala Asp Val Met Asn Arg Ile Ala Gly Val Thr Met Gln
100 105 110

Glu Glu Arg Tyr Gln His Gly Leu Lys Ser Ser Trp Phe Leu His Asp
115 120 125

Ala Asp Ala Ala Ala Leu Gly Glu Ile Glu Ala Ala Leu Leu Ala Ala
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Asp Ile Asp Ala Arg Ile Val Tyr Ser Ser Asp Arg Asp Leu Asp Ile
145 150 155 160

Leu Pro Lys Ala Ala Asp Lys Gly Ala Ala Leu Ala Trp Leu Cys Gly
165 170 175

Gln Leu Arg Ile Gly Leu Asp Glu Ser Val Val Ser Gly Asp Thr Gly
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Asn Asp Arg Ala Met Phe Glu Leu Lys Thr Ile Arg Gly Val Ile Val
195 200 205

Gly Asn Ala Leu Pro Glu Leu Val Ser Leu Ala His Gln Asp Asn Arg
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Arg His Trp Gly Leu Asn Pro Arg
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Arg Tyr Trp Leu Pro Thr Val Asp Thr Glu Val Lys Thr Pro Leu Ala
50 55 60

Ile Ala Lys Ala Ser Leu Ile Asp Pro Gln Thr Pro Phe Val Ile Val
65 70 75 80

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Thr Leu Glu Pro Ser Leu Tyr Leu Asn Lys Leu Pro Glu Arg Phe Ala
        115                 120                 125

Pro Gly Thr His Leu Leu Leu Leu Asp Pro Met Leu Ala Thr Gly Asn
    130                 135                 140

Thr Ile Met Ala Ala Leu Asp Leu Leu Met Ala Arg Asp Ile Asp Ala
145                 150                 155                 160

Asn Leu Ile Arg Leu Val Ser Val Val Ala Ala Pro Thr Ala Leu Gln
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Lys Leu Ser Asn Ala His Pro Asn Leu Thr Ile Tyr Thr Ala Met Ile
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Asp Glu Gln Leu Asn Asp Arg Gly Tyr Ile Val Pro Gly Leu Gly Asp
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Ala Gly Asp Arg Cys Phe Gly Thr
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<400> 114

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Arg Glu Trp Leu Pro Thr Ile Pro Ala Ala Val Gln Thr Pro Leu Ala
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Glu Thr Pro Ala Glu Phe Val Asp Phe Ser Gln Pro Leu Ala Ile Val
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Pro Ile Leu Arg Ala Gly Leu Gly Leu Val Glu Ser Val Gln Gln Val
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Leu Pro Thr Ala Arg Ile Phe His Val Gly Leu Lys Arg Asp Glu Val
100 105 110

Ser Leu Glu Pro Arg Cys Tyr Leu Asn His Leu Pro Glu Gln Leu Glu
115 120 125

Val Asn Ser Arg Val Leu Val Leu Asp Pro Met Leu Ala Thr Gly Gly
130 135 140

Ser Leu Leu Tyr Thr Leu Asp Leu Leu Arg Asp Arg Gly Val Ser Ala
145 150 155 160

Glu Gln Val Arg Val Leu Ser Ile Val Ala Ala Pro Pro Ala Leu Gln
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Lys Leu Ser Gln Ala Tyr Pro Ala Leu Thr Ile Tyr Ser Ala Ile Ile
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Ala Gly Asp Arg Leu Phe Gly Thr Pro
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<223> AflI restriction site

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305                 310                 315                 320

Pro Gln Gln Leu Asn Thr Leu Arg Thr Thr Ser Ile Val Pro Val Asp
                325                 330                 335

Leu Asn Ser Leu Met Phe Lys Met Glu Lys Ile Leu Ala Arg Ala Ser
            340                 345                 350

Lys Ala Ala Gly Asp Asn Ala Met Ala Asn Gln Tyr Glu Thr Leu Ala
        355                 360                 365

Asn Ala Arg Gln Lys Gly Ile Glu Lys Tyr Leu Trp Asn Asp Gln Gln
    370                 375                 380

Gly Trp Tyr Ala Asp Tyr Asp Leu Lys Ser His Lys Val Arg Asn Gln
385                 390                 395                 400

Leu Thr Ala Ala Ala Leu Phe Pro Leu Tyr Val Asn Ala Ala Ala Lys
                405                 410                 415

Asp Arg Ala Asn Lys Met Ala Thr Ala Thr Lys Thr His Leu Leu Gln
            420                 425                 430

Pro Gly Gly Leu Asn Thr Thr Ser Val Lys Ser Gly Gln Gln Trp Asp
        435                 440                 445

Ala Pro Asn Gly Trp Ala Pro Leu Gln Trp Val Ala Thr Glu Gly Leu
    450                 455                 460

Gln Asn Tyr Gly Gln Lys Glu Val Ala Met Asp Ile Ser Trp His Phe
465                 470                 475                 480

Leu Thr Asn Val Gln His Thr Tyr Asp Arg Glu Lys Lys Leu Val Glu
                485                 490                 495

Lys Tyr Asp Val Ser Thr Thr Gly Thr Gly Gly Gly Gly Gly Glu Tyr
            500                 505                 510

Pro Leu Gln Asp Gly Phe Gly Trp Thr Asn Gly Val Thr Leu Lys Met
        515                 520                 525

Leu Asp Leu Ile Cys Pro Lys Glu Gln Pro Cys Asp Asn Val Pro Ala
    530                 535                 540

Thr Arg Pro Thr Val Lys Ser Ala Thr Thr Gln Pro Ser Thr Lys Glu
545                 550                 555                 560

Ala Gln Pro Thr Pro
                565
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<210> 136
<211> 1738
<212> DNA
<213> Artificial Sequence

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<223> AflII restriction site

<220>
<221> misc_feature
<222> (1727)..(1732)
<223> XbaI restriction site

<400> 136
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aaaaatggcg ttaattccag cctgtatctt tttgtgtttc gctgcgctat cggtgcaggc 120

agaagaaaca ccggtaacac cacagccgcc tgatatttta ttagggccgc tgtttaatga 180

tgtgcaaaac gccaaacttt ttccggacca aaaaaccttt gccgatgccg tgccgaacag 240

cgatccgctg atgatccttg ctgattatcg gatgcagcaa aaccagagcg gatttgatct 300

gcgccatttc gttaacgtca atttcaccct gccgaaagaa ggcgagaaat atgttccgcc 360

agaggggcag tcactgcgcg aacatattga cggactttgg ccggtattaa cgcgttctac 420

cgaaaacacc gaaaaatggg attctctgtt accgctgccg gaaccttatg tcgtgccggg 480

cggacgcttt cgcgaggtat attactggga cagttacttc accatgttag gacttgccga 540

aagcggtcac tgggataaag tcgcggatat ggtggccaat tttgctcatg aaatagacac 600

ttacggtcat attcccaacg gcaaccgcag ttactattta agccgctcgc aaccgccctt 660

ctttgccctg atggtagagt tactggcgca gcatgaaggc gatgccgcgt tgaagcaata 720

cctgccgcaa atgcaaaaag aatatgctta ctggatggac ggtgttgaaa acctgcaagc 780

cggacaacag gaaaaacgcg ttgtcaaact tcaggatggt acccttctca accgctactg 840

ggacgatcgc gatacgccac gaccagagtc atgggtggaa gatattgcca ccgccaaaag 900

caatccgaat cgacctgcca ctgaaattta ccgcgacctg cgctctgccg ctgcgtctgg 960

ctgggatttc agctcgcgct ggatggacaa cccgcagcag ttaaatacct tacgcaccac 1020

cagcatcgta ccggtcgatc tgaacagcct gatgtttaaa atggaaaaaa tcctcgcccg 1080

cgccagcaaa gctgccggag ataacgcgat ggcaaaccag tacgaaacgc tggcaaatgc 1140

ccgtcaaaaa gggatcgaaa aatacctgtg gaacgatcaa caaggctggt atgccgatta 1200

cgacctgaaa agtcataaag tgcgcaatca gttaaccgcg gccgccctgt tcccgctgta 1260

cgtcaatgcg gcagcgaaag atcgcgccaa caaaatggcg acggcgacga aaacacatct 1320

gctgcaaccc ggcggcctga acaccacgtc ggtgaaaagt gggcaacaat gggatgcgcc 1380

aaatggctgg gcaccgttac agtgggtcgc gacagaagga ttacaaaact acgggcaaaa 1440

agaggtggcg atggacatta gctggcactt cctgaccaat gttcagcaca cctatgaccg 1500

ggagaaaaag ctggtggaaa aatatgatgt cagcaccacc ggaacggggg gcggcggtgg 1560

cgaatatcca ttacaggatg gctttggctg gaccaatggc gtgacgctga aaatgctgga 1620

tttgatctgc ccgaaagagc aaccgtgtga caatgttccg gcgacgcgtc cgaccgttaa 1680

gtcagcaacg acgcaaccct caaccaaaga ggcacaaccc acaccttcta gagcgctt 1738

<210> 137
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> treA with 6-His tag

<400> 137

Met Lys Ser Pro Ala Pro Ser Arg Pro Gln Lys Met Ala Leu Ile Pro
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Ala Cys Ile Phe Leu Cys Phe Ala Ala Leu Ser Val Gln Ala Glu Glu
20 25 30

Thr Pro Val Thr Pro Gln Pro Pro Asp Ile Leu Leu Gly Pro Leu Phe
35 40 45

Asn Asp Val Gln Asn Ala Lys Leu Phe Pro Asp Gln Lys Thr Phe Ala
50 55 60

Asp Ala Val Pro Asn Ser Asp Pro Leu Met Ile Leu Ala Asp Tyr Arg
65 70 75 80

Met Gln Gln Asn Gln Ser Gly Phe Asp Leu Arg His Phe Val Asn Val
85 90 95

Asn Phe Thr Leu Pro Lys Glu Gly Glu Lys Tyr Val Pro Pro Glu Gly
100 105 110

Gln Ser Leu Arg Glu His Ile Asp Gly Leu Trp Pro Val Leu Thr Arg
115 120 125

Ser Thr Glu Asn Thr Glu Lys Trp Asp Ser Leu Leu Pro Leu Pro Glu
130 135 140

Pro Tyr Val Val Pro Gly Gly Arg Phe Arg Glu Val Tyr Tyr Trp Asp
145 150 155 160

Ser Tyr Phe Thr Met Leu Gly Leu Ala Glu Ser Gly His Trp Asp Lys
165 170 175

Val Ala Asp Met Val Ala Asn Phe Ala His Glu Ile Asp Thr Tyr Gly
180 185 190

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His Ile Pro Asn Gly Asn Arg Ser Tyr Tyr Leu Ser Arg Ser Gln Pro
        195                 200                 205

Pro Phe Phe Ala Leu Met Val Glu Leu Leu Ala Gln His Glu Gly Asp
    210                 215                 220

Ala Ala Leu Lys Gln Tyr Leu Pro Gln Met Gln Lys Glu Tyr Ala Tyr
225                 230                 235                 240

Trp Met Asp Gly Val Glu Asn Leu Gln Ala Gly Gln Gln Glu Lys Arg
                245                 250                 255

Val Val Lys Leu Gln Asp Gly Thr Leu Leu Asn Arg Tyr Trp Asp Asp
            260                 265                 270

Arg Asp Thr Pro Arg Pro Glu Ser Trp Val Glu Asp Ile Ala Thr Ala
        275                 280                 285

Lys Ser Asn Pro Asn Arg Pro Ala Thr Glu Ile Tyr Arg Asp Leu Arg
    290                 295                 300

Ser Ala Ala Ala Ser Gly Trp Asp Phe Ser Ser Arg Trp Met Asp Asn
305                 310                 315                 320

Pro Gln Gln Leu Asn Thr Leu Arg Thr Thr Ser Ile Val Pro Val Asp
                325                 330                 335

Leu Asn Ser Leu Met Phe Lys Met Glu Lys Ile Leu Ala Arg Ala Ser
            340                 345                 350

Lys Ala Ala Gly Asp Asn Ala Met Ala Asn Gln Tyr Glu Thr Leu Ala
        355                 360                 365

Asn Ala Arg Gln Lys Gly Ile Glu Lys Tyr Leu Trp Asn Asp Gln Gln
    370                 375                 380

Gly Trp Tyr Ala Asp Tyr Asp Leu Lys Ser His Lys Val Arg Asn Gln
385                 390                 395                 400

Leu Thr Ala Ala Ala Leu Phe Pro Leu Tyr Val Asn Ala Ala Ala Lys
                405                 410                 415

Asp Arg Ala Asn Lys Met Ala Thr Ala Thr Lys Thr His Leu Leu Gln
            420                 425                 430

Pro Gly Gly Leu Asn Thr Thr Ser Val Lys Ser Gly Gln Gln Trp Asp
        435                 440                 445

Ala Pro Asn Gly Trp Ala Pro Leu Gln Trp Val Ala Thr Glu Gly Leu
    450                 455                 460
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Gln Asn Tyr Gly Gln Lys Glu Val Ala Met Asp Ile Ser Trp His Phe
465                 470                 475                 480

Leu Thr Asn Val Gln His Thr Tyr Asp Arg Glu Lys Lys Leu Val Glu
                485                 490                 495

Lys Tyr Asp Val Ser Thr Thr Gly Thr Gly Gly Gly Gly Gly Glu Tyr
            500                 505                 510

Pro Leu Gln Asp Gly Phe Gly Trp Thr Asn Gly Val Thr Leu Lys Met
        515                 520                 525

Leu Asp Leu Ile Cys Pro Lys Glu Gln Pro Cys Asp Asn Val Pro Ala
    530                 535                 540

Thr Arg Pro Thr Val Lys Ser Ala Thr Thr Gln Pro Ser Thr Lys Glu
545                 550                 555                 560

Ala Gln Pro Thr Pro Ser Arg His His His His His His
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<210> 138
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of partially deleted Synechococcus upp

<400> 138

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acaacagatc tctacttcac cccagaggat tgtgaggccg aagcgcagtt gattcctaag      120

gcgcactatt gcccaattcc ctcgatctgg ggtcaccgcg cgggcaaccc cagccaaaat      180

ccgcaggatg aaagcttcat tcggcaggcc gttcaggctt tgctcaacgc tgaagcctag      240

cgaattcagt cagcagatca aggagtacca aacaggcgat cgccagcatc ccccagcccc      300

ggcacgataa agcctttgtc gttcagctgc tcatcaatga tggcgctgta aatcgtcaac      360

gccgggtagg cttgactgag tttttgtagc gctggcgggg cagccacaat tgaaagcacc      420

cgcacttgct cagcagagac accgcgatcg cgcagcaaat caagggtata gagcagcgag      480

ccacctgtcg ccagcatcgg gtcgagaacc agaacgcgac tgttcacttc aagttgctct      540

ggcaggtgat tgaggtagca gcgcggttca agactgactt catcccgctc gcgcagaatc      600

ggcacgatcg ccaagggttg cgaaaaatcg acgaactccg ctggggtttc tgcaagagga      660

gtttgcaccg ccgctggaat cgttggtagc cattcccgca cagcctcata ggcgagccag      720

cggcccagct ctgcgatcgc ggtgcgaaac agaggcgtcg gcgtctggcg atcgcgggca      780

atgcccagcc agtgccgaat taagggatgg ggcggcacga agatacgcag ttgaggagcc      840

atgccaatca gcagaagaca gctcctgatt ttaacgttca gaccccaggg gaagcggaac      900

ggtgcaggaa ggcaagcgct tctgcttcgg gcagtggtgg gccatagaag aacccttgca      960
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cagcatcaca accaatcgct tctaagaagg cggcttgctc gaggcgttct acgccttctg 1020

cgatcgtgcg aagtttcaag accttggcca ttgcaacaat cgcctgcacg atcgcttgat 1080

cgtcatggtc gtgcggcaga tcgcgaataa agctgcgatc aattttgaga gcattgatgg 1140

gcaaacgctt gaggtaacca aggctggaat aacccgtccc aaaatcatct aaagcgactt 1200

gaaatcccat cgatcgggct tcctggagcc attgcagtgg gatcctctag agtcgacctg 1260

caggcatgc 1269

<210> 139
<211> 2686
<212> DNA
<213> Artificial Sequence

<220>
<223> pUC19

<400> 139
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cgacaggttt cccgactgga aagcgggcag tgagcgcaac gcaattaatg tgagttagct 120

cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt tgtgtggaat 180

tgtgagcgga taacaatttc acacaggaaa cagctatgac catgattacg ccaagcttgc 240

atgcctgcag gtcgactcta gaggatcccc gggtaccgag ctcgaattca ctggccgtcg 300

ttttacaacg tcgtgactgg gaaaaccctg gcgttaccca acttaatcgc cttgcagcac 360

atccccctttt cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac 420

agttgcgcag cctgaatggc gaatggcgcc tgatgcggta ttttctcctt acgcatctgt 480

gcggtatttc acaccgcata tggtgcactc tcagtacaat ctgctctgat gccgcatagt 540

taagccagcc ccgacacccg ccaacacccg ctgacgcgcc ctgacgggct tgtctgctcc 600

cggcatccgc ttacagacaa gctgtgaccg tctccgggag ctgcatgtgt cagaggtttt 660

caccgtcatc accgaaacgc gcgagacgaa agggcctcgt gatacgccta tttttatagg 720

ttaatgtcat gataataatg gtttcttaga cgtcaggtgg cacttttcgg ggaaatgtgc 780

gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg ctcatgagac 840

aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt attcaacatt 900

tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt gctcacccag 960

aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg ggttacatcg 1020

aactggatct caacagcggt aagatccttg agagttttcg ccccgaagaa cgttttccaa 1080

tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtatt gacgccgggc 1140

aagagcaact cggtcgccgc atacactatt ctcagaatga cttggttgag tactcaccag 1200

tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt gctgccataa 1260

ccatgagtga taacactgcg gccaacttac ttctgacaac gatcggagga ccgaaggagc 1320

taaccgcttt tttgcacaac atgggggatc atgtaactcg ccttgatcgt tgggaaccgg 1380

agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta gcaatggcaa 1440

caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg caacaattaa 1500

tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc cttccggctg 1560

gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggt atcattgcag 1620

cactggggcc agatggtaag ccctcccgta tcgtagttat ctacacgacg gggagtcagg 1680

caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg attaagcatt 1740

ggtaactgtc agaccaagtt tactcatata tactttagat tgatttaaaa cttcattttt 1800

aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa atcccttaac 1860

gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga tcttcttgag 1920

atccttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg ctaccagcgg 1980

tggtttgttt gccggatcaa gagctaccaa ctctttttcc gaaggtaact ggcttcagca 2040

gagcgcagat accaaatact gttcttctag tgtagccgta gttaggccac cacttcaaga 2100

actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg gctgctgcca 2160

gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg gataaggcgc 2220

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aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg agggagcttc 2400

caggggaaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc tgacttgagc 2460

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cccctgattc tgtggataac cgtattaccg cctttgagtg agctgatacc gctcgccgca 2640

gccgaacgac cgagcgcagc gagtcagtga gcgaggaagc ggaaga 2686

<210> 140
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> sll0626 (proposed invertase, aka lim17)

<400> 140
atgaaatccc cccaggctca acaaatccta gaccaggccc gccgtttgct ctacgaaaaa 60

gccatggtca aaatcaatgg gcaatacgtg gggacggtgg cggccattcc ccaatcggat 120

caccatgatt tgaactatac ggaagttttc attcgggaca atgtgccggt gatgatcttc 180

ttgttactgc aaaatgaaac ggaaattgtc caaaactttt tggaaatttg cctcaccctc 240

caaagtaagg gctttcccac ctacggcatt tttcccacta gttttgtgga aacggaaaac 300

catgaactca aggcagacta tggccaacgg gcgatcggtc gagtttgctc ggtggatgcg 360

tccctctggt ggcctatttt ggcctattac tacgtgcaaa gaaccggcaa tgaagcctgg 420

gctagacaaa cccatgtgca attggggcta caaaagtttt taaacctcat tctccatcca 480

gtctttcggg atgcacccac tttgtttgtg cccgacgggg cctttatgat tgaccgcccc 540

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ctccgccgcc gtcccacgga acagtacggt gaagaagcca gcaacgaaca taatgtccac 840

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gccggccatt ggccctgttt attttggttt ctggtggtgg cggtgctccg ccatagctgc 1200

cattccaact acggcacggt ggagtatgcg gaaatgggga acctaattcg caataactat 1260

gaggtgcttt tgcgccgttt gcccaagcat aaatgggctg aatattttga tggccccacg 1320

ggcttttggg tcgggcaaca atcccgttcc taccaaacct ggaccattgt gggcctattg 1380

ctagtacacc atttcacaga agttaacccc gacgatgctt tgatgttcga tttgcctagt 1440

ttgaaaagtt tgcatcaagc gctgcattaa 1470

<210> 141
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sll0626 (proposed invertase, aka lim17)

<400> 141

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

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

Val Ala Ala Ile Pro Gln Ser Asp His His Asp Leu Asn Tyr Thr Glu
35 40 45

Val Phe Ile Arg Asp Asn Val Pro Val Met Ile Phe Leu Leu Leu Gln
50 55 60

Asn Glu Thr Glu Ile Val Gln Asn Phe Leu Glu Ile Cys Leu Thr Leu
65 70 75 80

Gln Ser Lys Gly Phe Pro Thr Tyr Gly Ile Phe Pro Thr Ser Phe Val
85 90 95

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Glu Thr Glu Asn His Glu Leu Lys Ala Asp Tyr Gly Gln Arg Ala Ile
            100                 105                 110

Gly Arg Val Cys Ser Val Asp Ala Ser Leu Trp Trp Pro Ile Leu Ala
        115                 120                 125

Tyr Tyr Tyr Val Gln Arg Thr Gly Asn Glu Ala Trp Ala Arg Gln Thr
    130                 135                 140

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

Val Phe Arg Asp Ala Pro Thr Leu Phe Val Pro Asp Gly Ala Phe Met
                165                 170                 175

Ile Asp Arg Pro Met Asp Val Trp Gly Ala Pro Leu Glu Ile Gln Thr
            180                 185                 190

Leu Leu Tyr Gly Ala Leu Lys Ser Ala Ala Gly Leu Leu Leu Ile Asp
        195                 200                 205

Leu Lys Ala Lys Gly Tyr Cys Ser Asn Lys Asp His Pro Phe Asp Ser
    210                 215                 220

Phe Thr Met Glu Gln Ser His Gln Phe Asn Leu Ser Val Asp Trp Leu
225                 230                 235                 240

Lys Lys Leu Arg Thr Tyr Leu Leu Lys His Tyr Trp Ile Asn Cys Asn
                245                 250                 255

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

Ala Ser Asn Glu His Asn Val His Thr Glu Thr Ile Pro Asn Trp Leu
        275                 280                 285

Gln Asp Trp Leu Gly Asp Arg Gly Gly Tyr Leu Ile Gly Asn Ile Arg
    290                 295                 300

Thr Gly Arg Pro Asp Phe Arg Phe Phe Ser Leu Gly Asn Cys Leu Gly
305                 310                 315                 320

Ala Ile Phe Asp Val Thr Ser Leu Ala Gln Gln Arg Ser Phe Phe Arg
                325                 330                 335

Leu Val Leu Asn Asn Gln Arg Glu Leu Cys Ala Gln Met Pro Leu Arg
            340                 345                 350

Ile Cys His Pro Pro Leu Lys Asp Asp Asp Trp Arg Ser Lys Thr Gly
        355                 360                 365

Phe Asp Arg Lys Asn Leu Pro Trp Cys Tyr His Asn Ala Gly His Trp
```

370 375 380

Pro Cys Leu Phe Trp Phe Leu Val Val Ala Val Leu Arg His Ser Cys
385 390 395 400

His Ser Asn Tyr Gly Thr Val Glu Tyr Ala Glu Met Gly Asn Leu Ile
405 410 415

Arg Asn Asn Tyr Glu Val Leu Leu Arg Arg Leu Pro Lys His Lys Trp
420 425 430

Ala Glu Tyr Phe Asp Gly Pro Thr Gly Phe Trp Val Gly Gln Gln Ser
435 440 445

Arg Ser Tyr Gln Thr Trp Thr Ile Val Gly Leu Leu Val His His
450 455 460

Phe Thr Glu Val Asn Pro Asp Asp Ala Leu Met Phe Asp Leu Pro Ser
465 470 475 480

Leu Lys Ser Leu His Gln Ala Leu His
485

<210> 142
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Sspinvdel-F

<400> 142
ggaagatcta gacacctatg tccagctcat ccatg 35

<210> 143
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Sspinvdel-R

<400> 143
caaacggcgc aaaagcacct gcaggcggtc gaccatggct ttttcgtaga gcaaac 56

<210> 144
<211> 650
<212> DNA
<213> Artificial Sequence

<220>
<223> Ssp6803 Invertase Deletion PCR 1

<400> 144
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cttggacaat ggacagtggt acgatcgcca gaagatccgt caccagttgc ccgctagcaa 120

aaccattgat tgcctgttag tagatggacc gcccgcctac cgagaagaca ttcaatattc 180

ccggtttcct gcagtgcctt ttttccaacc gcaattggca ccccacagca ccatcatttt 240

ggatgacatt aaccgtaggg gagaacagga aattttagcc cgttggcaaa cattgctcaa 300

tgttagtttt gatagctcca ttggcaatgt ggcgatcgcc catctgtcgg cctagggtaa 360

attttaaaaa tcccctgatc caccagtttc agggaaagcc gggtaaaaat ctgccagtgt 420

tgggatattg gatattgagg gaacgagcta gaaccctact atctgtcagc ctagcaaacc 480

aaatgcttta catcgtcaga ctagttcagg aaaattaagt ttgacccata gattaatcct 540

aatcttttgc tatgaaatcc ccccaggctc aacaaatcct agaccaggcc cgccgtttgc 600

tctacgaaaa agccatggtc gaccgcctgc aggtgctttt gcgccgtttg 650

<210> 145
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Sspinvdel-R2

<400> 145
ccgggtgcat gccagtttag caggaggagc caatcgtc 38

<210> 146
<211> 1427
<212> DNA
<213> Artificial Sequence

<220>
<223> Ssp6803 Invertase Deletion PCR 2

<400> 146
ggaagatcta gacacctatg tccagctcat ccatgccccc ttggaaccct gcgaactggc 60

cttggacaat ggacagtggt acgatcgcca gaagatccgt caccagttgc ccgctagcaa 120

aaccattgat tgcctgttag tagatggacc gcccgcctac cgagaagaca ttcaatattc 180

ccggtttcct gcagtgcctt ttttccaacc gcaattggca ccccacagca ccatcatttt 240

ggatgacatt aaccgtaggg gagaacagga aattttagcc cgttggcaaa cattgctcaa 300

tgttagtttt gatagctcca ttggcaatgt ggcgatcgcc catctgtcgg cctagggtaa 360

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