

Supplementary Table 1. List of all experimental treatments conducted in this study.

Experiments on <i>Halotheca</i> sp. PCC 7418 and <i>Fischerella muscicola</i> PCC 73103			
Treatments			Description
[Low PO ₄ ³⁻ - Low Fe]	[Medium PO ₄ ³⁻ - Low Fe]	[High PO ₄ ³⁻ - Low Fe]	1 st experiment Optimal NO ₃ ⁻ (4.4 mM) for <i>Halotheca</i> sp.
[Low PO ₄ ³⁻ - Medium Fe]	[Medium PO ₄ ³⁻ - Medium Fe]	[High PO ₄ ³⁻ - Medium Fe]	2 nd experiment Low NO ₃ ⁻ (0.15 mM) for <i>Halotheca</i> sp. and N ₂ as sole N source for <i>F.</i> <i>muscicola</i>
[Low PO ₄ ³⁻ - High Fe]	[Medium PO ₄ ³⁻ - High Fe]	[High PO ₄ ³⁻ - High Fe]	3 rd experiment Extremely limiting NO ₃ ⁻ conditions (6.66 nM), comparing with optimal NO ₃ ⁻ in selected treatments ([Low PO ₄ ³⁻ - Low Fe], [High PO ₄ ³⁻ - Low Fe], [Low PO ₄ ³⁻ - High Fe] and [High PO ₄ ³⁻ - High Fe]) for <i>Halotheca</i> sp.
Recovery experiments on <i>Halotheca</i> sp. PCC 7418			
Initial Treatment	Condition of NO₃⁻	Nutrient added (at day 12)	Resulting treatment (maintained for 4 days)
[Low PO ₄ ³⁻ - Low Fe]	Optimal NO ₃ ⁻ (4.4 mM)	PO ₄ ³⁻ and Fe	[High PO ₄ ³⁻ - High Fe] in optimal NO ₃ ⁻ treatment
[Low PO ₄ ³⁻ - Low Fe]	Extremely limiting NO ₃ ⁻ conditions (6.66 nM)	PO ₄ ³⁻ , Fe and NO ₃ ⁻	[High PO ₄ ³⁻ - High Fe] in optimal NO ₃ ⁻ treatment
[High PO ₄ ³⁻ - High Fe]	Extremely limiting NO ₃ ⁻ conditions (6.66 nM)	NO ₃ ⁻	[High PO ₄ ³⁻ - High Fe] in optimal NO ₃ ⁻ treatment

In the recovery experiments, PO₄³⁻, Fe, and/or NO₃⁻ were added to the different initial treatments to achieve optimal conditions (45 µM, 7.5 µM and 4.4 mM, respectively). Initial treatment for PO₄³⁻: [Low PO₄³⁻] (0.1 µM), [Medium PO₄³⁻] (1 µM) and [High PO₄³⁻] (45 µM). Initial treatments for Fe: [Low Fe] (2 nM), [Medium Fe] (20 nM) and [High Fe] (7.5 µM).

Supplementary multifasta 1, for PHO boxes in cyanobacteria:

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>SYNPCC7002_A1357(SYNPCC7002_A1357) Score=7.8 Pos=-125 [Synechococcus sp. PCC 7002]
GCTAACCTNNNCTATATTTNNNTTTTATTT
>SYNPCC7002_A2352(phoA1) Score=7.5 Pos=-182 [Synechococcus sp. PCC 7002]
ATTTAATTNNNTTTAGTTGNNNCTTAGCTA
>SYNPCC7002_A2352(phoA1) Score=9.5 Pos=-91 [Synechococcus sp. PCC 7002]
ATTAAACTNNNCTTAGTTTNNNTTTAACTC
>SYNPCC7002_A1232(cysR) Score=8.7 Pos=-126 [Synechococcus sp. PCC 7002]
CTTAAACTNNNGATTACATNNNATTTAACT
>SYNPCC7002_A2120(ndbB) Score=7.6 Pos=-309 [Synechococcus sp. PCC 7002]
CTAAAATTNNNTTTTACTANNNTTTGATCA
>sll0679(sphX) Score=10.9 Pos=-135 [Synechocystis sp. PCC 6803]
TTTAACCANNNCTTTACTANNNCTTAACCT
>sll0654(phoA) Score=7.3 Pos=-210 [Synechocystis sp. PCC 6803]
TTTTACTTNNNCTTTCCCTNNNGTTAGCAA
>sll0654(phoA) Score=8.8 Pos=-175 [Synechocystis sp. PCC 6803]
CTTAACCTNNNCATAGTCTNNNCATAAGTT
>slr1247(pstS) Score=10.5 Pos=-342 [Synechocystis sp. PCC 6803]
CTTAATCTNNNCTTAATTCNNNCTTAATTT
>slr0115(rpaA) Score=7 Pos=-174 [Synechocystis sp. PCC 6803]
ATTACCCANNNTTTAGATGNNNTTTTCTT
>cce_1163(pstS) Score=9.7 Pos=-109 [Cyanotheca sp. ATCC 51142]
CTTAATCTNNNTTTTACTGNNNTTTAACCC
>cce_1859(sphX) Score=8.8 Pos=-141 [Cyanotheca sp. ATCC 51142]
CTTAATAANNNGTTTAACTNNNCTTCATAT
>cce_0886(pstS) Score=7.5 Pos=-53 [Cyanotheca sp. ATCC 51142]
GTTAGATTNNNCTTTAAGANNNGTTTAGTT
>cce_0886(pstS) Score=6.9 Pos=-358 [Cyanotheca sp. ATCC 51142]
CTTGAAAANNNTATAAATANNNGTTATCAT
>cce_3317(SYNPCC7002_A1357) Score=8.4 Pos=-44 [Cyanotheca sp. ATCC 51142]
CTTATCTANNNCTTTATTTNNNTTTTACT
>cce_1211(purF) Score=7.7 Pos=-143 [Cyanotheca sp. ATCC 51142]
TATAATCTNNNGTTTATTNNNGTCTATTT
>cce_4621(phoA) Score=8.7 Pos=-88 [Cyanotheca sp. ATCC 51142]
TTTAAAGTNNNTTTAACATNNNCTTTAAAT
>cce_4758(fbp) Score=8.3 Pos=-125 [Cyanotheca sp. ATCC 51142]
ATTAACTNNNCTGAAATTNNNCTAAAGTT
>cce_5183(ackA) Score=9.6 Pos=-74 [Cyanotheca sp. ATCC 51142]
GTTAATTTNNNTTTAATCANNNCTTAAAT
>cce_4392(cce_4392) Score=8.8 Pos=20 [Cyanotheca sp. ATCC 51142]
CTTTAACCNNNCTCAATCTNNNCTTAAACT
>cce_5174(ppk) Score=8.4 Pos=-70 [Cyanotheca sp. ATCC 51142]
GATAAAAANNNCATAAAGTNNNCTTAAACT
>cce_0154(ndbB) Score=7.6 Pos=-83 [Cyanotheca sp. ATCC 51142]
TTTTATCTNNNGATAATTANNNATTAATGA
>PCC8801_1024(pstS) Score=9.8 Pos=-108 [Cyanotheca sp. PCC 8801]
TTTTATCANNNGTTTACCTNNNCTTAACCC
>PCC8801_4067(sphX) Score=8.1 Pos=-157 [Cyanotheca sp. PCC 8801]
CTTAGCATNNNCTTTTCTNNNGCTAAACT
>PCC8801_1433(spoT) Score=8.5 Pos=-224 [Cyanotheca sp. PCC 8801]
TTTAACAGNNNCTAAACCTNNNTTTAAACT
>PCC8801_1847(SYNPCC7002_A1357) Score=7.5 Pos=-43 [Cyanotheca sp. PCC 8801]
AATAAATTNNNTCTTATTTNNNATTATCTT
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>PCC8801_4178(purF) Score=7.5 Pos=-104 [Cyanotheca sp. PCC 8801]
 GATAAGATNNNGTTAAAGANNNGTTAAAT
 >PCC8801_1683(nucH) Score=9.8 Pos=-246 [Cyanotheca sp. PCC 8801]
 ATTAACTNNNCTTAAATTNNNGTTAAATA
 >PCC8801_0430(fbp) Score=7.9 Pos=-278 [Cyanotheca sp. PCC 8801]
 TTAATAATTNNNTTTTATTTNNNCTTTTATT
 >PCC8801_0346(cysR) Score=9.7 Pos=-91 [Cyanotheca sp. PCC 8801]
 TTTAATCTNNNGATTACCTNNNGTTTACCT
 >PCC8801_3887(ackA) Score=9.1 Pos=-183 [Cyanotheca sp. PCC 8801]
 CTTTGACCNNNGTTTACCANNNCTTAACCT
 >PCC8801_1625(ppk) Score=7.2 Pos=-95 [Cyanotheca sp. PCC 8801]
 TATTACCTNNNTATAGCTNNNGATAGCCT
 >PCC8801_3662(rsbU) Score=7.4 Pos=-162 [Cyanotheca sp. PCC 8801]
 ATTAACGCNNNGATTAAACNNNCCTAATTA
 >PCC8801_2302(SYNPCC7002_A0979) Score=7.1 Pos=-232 [Cyanotheca sp. PCC 8801]
 CATAATGANNNTTTTAAAGANNNGTTAAAAA
 >Cyan7425_0207 Score=7.8 Pos=-81 [Cyanotheca sp. PCC 7425]
 TTTAACGANNNCTTTAGCANNNGATTACCT
 >Cyan7425_4261(phoA1) Score=9 Pos=-146 [Cyanotheca sp. PCC 7425]
 ATTAATCANNNGTTTACCTNNNCATAAATC
 >Cyan7425_4387(SYNPCC7002_A2263) Score=7.5 Pos=-102 [Cyanotheca sp. PCC 7425]
 ATTATCATNNNTATTACCTNNNCCTTACCC
 >Cyan7425_1977(ppk) Score=8.4 Pos=-238 [Cyanotheca sp. PCC 7425]
 GTTATCCCNNNGTTAATTTNNNATTAAATC
 >Cyan7425_0664(pstS) Score=10.1 Pos=-80 [Cyanotheca sp. PCC 7425]
 ATTAATCTNNNCTTAATCTNNNCTTTATCC
 >MAE_18380(pstS) Score=9.5 Pos=-87 [Microcystis aeruginosa NIES-843]
 TTTATTCANNNCTTAACCTNNNCTTTACCA
 >MAE_23860(fbp) Score=7.6 Pos=-129 [Microcystis aeruginosa NIES-843]
 ATTAGCCANNNCTAAACTNNNCTAAAAAT
 >MAE_18440(cysR) Score=9.6 Pos=-86 [Microcystis aeruginosa NIES-843]
 GTTAATCTNNNGATTACCTNNNGTTTACCT
 >MAE_02800(ackA) Score=8.8 Pos=-66 [Microcystis aeruginosa NIES-843]
 TTTTATCTNNNCTTAACCTNNNTTTGATTA
 >MAE_18310(pstS) Score=9.6 Pos=-139 [Microcystis aeruginosa NIES-843]
 ATTAACCGNNNTTTTACCGNNNCTTAACCA
 >all3651(purF) Score=7.7 Pos=-119 [Nostoc sp. PCC 7120]
 TTTAATATNNNGTTAAAGANNNGTTAAGAC
 >alr5291(phoA1) Score=10.4 Pos=-229 [Nostoc sp. PCC 7120]
 GTTAACCTNNNTTTATATNNNCTTAACCT
 >all4021(fbp) Score=7 Pos=-136 [Nostoc sp. PCC 7120]
 CGTAAACTNNNGATTTCTTNNNTTTATCTA
 >alr5259(SYNPCC7002_A2263) Score=8.7 Pos=-329 [Nostoc sp. PCC 7120]
 GTAAACTNNNTTTATTTANNNCTTAATTT
 >all1758(rsbU) Score=7.5 Pos=-49 [Nostoc sp. PCC 7120]
 ATTTATTANNNGTCAATCTNNNATTAACCC
 >all0129(rpaA) Score=7.3 Pos=-101 [Nostoc sp. PCC 7120]
 TTTATGTTNNNTTTAAATNNNTTTTATAA
 >all3822(SYNPCC7002_A0979) Score=8.6 Pos=-149 [Nostoc sp. PCC 7120]
 CTTAATTTNNNCTTAAGTANNNCTCAAATT
 >alr4975(alr4975) Score=7.6 Pos=-10 [Nostoc sp. PCC 7120]
 ATTAATTANNNTGTTACCTNNNATTTATAT
 >alr2234(phoD) Score=9.6 Pos=-275 [Nostoc sp. PCC 7120]
 ATTAACCTNNNCTTAGTCANNNATTAATTT
 >all0207(phoD) Score=9.3 Pos=-98 [Nostoc sp. PCC 7120]

ATTAACCCNNNGATAACTCNNNCTTTACTT
 >all0911(pstS) Score=10.8 Pos=-105 [Nostoc sp. PCC 7120]
 CTTAACTTNNNGTTTACCTNNNCTTAACTT
 >all4575(pstS) Score=8 Pos=-324 [Nostoc sp. PCC 7120]
 TTTTATCTNNNCTTTTATTNNNCTTTTTTTT
 >Tery_3534(pstS) Score=9.7 Pos=-192 [Trichodesmium erythraeum IMS101]
 TTTGATATNNNTTTAACCTNNNCTTAATCT
 >Tery_2653(spoT) Score=7.8 Pos=-43 [Trichodesmium erythraeum IMS101]
 AATAAACTNNNATTTGATANNNATTAAGTC
 >Tery_4322(SYNPCC7002_A1357) Score=7 Pos=-395 [Trichodesmium erythraeum IMS101]
 CTTATTATNNNAATTATTNNNATTTAGCT
 >Tery_3699(purF) Score=8.3 Pos=-97 [Trichodesmium erythraeum IMS101]
 GTTAAGGANNNCTTAAAGTNNNTTTAAGCT
 >Tery_0682(fbp) Score=6.5 Pos=-336 [Trichodesmium erythraeum IMS101]
 TTTTAGATNNNGTTTTTGTNNNCATTATCA
 >Tery_2568(SYNPCC7002_A2263) Score=7.5 Pos=-208 [Trichodesmium erythraeum IMS101]
 GATAAGATNNNATTAACCTNNNGTTTGCTA
 >Tery_0739(rsuU) Score=8.3 Pos=-250 [Trichodesmium erythraeum IMS101]
 TTAAAACCTNNNCTTAATCTNNNACTAACTC
 >Tery_4937(rpaA) Score=7 Pos=-158 [Trichodesmium erythraeum IMS101]
 CTTGACAANNNAATAAATTNNNGTTAAAGA
 >Tery_0954(SYNPCC7002_A0979) Score=8.3 Pos=-309 [Trichodesmium erythraeum IMS101]
 ATTAACCANNNATTGAATTNNNATTGACTT
 >Tery_2902(sphR) Score=10.4 Pos=-365 [Trichodesmium erythraeum IMS101]
 GATAACCCNNNGTTAACCTNNNCTTAACCT
 >Tery_3661(ndbB) Score=7.8 Pos=-342 [Trichodesmium erythraeum IMS101]
 TTTTAATANNNAATTACCCNNNCTTAGCCT
 >Synpcc7942_0004(purF) Score=7.8 Pos=-76 [Synechococcus elongatus PCC 7942]
 GTTAAGTCNNNGTTAAATTNNNATTAGCCG
 >Synpcc7942_1392(phoA) Score=9.4 Pos=-233 [Synechococcus elongatus PCC 7942]
 TTTAACTANNNCATAATCTNNNCTCAATCT
 >CYA_1552(pstS) Score=10.2 Pos=-203 [Synechococcus sp. JA-3-3Ab]
 AATAACCTNNNTTTAACCTNNNGTTAACCA
 >CYA_1732(pstS) Score=9.6 Pos=-75 [Synechococcus sp. JA-3-3Ab]
 GTTAACCTNNNGATATCCTNNNGTTAACTT
 >CYA_1541(cysR) Score=10.5 Pos=-172 [Synechococcus sp. JA-3-3Ab]
 CTTAACCTNNNCATAACCTNNNCTTTACTT
 >CYA_2506(phoD) Score=7.9 Pos=-129 [Synechococcus sp. JA-3-3Ab]
 CTTAAACANNGCTAACCCNNNTTTCACCG
 >SYNW2391(phoA1) Score=9.2 Pos=-78 [Synechococcus sp. WH 8102]
 TTTGATCANNNCTTAAACTNNNCCTAACTT
 >tlr2164(pstS) Score=10.9 Pos=-51 [Thermosynechococcus elongatus BP-1]
 TTTAAACANNNTTTTACCTNNNCTTAACTT
 >tll1671(cysR) Score=8.1 Pos=-171 [Thermosynechococcus elongatus BP-1]
 CTTAACCCNNNCTTGAACCNNNGATTATCT
 >null(SYNPCC7002_A1357) Score=7.1 Pos=-268 [Thermosynechococcus elongatus BP-1]
 ATTAAAAANNNATTAAAAANNNTTCTCTT

Supplementary multifasta 2, for Fur boxes in cyanobacteria:

>SYNPCC7002_A2347(chlL) Score=3.6 Pos=-126 [Synechococcus sp. PCC 7002]
TTTTATAAAACTCTAAGT
>SYNPCC7002_G0137(exbB) Score=4.2 Pos=-279 [Synechococcus sp. PCC 7002]
ATTAAGAGATTATCTCAAT
>SYNPCC7002_G0099(pchR) Score=3.7 Pos=-94 [Synechococcus sp. PCC 7002]
ATTTCTTATTAATATAAAT
>SYNPCC7002_G0006(iutA) Score=4.6 Pos=-38 [Synechococcus sp. PCC 7002]
TTTGAGAATTATTTTGTAGT
>SYNPCC7002_A1631(apcF) Score=3.3 Pos=-257 [Synechococcus sp. PCC 7002]
TTTTATTATTTTAAAA
>SYNPCC7002_A0913(SYNPCC7002_A0913) Score=2.2 Pos=-146 [Synechococcus sp. PCC 7002]
TTTTTACAACATTTTAAAA
>SYNPCC7002_A0913(SYNPCC7002_A0913) Score=3.8 Pos=-68 [Synechococcus sp. PCC 7002]
AATGAGAAAATTTTGATAT
>SYNPCC7002_A1018(chlH) Score=3.8 Pos=-57 [Synechococcus sp. PCC 7002]
ATAGTTATAAATTTTAAAT
>SYNPCC7002_A1443(nifJ) Score=2.2 Pos=-165 [Synechococcus sp. PCC 7002]
TTTTCTTATAACTTTTAGC
>SYNPCC7002_A0871(afuC) Score=5.1 Pos=-83 [Synechococcus sp. PCC 7002]
GTTGAGAATAGTTCTTAAT
>SYNPCC7002_A2351(SYNPCC7002_A2351) Score=2.9 Pos=-216 [Synechococcus sp. PCC 7002]
TTTATTATTGTTTTTGTAGT
>SYNPCC7002_A1961(psaA) Score=3.4 Pos=-206 [Synechococcus sp. PCC 7002]
AGTTTTAAATATTGTTAAT
>SYNPCC7002_G0061(SYNPCC7002_G0061) Score=4.1 Pos=-62 [Synechococcus sp. PCC 7002]
ATTGATAAATAATTTAAGT
>SYNPCC7002_A1649(fur) Score=3.5 Pos=-88 [Synechococcus sp. PCC 7002]
GTTAGTATTTATTTGCAAT
>SYNPCC7002_G0138(iutA) Score=4.6 Pos=-67 [Synechococcus sp. PCC 7002]
ATTGAGATAATCTCTTAAT
>SYNPCC7002_G0090(SYNPCC7002_G0090) Score=5.2 Pos=-83 [Synechococcus sp. PCC 7002]
ATTGAAATAAATTCTTATT
>SYNPCC7002_G0104(pchR) Score=5.4 Pos=-68 [Synechococcus sp. PCC 7002]
ATTGAGAATAATTAGTAAT
>SYNPCC7002_G0103(fhuA) Score=3.2 Pos=-46 [Synechococcus sp. PCC 7002]
ATTAAGAACTTTTTGAAGT
>slr0749(chlL) Score=3.3 Pos=-173 [Synechocystis sp. PCC 6803]
ATTTTATTTTTGTCTCAAT
>ssr2333(feoA) Score=4.5 Pos=-31 [Synechocystis sp. PCC 6803]
GTTGAGAATTATTTGCAGT
>slr1406(fhuA) Score=3.4 Pos=-38 [Synechocystis sp. PCC 6803]
ATTAATAAACTTTTTAAC
>slr1404(exbB) Score=6 Pos=-110 [Synechocystis sp. PCC 6803]
ATTGAAAATAGTTATCAAT
>slr1490(fhuA) Score=4.1 Pos=-86 [Synechocystis sp. PCC 6803]
TTTGAGAATTAGTTGCAGT
>slr1484(SYNPCC7002_G0090) Score=5.6 Pos=-255 [Synechocystis sp. PCC 6803]
ATTGATAACTATTTTCAAT

>slr1318(fecE) Score=4.1 Pos=-176 [Synechocystis sp. PCC 6803]
 ATTCCTAATTATTCTTAAC
 >slr1485(SYNPCC7002_G0089) Score=2.2 Pos=-9 [Synechocystis sp. PCC 6803]
 GTTTTAATAATGTTTAAAT
 >slr1316(fecC) Score=4.2 Pos=-78 [Synechocystis sp. PCC 6803]
 ATTGATAATCTTTCCTAGT
 >slr1485(SYNPCC7002_G0089) Score=2.7 Pos=-42 [Synechocystis sp. PCC 6803]
 ACTGTGAAATTTATTTAAC
 >sll1404(exbB) Score=4.6 Pos=-64 [Synechocystis sp. PCC 6803]
 ATTGAGAATTACTCTTAAC
 >sll1404(exbB) Score=4.6 Pos=-286 [Synechocystis sp. PCC 6803]
 TATGTGAAATATTATTATT
 >slr1295(sufA) Score=4.9 Pos=-44 [Synechocystis sp. PCC 6803]
 ATTGAGAATTACTTTTATT
 >sll1911(SYNPCC7002_A0913) Score=4.2 Pos=-59 [Synechocystis sp. PCC 6803]
 GTTGTTAAAATTTAACAAT
 >slr0513(sufA) Score=3.9 Pos=-240 [Synechocystis sp. PCC 6803]
 AATAATAATCTCTTGCAAT
 >slr0513(sufA) Score=4.1 Pos=-187 [Synechocystis sp. PCC 6803]
 ATTGCACCTTTATTTGCAAT
 >sll0849(psbD) Score=3.3 Pos=-298 [Synechocystis sp. PCC 6803]
 AATGTAAAATATTTGCTAA
 >slr1181(psbA) Score=2.8 Pos=-242 [Synechocystis sp. PCC 6803]
 ATTAAAATCTTTTTTTTAC
 >slr1181(psbA) Score=4 Pos=-182 [Synechocystis sp. PCC 6803]
 TTAAAGAAATATTATTAAT
 >sll1867(psbA) Score=3.4 Pos=-124 [Synechocystis sp. PCC 6803]
 ATTTACAAATTGTTACAAT
 >slr1738(perR) Score=3 Pos=-194 [Synechocystis sp. PCC 6803]
 ATTAATATTTTTTTTATAA
 >sll0247(isiA) Score=2.8 Pos=-269 [Synechocystis sp. PCC 6803]
 ATTTCTTAATAATTTTAGT
 >ssr2333(feoA) Score=4.4 Pos=-69 [Synechocystis sp. PCC 6803]
 TTTGATATTTATTCTGAAC
 >slr1392(feoB) Score=4.5 Pos=-278 [Synechocystis sp. PCC 6803]
 GTTGAGAATTATTTGCAGT
 >cce_4533(cce_4533) Score=3.7 Pos=-118 [Cyanothecce sp. ATCC 51142]
 TTTGAGTTTTATTTAAAAT
 >cce_0033(feoA) Score=4.5 Pos=-47 [Cyanothecce sp. ATCC 51142]
 GATAAGAATTATTCTTAAT
 >cce_0033(feoA) Score=3.3 Pos=-298 [Cyanothecce sp. ATCC 51142]
 ATTAAAAAATACTGTTAAC
 >cce_0660(psbD) Score=3.4 Pos=-298 [Cyanothecce sp. ATCC 51142]
 ATTGTAAATTTTTTGCTAA
 >cce_0479(dpsA) Score=4.7 Pos=-144 [Cyanothecce sp. ATCC 51142]
 GATGCAATATATTCTCAAT
 >cce_2632(sufA) Score=4.8 Pos=-20 [Cyanothecce sp. ATCC 51142]
 ATCAATAATAATTTTCAAT
 >cce_4358(chlH) Score=2.7 Pos=-183 [Cyanothecce sp. ATCC 51142]
 AATAAATAATTTTTGTAAA
 >cce_4358(chlH) Score=2.3 Pos=-138 [Cyanothecce sp. ATCC 51142]
 ATTTGTCAATATTTGTAAC
 >cce_3801(afuC) Score=4.2 Pos=-163 [Cyanothecce sp. ATCC 51142]
 ATTGAAAATTAATGCTAAT
 >cce_0989(psaA) Score=3.4 Pos=-205 [Cyanothecce sp. ATCC 51142]

AATTTTAATTATTGTAAAG
 >cce_3809(SYNPCC7002_A2351) Score=3.2 Pos=-132 [Cyanotherce sp. ATCC 51142]
 GTTTTTATTTTCTGTCAAT
 >cce_1977(coxB) Score=3.7 Pos=-136 [Cyanotherce sp. ATCC 51142]
 AATTTCAATCAATTTCAAT
 >cce_0019(SYNPCC7002_A0913) Score=3.1 Pos=-75 [Cyanotherce sp. ATCC 51142]
 TTTTTTAATATTTTTTGAT
 >cce_1944(apcF) Score=4.4 Pos=-151 [Cyanotherce sp. ATCC 51142]
 ATTGCTAAAATCTATAATT
 >cce_3895(SYNPCC7002_G0062) Score=2.8 Pos=16 [Cyanotherce sp. ATCC 51142]
 GTTTAAAAATTCTTTTAGT
 >cce_0892(fdx) Score=3 Pos=-29 [Cyanotherce sp. ATCC 51142]
 TTTCTTATAATTCTTAAC
 >cce_1785(isiA) Score=4.4 Pos=-18 [Cyanotherce sp. ATCC 51142]
 ATTGCAAATCTTTTAAAT
 >cce_3031(isiB) Score=4.9 Pos=-66 [Cyanotherce sp. ATCC 51142]
 ATTGAGAATTATTCTAAAC
 >cce_2330(fur) Score=5.1 Pos=-96 [Cyanotherce sp. ATCC 51142]
 GTTGCTAATTATTTTCAAT
 >PCC8801_0791(chlL) Score=2.7 Pos=-242 [Cyanotherce sp. PCC 8801]
 ATTTAGTAAATTTTAAAGT
 >PCC8801_2575(SYNPCC7002_A2351) Score=3.1 Pos=-247 [Cyanotherce sp. PCC 8801]
 ATTTCTCCTTATTTTAAAT
 >PCC8801_0349(sll1407) Score=3.3 Pos=-107 [Cyanotherce sp. PCC 8801]
 AATAATTAATTTTTTTTAT
 >PCC8801_0256(ctaA) Score=2.2 Pos=-185 [Cyanotherce sp. PCC 8801]
 TTTTATTAACCTATGTAA
 >PCC8801_2812(SYNPCC7002_A0913) Score=4.4 Pos=-67 [Cyanotherce sp. PCC 8801]
 TATGATAAAATTTATTAA
 >PCC8801_4320(chlH) Score=2.3 Pos=-186 [Cyanotherce sp. PCC 8801]
 ATTTGTCAATATTTGTAAAC
 >PCC8801_0567(coxB) Score=2.7 Pos=-152 [Cyanotherce sp. PCC 8801]
 TTTGTTTATTATTTGTTAC
 >PCC8801_3918(nifJ) Score=3.4 Pos=-67 [Cyanotherce sp. PCC 8801]
 TTTGTCAATAATTTGTAAAC
 >PCC8801_1443(sufA) Score=4 Pos=-90 [Cyanotherce sp. PCC 8801]
 ATTAGGAATAATTAGCAAC
 >PCC8801_1928(SYNPCC7002_G0061) Score=2 Pos=-184 [Cyanotherce sp. PCC 8801]
 AATATTTTATATTTATAGT
 >PCC8801_2860(fdx) Score=3.8 Pos=-49 [Cyanotherce sp. PCC 8801]
 ATTGTAAAAAATATTAAC
 >PCC8801_0870(fur) Score=4.6 Pos=-97 [Cyanotherce sp. PCC 8801]
 GTTGCAAATTATTTGCAAT
 >PCC8801_3039(SYNPCC7002_G0098) Score=5.5 Pos=-89 [Cyanotherce sp. PCC 8801]
 GTTGACAAAAATTCTCATT
 >PCC8801_3017(exbB) Score=5.7 Pos=-38 [Cyanotherce sp. PCC 8801]
 ATTGATAACTTTTCTCAAT
 >Cyan7425_2411(pchR) Score=4.9 Pos=-71 [Cyanotherce sp. PCC 7425]
 ATTGTTAATCTTTTTCATT
 >Cyan7425_2410(fhuA) Score=5.8 Pos=-56 [Cyanotherce sp. PCC 7425]
 ATTGAGAATAATTCTTATT
 >Cyan7425_2418(exbB) Score=4.6 Pos=-264 [Cyanotherce sp. PCC 7425]
 ATTGATGATTATTTTCAAC
 >Cyan7425_2438(pchR) Score=4.5 Pos=-37 [Cyanotherce sp. PCC 7425]
 ATTAAGAATAAGTCTCAGT

>Cyan7425_2439(fhuA) Score=5.1 Pos=-66 [Cyanothecae sp. PCC 7425]
 ATTGAGAGTATTTCTTATT
 >Cyan7425_1597(perR) Score=4.9 Pos=-88 [Cyanothecae sp. PCC 7425]
 TTTGAGAATTATACTAAAT
 >Cyan7425_5031(psbD) Score=3.1 Pos=-91 [Cyanothecae sp. PCC 7425]
 GTTTATAAACTTTTCGTAAA
 >Cyan7425_4671(psaA) Score=3.4 Pos=-292 [Cyanothecae sp. PCC 7425]
 TCTATGAATTTTTATTAAT
 >Cyan7425_3510(afuC) Score=4 Pos=-60 [Cyanothecae sp. PCC 7425]
 GTTGAATAATAGTCTTAAT
 >Cyan7425_3510(afuC) Score=5.3 Pos=-105 [Cyanothecae sp. PCC 7425]
 ATTGAGAATAATTTTCAAA
 >Cyan7425_1838(apcF) Score=3 Pos=-245 [Cyanothecae sp. PCC 7425]
 TTTTATATTATCTTTTAAC
 >Cyan7425_1059(psbA) Score=3.4 Pos=-182 [Cyanothecae sp. PCC 7425]
 ATTATTAATAAGTTTCAAA
 >Cyan7425_2984(cce_4396) Score=2.7 Pos=-78 [Cyanothecae sp. PCC 7425]
 TATATGAATATCTTGTAAT
 >Cyan7425_2984(cce_4396) Score=3.9 Pos=-48 [Cyanothecae sp. PCC 7425]
 ATTGCAATTATATTACAAT
 >Cyan7425_2434(isiA) Score=4.7 Pos=-61 [Cyanothecae sp. PCC 7425]
 ATTGAGTTTATTTCTCAAC
 >Cyan7425_3508(sufA) Score=3.5 Pos=-165 [Cyanothecae sp. PCC 7425]
 ATTAGGAATGAATCGTAAT
 >MAE_16250(chlN) Score=2.8 Pos=-107 [Microcystis aeruginosa NIES-843]
 ATTAAGTAATTCTTTATAT
 >MAE_16230(chlL) Score=2.8 Pos=-150 [Microcystis aeruginosa NIES-843]
 ATTTATATAATTTTAAAGC
 >MAE_12190(chlH) Score=2.8 Pos=-247 [Microcystis aeruginosa NIES-843]
 ATTAAATATTAATTTTGT
 >MAE_41160(psbD) Score=2.9 Pos=-274 [Microcystis aeruginosa NIES-843]
 ATTTGTAATTTTTTGCTAA
 >MAE_47560(psaA) Score=3.2 Pos=-297 [Microcystis aeruginosa NIES-843]
 ATTAATAAACTTTTGTAAG
 >MAE_22930(coxB) Score=2.5 Pos=-216 [Microcystis aeruginosa NIES-843]
 TTTTAGATATTCTTTAGAT
 >MAE_38140(nifJ) Score=3.9 Pos=-292 [Microcystis aeruginosa NIES-843]
 ATTCTGAATATTAATTAAT
 >MAE_12460(afuC) Score=4.4 Pos=-117 [Microcystis aeruginosa NIES-843]
 TTTGAGAAAGTTTCCTAAT
 >MAE_56680(sufA) Score=4.9 Pos=-61 [Microcystis aeruginosa NIES-843]
 GATAAGAATTATTCTCAAT
 >MAE_22920(ctaA) Score=2.5 Pos=-282 [Microcystis aeruginosa NIES-843]
 TCTTTTCAATATTTTAAAT
 >all4365(chlH) Score=2.9 Pos=-272 [Nostoc sp. PCC 7120]
 GTTTTTTATTTTTTCATC
 >all4365(chlH) Score=3 Pos=-232 [Nostoc sp. PCC 7120]
 AATATTAATTTTTCTTTAC
 >alr5154(psaA) Score=3.4 Pos=-177 [Nostoc sp. PCC 7120]
 ATTTTGAATTATTGTAAA
 >alr0950(coxB) Score=3.7 Pos=-134 [Nostoc sp. PCC 7120]
 TTTACTCAAGATTATTAAT
 >alr2803(nifJ) Score=3.8 Pos=-92 [Nostoc sp. PCC 7120]
 ATTTTAAATCAGTATTAAT
 >alr3808(dpsA) Score=3.5 Pos=-204 [Nostoc sp. PCC 7120]

GTTTAGAAATTATTGCAAT
 >alr2514(coxB) Score=3 Pos=-190 [Nostoc sp. PCC 7120]
 AGTTAAAAAGTTAATAAGT
 >all4001(isiA) Score=4.8 Pos=-161 [Nostoc sp. PCC 7120]
 ATTAAGAATCTTTTCAAT
 >alr3727(psbA) Score=3.7 Pos=-105 [Nostoc sp. PCC 7120]
 TTTAGTAATATTAATTAAT
 >alr4592(psbA) Score=4.1 Pos=-28 [Nostoc sp. PCC 7120]
 ATAAATAATTAATCGCAAT
 >asl0884(fdx) Score=3.5 Pos=-90 [Nostoc sp. PCC 7120]
 ATTCTTAATTTTTGTAAAT
 >alr3155(SYNPCC7002_G0061) Score=4.1 Pos=-98 [Nostoc sp. PCC 7120]
 ATTACGAATTAATATAAAAT
 >all3903(cce_4396) Score=4.6 Pos=-47 [Nostoc sp. PCC 7120]
 TTTAATATAAATTGTCAAT
 >all2367(all2367) Score=3.2 Pos=-181 [Nostoc sp. PCC 7120]
 TATTGTAATATCTTTTAAT
 >alr2405(isiB) Score=5 Pos=-235 [Nostoc sp. PCC 7120]
 ATTGAAATAAATATTCAAT
 >all1691(fur) Score=5.2 Pos=-94 [Nostoc sp. PCC 7120]
 TTTAATAAATATTCTCAAT
 >all1692(sigC) Score=3.5 Pos=-320 [Nostoc sp. PCC 7120]
 AATAAACATAATTTTTACT
 >all2158(fhuA) Score=4.6 Pos=-62 [Nostoc sp. PCC 7120]
 ATTAAGAATTATTAGCAGT
 >alr2175(fhuE) Score=4.4 Pos=-120 [Nostoc sp. PCC 7120]
 GTTAATAATCTTTCGCAAT
 >alr2626(fhuE) Score=4.7 Pos=-106 [Nostoc sp. PCC 7120]
 TTTGATATTAATTACTAAT
 >all2586(fecC) Score=4.6 Pos=-100 [Nostoc sp. PCC 7120]
 TCTTATATTAATTCTCAAT
 >all2586(fecC) Score=5 Pos=-32 [Nostoc sp. PCC 7120]
 AATGACTATATTTTTCAAT
 >all2237(pchR) Score=5.1 Pos=-40 [Nostoc sp. PCC 7120]
 TTTGAGAAAGTTTATCTAT
 >all2235(fecB) Score=3.5 Pos=12 [Nostoc sp. PCC 7120]
 TTTTATTATCATATTCAAC
 >all1101(fhuA) Score=3.8 Pos=-238 [Nostoc sp. PCC 7120]
 ATTAATATTAATCCTAAT
 >all4924(fhuE) Score=5.5 Pos=-32 [Nostoc sp. PCC 7120]
 ATTGAGAATTTTTATCTAT
 >all5047(exbB) Score=4.7 Pos=-102 [Nostoc sp. PCC 7120]
 TTTGATAATAATTTGCATC
 >alr2184(pchR) Score=5.1 Pos=-39 [Nostoc sp. PCC 7120]
 ATTGAGAAATAATATTATT
 >alr2185(fhuE) Score=4.3 Pos=-69 [Nostoc sp. PCC 7120]
 TTTGCAAAAAATTATTAAC
 >alr2211(fhuA) Score=2.9 Pos=-272 [Nostoc sp. PCC 7120]
 ATTTATTTAATTATTTAGT
 >all2580(pchR) Score=5.5 Pos=-48 [Nostoc sp. PCC 7120]
 ATTGAGAAATAATATCATT
 >alr2174(pchR) Score=5.6 Pos=-96 [Nostoc sp. PCC 7120]
 ATTGATAAATACTATCATT
 >Tery_2879(feoA) Score=3.5 Pos=-270 [Trichodesmium erythraeum IMS101]
 TTTTCCAAATTTTTTCAGT

>Tery_2644(SYNPCC7002_A2351) Score=4.2 Pos=-122 [Trichodesmium erythraeum IMS101]
 AATTAGATTAATTTTGAAT
 >Tery_4282(dpsA) Score=2.4 Pos=-285 [Trichodesmium erythraeum IMS101]
 ATTTTAAACAATTGAAAT
 >Tery_0513(psbC) Score=3.5 Pos=-195 [Trichodesmium erythraeum IMS101]
 TTTACAAAAAATTGTAAAT
 >Tery_1780(ctaA) Score=3.3 Pos=-167 [Trichodesmium erythraeum IMS101]
 ATTAAAAAAAATTTAAAA
 >Tery_4773(SYNPCC7002_A0913) Score=2.4 Pos=-64 [Trichodesmium erythraeum IMS101]
 TTTATGAAATATTTATGAT
 >Tery_3224(chlH) Score=3 Pos=-65 [Trichodesmium erythraeum IMS101]
 GTTTAAAATTTTTTGATAT
 >Tery_1781(ctaB) Score=4.1 Pos=-41 [Trichodesmium erythraeum IMS101]
 AATTATAACCAGTTTCAAT
 >Tery_4669(psaA) Score=4 Pos=-80 [Trichodesmium erythraeum IMS101]
 ATTGATAATTCTTTACAAC
 >Tery_3222(afuC) Score=5.1 Pos=-94 [Trichodesmium erythraeum IMS101]
 AATGAAAAAAATATTCAAT
 >Tery_2878(feoB) Score=3 Pos=-43 [Trichodesmium erythraeum IMS101]
 TATTACATAATTTTTATAT
 >Tery_3377(sufA) Score=4.4 Pos=-97 [Trichodesmium erythraeum IMS101]
 ATTAAGAATAAATTGCAAT
 >Tery_1667(isiA) Score=3.2 Pos=-156 [Trichodesmium erythraeum IMS101]
 TTTTATAATTTCTTTTAAA
 >Tery_4504(fdx) Score=2.6 Pos=-35 [Trichodesmium erythraeum IMS101]
 GTTAATATTTTTTTATAAC
 >Tery_1958(fur) Score=4.7 Pos=-44 [Trichodesmium erythraeum IMS101]
 ATTGTGTATCATTGTCAAT
 >Tery_1780(ctaA) Score=3.5 Pos=-278 [Trichodesmium erythraeum IMS101]
 ATTGTTAAAATTATGAAAT
 >Synpcc7942_2601(ctaA) Score=4.3 Pos=-158 [Synechococcus elongatus PCC 7942]
 GATGACAATATTTTTTCGAT
 >Synpcc7942_1406(afuC) Score=4.2 Pos=-81 [Synechococcus elongatus PCC 7942]
 ATTGAGAATAAATCGCAGA
 >Synpcc7942_0938(ccc_4396) Score=4 Pos=-30 [Synechococcus elongatus PCC 7942]
 AATAAAAAAGTTTCGTAAT
 >Synpcc7942_1542(isiA) Score=5.2 Pos=-45 [Synechococcus elongatus PCC 7942]
 ATTGAGAATTATTGTAAAT
 >Synpcc7942_2049(psaA) Score=3.3 Pos=-296 [Synechococcus elongatus PCC 7942]
 TCTTTGAATTATTGTAAAT
 >PMT1340(ctaA) Score=2.6 Pos=-30 [Prochlorococcus marinus str. MIT 9313]
 ATTTAAATTATTTTATTGT
 >CYA_2647(psbD) Score=3 Pos=-106 [Synechococcus sp. JA-3-3Ab]
 TTTATTAATTTTTTCGTAAG
 >CYA_2794(afuC) Score=3.8 Pos=-26 [Synechococcus sp. JA-3-3Ab]
 AGTGAAAATCTTTTGCAAC
 >CYA_0643(fdx) Score=2.8 Pos=-92 [Synechococcus sp. JA-3-3Ab]
 ATTAAAAATATGATTTAAA
 >gvip470(psaA) Score=2.2 Pos=-195 [Gloeobacter violaceus PCC 7421]
 TTTTAAAAAATTGTAAAGT
 >glr3733(perR) Score=4.2 Pos=-58 [Gloeobacter violaceus PCC 7421]
 AATTAGATCTATTCTAAAT
 >gll1014(afuA) Score=3.7 Pos=-64 [Gloeobacter violaceus PCC 7421]
 ATTGACAATTAATTGCAGC
 >null(chlL) Score=2.8 Pos=-211 [Thermosynechococcus elongatus BP-1]

TTTTGTATTTTGTTTAAT
>null(psbA) Score=3.8 Pos=-135 [Thermosynechococcus elongatus BP-1]
ATTTAGTTTACTAACAAT
>null(apcF) Score=3.1 Pos=-157 [Thermosynechococcus elongatus BP-1]
AATTATGAACTTTTGTAAT
>null(cce_4396) Score=4 Pos=-45 [Thermosynechococcus elongatus BP-1]
AATTAAAATTATATTCATC
>null(isiA) Score=5.5 Pos=-121 [Thermosynechococcus elongatus BP-1]
AATGCTATTAATTCTCAAT
>null(fur) Score=4.4 Pos=-59 [Thermosynechococcus elongatus BP-1]
CATTGTAATTATTCTCAAT

Supplementary multifasta 3, for NtcA boxes in cyanobacteria:

>SYNPCC7002_A2208(amt1) Score=3.7 Pos=-52 [Synechococcus sp. PCC 7002]
GGTTACTTCTGCTACC
>SYNPCC7002_A0076(SYNPCC7002_A0076) Score=4.2 Pos=-97 [Synechococcus sp. PCC 7002]
AGTATTGAAATATACA
>SYNPCC7002_A2395(SYNPCC7002_A2395) Score=4.5 Pos=-200 [Synechococcus sp. PCC 7002]
TGTTACTTAAATTACA
>SYNPCC7002_A2395(SYNPCC7002_A2395) Score=4.5 Pos=-92 [Synechococcus sp. PCC 7002]
TGTAGTAGACGTTACA
>SYNPCC7002_A1954(SYNPCC7002_A1954) Score=4.7 Pos=-243 [Synechococcus sp. PCC 7002]
TGTAACAGGAGTTACA
>SYNPCC7002_A0643(cynS) Score=4.5 Pos=-237 [Synechococcus sp. PCC 7002]
CGTATCTTTAATTACA
>SYNPCC7002_A0860(cynA) Score=4.1 Pos=-221 [Synechococcus sp. PCC 7002]
TGTAATTGATTTAACA
>SYNPCC7002_A0582(gifA) Score=5 Pos=-96 [Synechococcus sp. PCC 7002]
TGTATCAAATTTTACA
>SYNPCC7002_A1630(glnA) Score=3.5 Pos=-125 [Synechococcus sp. PCC 7002]
TGTGACCCAGACTACA
>SYNPCC7002_A1827(nirA) Score=4 Pos=-111 [Synechococcus sp. PCC 7002]
CGTAGTTAACTACTACA
>SYNPCC7002_A0496(nrrA) Score=4.1 Pos=-75 [Synechococcus sp. PCC 7002]
CGTAACCACGGTTACA
>SYNPCC7002_A1675(ntcA) Score=3.9 Pos=-177 [Synechococcus sp. PCC 7002]
TGAAGCAAAAAGTACA
>SYNPCC7002_A1632(ntcB) Score=3.9 Pos=-87 [Synechococcus sp. PCC 7002]
TGTAACATCCGGAACA
>SYNPCC7002_A2101(SYNPCC7002_A2101) Score=5 Pos=67 [Synechococcus sp. PCC 7002]
TGTATCATTAATACA
>SYNPCC7002_A0264(SYNPCC7002_A0264) Score=5 Pos=-29 [Synechococcus sp. PCC 7002]
TGTATCAAATACTACA
>SYNPCC7002_A0398(urta) Score=4.1 Pos=-127 [Synechococcus sp. PCC 7002]
TGTATCAAGTGTACACA
>SYNPCC7002_A1443(nifJ) Score=4.1 Pos=-272 [Synechococcus sp. PCC 7002]
TTTATCATTTTCTACA
>sll0108(amt1) Score=4 Pos=-189 [Synechocystis sp. PCC 6803]
AGTAGTAAATCATACA
>sll0108(amt1) Score=4.4 Pos=-18 [Synechocystis sp. PCC 6803]
TGTAAGATTAAAGTACA
>ssr1562(SYNPCC7002_A0076) Score=4.5 Pos=-78 [Synechocystis sp. PCC 6803]
TGTAATCGATAATACA
>slr1147(SYNPCC7002_A1954) Score=4.7 Pos=-214 [Synechocystis sp. PCC 6803]
TGTAATGATAGTTACA
>ssl1911(gifA) Score=5 Pos=-89 [Synechocystis sp. PCC 6803]
TGTATAAAATGTTACA
>slr1756(glnA) Score=4.3 Pos=-98 [Synechocystis sp. PCC 6803]
GGTAGCGAAAAATACA
>ssl0707(glnB) Score=3.7 Pos=-184 [Synechocystis sp. PCC 6803]

GGTACTGATTTTACA
>slr0851(ndh) Score=4.1 Pos=-72 [Synechocystis sp. PCC 6803]
TGTAACAACCATTACC
>slr1450(nrtA) Score=3.9 Pos=-96 [Synechocystis sp. PCC 6803]
AGTTACAACTATACA
>slr0898(nirA) Score=4.7 Pos=-74 [Synechocystis sp. PCC 6803]
TGTAATTTACGTTACA
>slr1330(nrrA) Score=4.6 Pos=-75 [Synechocystis sp. PCC 6803]
GGTAACTGTTGTTACA
>slr0653(rpoD) Score=3.9 Pos=-246 [Synechocystis sp. PCC 6803]
TGTTATCGAGGCTACA
>slr1515(gifB) Score=4.2 Pos=-119 [Synechocystis sp. PCC 6803]
CGTAAAAATGGATACA
>slr0447(urtA) Score=4.5 Pos=-211 [Synechocystis sp. PCC 6803]
GGTATCCTATGCTACA
>slr0009(rbcL) Score=4.3 Pos=-228 [Synechocystis sp. PCC 6803]
TGTAATTTAAAAACA
>slr0741(nifJ) Score=3.3 Pos=-181 [Synechocystis sp. PCC 6803]
AGAATCAACAAAAACA
>slr1733(ndhD) Score=4 Pos=-252 [Synechocystis sp. PCC 6803]
TGTAACAATTTTGTAGT
>slr1732(ndhF) Score=4 Pos=-244 [Synechocystis sp. PCC 6803]
TGTAACAAATAACACT
>slr1712(hanA) Score=3.8 Pos=-264 [Synechocystis sp. PCC 6803]
GGTAGTTTTTGAAACT
>cce_3261(amt1) Score=3.5 Pos=-152 [Cyanothecce sp. ATCC 51142]
TGTTAAGGTTGTAACA
>cce_0537(SYNPCC7002_A0076) Score=4 Pos=-137 [Cyanothecce sp. ATCC 51142]
TGTAAACTATGATATA
>cce_0537(SYNPCC7002_A0076) Score=4.8 Pos=-93 [Cyanothecce sp. ATCC 51142]
TGTAGTCTTTGTTACA
>cce_4355(SYNPCC7002_A0077) Score=4.7 Pos=-172 [Cyanothecce sp. ATCC 51142]
TGTTACAATAGCTACA
>cce_2729(SYNPCC7002_A2395) Score=4 Pos=-148 [Cyanothecce sp. ATCC 51142]
TGTAACATATGATAAC
>cce_2729(SYNPCC7002_A2395) Score=4.6 Pos=-87 [Cyanothecce sp. ATCC 51142]
TGTAATATTGATTACA
>cce_3327(SYNPCC7002_A1954) Score=4.7 Pos=-210 [Cyanothecce sp. ATCC 51142]
TGTAGTCATAGTTACA
>cce_3327(SYNPCC7002_A1954) Score=4 Pos=-46 [Cyanothecce sp. ATCC 51142]
TTTATTTTCTGTTACA
>cce_3797(cce_3797) Score=4.9 Pos=-70 [Cyanothecce sp. ATCC 51142]
TGTAGCTTAATATACA
>cce_0259(gifA) Score=5.2 Pos=-95 [Cyanothecce sp. ATCC 51142]
TGTAGCAAATGTTACA
>cce_4432(glnA) Score=4.5 Pos=-89 [Cyanothecce sp. ATCC 51142]
AGTATCCAATTATACA
>cce_4432(glnA) Score=4 Pos=-30 [Cyanothecce sp. ATCC 51142]
TGTATATATTGAAACC
>cce_1063(hupS) Score=4.8 Pos=-204 [Cyanothecce sp. ATCC 51142]
TGTAATAATTAATACA
>cce_1063(hupS) Score=3.8 Pos=-159 [Cyanothecce sp. ATCC 51142]
GGTAATAATTAATAGA
>cce_0624(ndh) Score=4.7 Pos=-47 [Cyanothecce sp. ATCC 51142]
TGTAAGTGTAGTTACT

>cce_1223(nirA) Score=4.7 Pos=-76 [Cyanothecae sp. ATCC 51142]
 TGTTACATTAGCTACA
 >cce_1808(nrrA) Score=4.3 Pos=-76 [Cyanothecae sp. ATCC 51142]
 CGTAGCCGATGTTACA
 >cce_0198(nteB) Score=4.2 Pos=-73 [Cyanothecae sp. ATCC 51142]
 AGTATCAATTTCTACG
 >cce_3797(SYNPCC7002_A2101) Score=4.9 Pos=-70 [Cyanothecae sp. ATCC 51142]
 TGTAGCTTAATATACA
 >cce_0267(psbA3) Score=4.4 Pos=-58 [Cyanothecae sp. ATCC 51142]
 GGTAATCATTGATACA
 >cce_0875(rpoD) Score=4.3 Pos=-232 [Cyanothecae sp. ATCC 51142]
 AGTAATCAAGGCTACA
 >cce_2638(gifB) Score=5.2 Pos=-144 [Cyanothecae sp. ATCC 51142]
 TGTAACAATAGATACA
 >cce_1944(apcF) Score=3.8 Pos=-177 [Cyanothecae sp. ATCC 51142]
 TGTGATAAGAAATACA
 >cce_2390(trxQ) Score=3.7 Pos=-332 [Cyanothecae sp. ATCC 51142]
 AATAGCTATAATTACT
 >cce_3633(psbZ) Score=4.2 Pos=-20 [Cyanothecae sp. ATCC 51142]
 TGTAAGTGTATTAACA
 >cce_0953(nifJ) Score=3.8 Pos=-52 [Cyanothecae sp. ATCC 51142]
 TGCAACAAAAATTACC
 >PCC8801_1229(amt1) Score=5 Pos=-264 [Cyanothecae sp. PCC 8801]
 TGTATTTTTTGATACA
 >PCC8801_1229(amt1) Score=4.1 Pos=-229 [Cyanothecae sp. PCC 8801]
 AGTAATAAAAAAACA
 >PCC8801_3101(SYNPCC7002_A0076) Score=4.6 Pos=-95 [Cyanothecae sp. PCC 8801]
 TGTATTGGTTGTTACA
 >PCC8801_2066(SYNPCC7002_A2395) Score=4.8 Pos=-53 [Cyanothecae sp. PCC 8801]
 TGTAATATTAATTACA
 >PCC8801_3053(SYNPCC7002_A1954) Score=4.8 Pos=-198 [Cyanothecae sp. PCC 8801]
 TGTAATCATAGTTACA
 >PCC8801_3848(cce_3797) Score=5.1 Pos=-165 [Cyanothecae sp. PCC 8801]
 TGTAAGTTTAGATACA
 >PCC8801_2371(gifA) Score=4.9 Pos=-94 [Cyanothecae sp. PCC 8801]
 TGTATAAATTGCTACA
 >PCC8801_0808(glnA) Score=4 Pos=-92 [Cyanothecae sp. PCC 8801]
 CGTATCATGGTATACA
 >PCC8801_3212(hupS) Score=4.3 Pos=-127 [Cyanothecae sp. PCC 8801]
 TGTAACAACAATAACA
 >PCC8801_3485(ndh) Score=4.6 Pos=-117 [Cyanothecae sp. PCC 8801]
 TGTAACCATAGCTACT
 >PCC8801_3485(ndh) Score=3.8 Pos=-92 [Cyanothecae sp. PCC 8801]
 CGTAATTGGTTTTACA
 >PCC8801_4396(nrtA) Score=4.6 Pos=-184 [Cyanothecae sp. PCC 8801]
 TGTAAGCAAATAATACG
 >PCC8801_4396(nrtA) Score=3.9 Pos=-106 [Cyanothecae sp. PCC 8801]
 AGTATTTATAGACACA
 >PCC8801_2468(nirA) Score=4.6 Pos=-75 [Cyanothecae sp. PCC 8801]
 TGTTACAATTAATACA
 >PCC8801_2463(narB) Score=4.4 Pos=-165 [Cyanothecae sp. PCC 8801]
 TGTATTACCAAATACA
 >PCC8801_3375(nrrA) Score=4.5 Pos=-76 [Cyanothecae sp. PCC 8801]
 CGTAGCAGATGTTACA
 >PCC8801_2329(nteB) Score=4.7 Pos=-80 [Cyanothecae sp. PCC 8801]

TGTATCAAATTCTACT
 >PCC8801_3848(SYNPCC7002_A2101) Score=5.1 Pos=-165 [Cyanothecae sp. PCC 8801]
 TGTAACCTTAGATACA
 >PCC8801_3216(psbA3) Score=4.4 Pos=-59 [Cyanothecae sp. PCC 8801]
 AGTAGTTATTGCTACT
 >PCC8801_0154(rpoD) Score=4.4 Pos=-257 [Cyanothecae sp. PCC 8801]
 TGTAATCGAGGCTACA
 >PCC8801_0807(apcF) Score=4 Pos=-251 [Cyanothecae sp. PCC 8801]
 TGTATACCATGATACG
 >PCC8801_0870(fur) Score=3.4 Pos=-380 [Cyanothecae sp. PCC 8801]
 TGTTTATGCTAAAACA
 >PCC8801_0567(coxB) Score=3.8 Pos=-148 [Cyanothecae sp. PCC 8801]
 TTTATTATTTGTTACC
 >PCC8801_3918(nifJ) Score=3.5 Pos=-265 [Cyanothecae sp. PCC 8801]
 AGTAACCATAATTATT
 >PCC8801_4247(ndhF) Score=3.6 Pos=-238 [Cyanothecae sp. PCC 8801]
 CGTATTATGAGTTAGA
 >Cyan7425_0782(amt1) Score=4.4 Pos=-228 [Cyanothecae sp. PCC 7425]
 TGTATAACGTGATACA
 >Cyan7425_0729(SYNPCC7002_A0076) Score=4.3 Pos=-128 [Cyanothecae sp. PCC 7425]
 TGTAACATTTGTTATT
 >Cyan7425_0729(SYNPCC7002_A0076) Score=4.1 Pos=-71 [Cyanothecae sp. PCC 7425]
 AGTATTGGTGGATACA
 >Cyan7425_0833(SYNPCC7002_A2395) Score=3.7 Pos=-38 [Cyanothecae sp. PCC 7425]
 AGTAGTTTAATAAACT
 >Cyan7425_0732(ccc_3797) Score=5.2 Pos=-33 [Cyanothecae sp. PCC 7425]
 TGTATCATAAGCTACA
 >Cyan7425_1839(glnA) Score=4.9 Pos=-221 [Cyanothecae sp. PCC 7425]
 TGTAACATCATGATACA
 >Cyan7425_4042(Cyan7425_4042) Score=4.4 Pos=-151 [Cyanothecae sp. PCC 7425]
 AGTAGCTCGTGATACA
 >Cyan7425_4573(nirA) Score=4.5 Pos=-123 [Cyanothecae sp. PCC 7425]
 TGTAACCTAATATACC
 >Cyan7425_0851(nrrA) Score=4.1 Pos=-82 [Cyanothecae sp. PCC 7425]
 AGTAGCTAGAGTTACG
 >Cyan7425_0755(ntcA) Score=4.8 Pos=-173 [Cyanothecae sp. PCC 7425]
 TGTATCCGATGATACA
 >Cyan7425_1599(ntcB) Score=4.6 Pos=-78 [Cyanothecae sp. PCC 7425]
 TGTATCACTATCTACA
 >Cyan7425_0732(SYNPCC7002_A2101) Score=5.2 Pos=-33 [Cyanothecae sp. PCC 7425]
 TGTATCATAAGCTACA
 >Cyan7425_1838(apcF) Score=4.9 Pos=-281 [Cyanothecae sp. PCC 7425]
 TGTATCATGAGTTACA
 >Cyan7425_4369(nifJ) Score=3.1 Pos=-120 [Cyanothecae sp. PCC 7425]
 TCTAACGTATTCTCCA
 >Cyan7425_2260(urta) Score=3.7 Pos=-148 [Cyanothecae sp. PCC 7425]
 TGTATAATAGATCACA
 >Cyan7425_1393(gifB) Score=4.7 Pos=-158 [Cyanothecae sp. PCC 7425]
 GGTATCATATAATACA
 >MAE_62530(ica) Score=3.7 Pos=-30 [Microcystis aeruginosa NIES-843]
 CGTATAGATAAAATACT
 >MAE_40010(amt1) Score=4.6 Pos=-213 [Microcystis aeruginosa NIES-843]
 TGTATCAACGAATACA
 >MAE_39690(SYNPCC7002_A0076) Score=4.3 Pos=-99 [Microcystis aeruginosa NIES-843]
 TGTAATCGTCGATACA

>MAE_38700(SYNPCC7002_A2395) Score=4.2 Pos=-87 [Microcystis aeruginosa NIES-843]
 TGTAATCATCTTTACA
 >MAE_14410(SYNPCC7002_A1954) Score=3.7 Pos=-75 [Microcystis aeruginosa NIES-843]
 TGTAAACTGGGAAACA
 >MAE_14840(ccc_3797) Score=4.9 Pos=-38 [Microcystis aeruginosa NIES-843]
 TGTAAATTTAGATACA
 >MAE_49490(gifA) Score=4.9 Pos=-42 [Microcystis aeruginosa NIES-843]
 TGTAAAAATAGATACA
 >MAE_19270(glnA) Score=4.7 Pos=-92 [Microcystis aeruginosa NIES-843]
 TGTATCGAAAAATACA
 >MAE_09050(glnN) Score=4.7 Pos=-244 [Microcystis aeruginosa NIES-843]
 TGTAATGTTTGATACA
 >MAE_18410(nirA) Score=4.1 Pos=-190 [Microcystis aeruginosa NIES-843]
 TGTTACAGACAATACA
 >MAE_14810(MAE_14810) Score=4.2 Pos=-177 [Microcystis aeruginosa NIES-843]
 TGTAACAATCTATACG
 >MAE_53960(narB) Score=4.8 Pos=-88 [Microcystis aeruginosa NIES-843]
 TGTATTAATAACTACA
 >MAE_09380(ntcB) Score=4.1 Pos=-80 [Microcystis aeruginosa NIES-843]
 GGTAGCAATTTCTACC
 >MAE_14840(SYNPCC7002_A2101) Score=4.9 Pos=-38 [Microcystis aeruginosa NIES-843]
 TGTAAATTTAGATACA
 >MAE_54470(rpoD) Score=4.9 Pos=-126 [Microcystis aeruginosa NIES-843]
 TGTAATTAAAGCTACA
 >MAE_18580(SYNPCC7002_A0264) Score=4.8 Pos=-68 [Microcystis aeruginosa NIES-843]
 TGTATCTTTAGCTACT
 >MAE_06220(urta) Score=4.6 Pos=-140 [Microcystis aeruginosa NIES-843]
 AGTAGCGAAAGTTACA
 >MAE_06180(urte) Score=3.8 Pos=-8 [Microcystis aeruginosa NIES-843]
 GGTTGACAATGTTACA
 >MAE_37080(fur) Score=3.7 Pos=-118 [Microcystis aeruginosa NIES-843]
 AGTAATTTTTCATACT
 >MAE_22930(coxB) Score=3.8 Pos=-141 [Microcystis aeruginosa NIES-843]
 AGTTATTTTAAATACT
 >MAE_06220(urta) Score=4.7 Pos=-170 [Microcystis aeruginosa NIES-843]
 AGTAGCAAAAATTACA
 >all4968(gor) Score=4.1 Pos=-48 [Nostoc sp. PCC 7120]
 AATAACAACCTGTTACA
 >alr1827(ica) Score=3.4 Pos=-6 [Nostoc sp. PCC 7120]
 TGAAATATGTACAACA
 >alr0992(amt1) Score=4.7 Pos=-50 [Nostoc sp. PCC 7120]
 TGTAACCTAAGTATACA
 >alr0990(amt1) Score=4.7 Pos=-250 [Nostoc sp. PCC 7120]
 TGTATTAACCTAATACA
 >asr0064(SYNPCC7002_A0076) Score=3.7 Pos=-107 [Nostoc sp. PCC 7120]
 CGTATAGCAAAAATACA
 >alr4308(SYNPCC7002_A2395) Score=3.9 Pos=-64 [Nostoc sp. PCC 7120]
 GGTAGTCGGAGTTACA
 >alr3982(SYNPCC7002_A1954) Score=4.6 Pos=-250 [Nostoc sp. PCC 7120]
 TGTAGTGATAGCTACA
 >asl2329(gifA) Score=4.7 Pos=-78 [Nostoc sp. PCC 7120]
 CGTAGCATAAGATACA
 >alr2328(glnA) Score=4.8 Pos=-142 [Nostoc sp. PCC 7120]
 TGTAACAAAGACTACA
 >all2319(glnB) Score=3.8 Pos=-214 [Nostoc sp. PCC 7120]

AGTTACACAGACTACA
 >all1127(ndh) Score=4.7 Pos=-146 [Nostoc sp. PCC 7120]
 TGTAGCTTAAATTACT
 >all4312(nrrA) Score=4.5 Pos=-75 [Nostoc sp. PCC 7120]
 AGTAACAAAGACTACA
 >alr4392(ntcA) Score=3.7 Pos=-151 [Nostoc sp. PCC 7120]
 GGTATCATTATGAACA
 >alr4392(ntcA) Score=3.7 Pos=-111 [Nostoc sp. PCC 7120]
 AGTATAGGAAAGTACA
 >all0602(ntcB) Score=4.5 Pos=-80 [Nostoc sp. PCC 7120]
 TGTAACAAAATCTACC
 >all0602(ntcB) Score=4.7 Pos=-21 [Nostoc sp. PCC 7120]
 TGTAATTAAGGCTACA
 >all1327(SYNPCC7002_A0264) Score=4.3 Pos=-52 [Nostoc sp. PCC 7120]
 CGTAGTGTATGTTACA
 >all2327(apcF) Score=4.8 Pos=-233 [Nostoc sp. PCC 7120]
 TGTAGTCTTTGTTACA
 >all1691(fur) Score=4.1 Pos=-218 [Nostoc sp. PCC 7120]
 TGTAGCTTGAGATTCA
 >alr1690(alr1690) Score=3.6 Pos=-91 [Nostoc sp. PCC 7120]
 TGTGAATATAGAAACA
 >alr2514(coxB) Score=3.5 Pos=-291 [Nostoc sp. PCC 7120]
 AGAAGTAGAAGCTACT
 >all4001(isiA) Score=3.7 Pos=-37 [Nostoc sp. PCC 7120]
 AGTATTTCTGGCAACA
 >alr1524(rbcL) Score=3.6 Pos=-32 [Nostoc sp. PCC 7120]
 AGTAAAAAGAGTGACA
 >alr4344(gltS) Score=3.5 Pos=-265 [Nostoc sp. PCC 7120]
 TGGAAAAATTAAAACA
 >all1258(psbZ) Score=3.4 Pos=-161 [Nostoc sp. PCC 7120]
 TGTTACAAAAATTAGG
 >alr1911(nifJ) Score=3.2 Pos=-281 [Nostoc sp. PCC 7120]
 TGAATTTGATGTAACC
 >alr4156(ndhF) Score=4 Pos=-260 [Nostoc sp. PCC 7120]
 TGTCTTATAAAATACA
 >alr0052(trxA) Score=3.7 Pos=17 [Nostoc sp. PCC 7120]
 AGTTACAGATTCTACT
 >asr3935(hanA) Score=3.6 Pos=-279 [Nostoc sp. PCC 7120]
 GGTATTTTTTCCTACT
 >all1951(urtA) Score=4.3 Pos=-116 [Nostoc sp. PCC 7120]
 AGTATCAAAAATAACA
 >Tery_4477(amt1) Score=4.9 Pos=-83 [Trichodesmium erythraeum IMS101]
 AGTAGCATTTGATACA
 >Tery_2891(SYNPCC7002_A0076) Score=4.1 Pos=-191 [Trichodesmium erythraeum IMS101]
 TGTAATTTAGACAACA
 >Tery_2891(SYNPCC7002_A0076) Score=4.6 Pos=-110 [Trichodesmium erythraeum IMS101]
 TGTAACATATATACT
 >Tery_0672(SYNPCC7002_A2395) Score=4.3 Pos=-94 [Trichodesmium erythraeum IMS101]
 AGTATTCAAAAATTACA
 >Tery_3912(SYNPCC7002_A1954) Score=4.3 Pos=-156 [Trichodesmium erythraeum IMS101]
 TGTAGTTATGGCTACC
 >Tery_3834(glnA) Score=4 Pos=-250 [Trichodesmium erythraeum IMS101]
 CGTAACACCCGATACA
 >Tery_3369(hupS) Score=4.3 Pos=-188 [Trichodesmium erythraeum IMS101]
 AGTATCAAAAATAACA

>Tery_3368(hupL) Score=4.1 Pos=-64 [Trichodesmium erythraeum IMS101]
 TGTAGCTACTGATAAA
 >Tery_1068(nirA) Score=3.8 Pos=-276 [Trichodesmium erythraeum IMS101]
 TGTATTTTTATATAGT
 >Tery_1068(nirA) Score=4.1 Pos=-199 [Trichodesmium erythraeum IMS101]
 TGTTATATAAGCTACG
 >Tery_0675(nrrA) Score=4.7 Pos=-89 [Trichodesmium erythraeum IMS101]
 AGTAGCTTCTGTTACA
 >Tery_4333(ntcB) Score=4 Pos=-27 [Trichodesmium erythraeum IMS101]
 TGTATAAAATAACACA
 >Tery_5068(rpoD) Score=4 Pos=-199 [Trichodesmium erythraeum IMS101]
 TGTAAAATTTTGTACC
 >Tery_5068(rpoD) Score=3.7 Pos=-46 [Trichodesmium erythraeum IMS101]
 TGTAAAATAATTTATT
 >Tery_3029(gifB) Score=3.8 Pos=-349 [Trichodesmium erythraeum IMS101]
 TGTATCTGATGTTAGG
 >Tery_1958(fur) Score=3.5 Pos=-40 [Trichodesmium erythraeum IMS101]
 TGTATCATTGTCAATA
 >Tery_4410(rbcL) Score=3.4 Pos=-293 [Trichodesmium erythraeum IMS101]
 GATAACTATTACTACG
 >Tery_1667(isiA) Score=3.6 Pos=-134 [Trichodesmium erythraeum IMS101]
 AGTAATTGATCATACT
 >Tery_0466(gltS) Score=4.2 Pos=-228 [Trichodesmium erythraeum IMS101]
 TGTATCCTAGGCAACA
 >Tery_0130(urtA) Score=3.8 Pos=-390 [Trichodesmium erythraeum IMS101]
 AGTTACAAAAAAACA
 >Tery_4747(gor) Score=3.9 Pos=-208 [Trichodesmium erythraeum IMS101]
 TGTAGTCGTAGATATA
 >Tery_4747(gor) Score=4.7 Pos=-120 [Trichodesmium erythraeum IMS101]
 TGTAACATAATTATACT
 >Synpcc7942_0442(amt1) Score=4.1 Pos=-151 [Synechococcus elongatus PCC 7942]
 TGTTACATCGATTACA
 >Synpcc7942_1845(cce_3797) Score=4.3 Pos=-27 [Synechococcus elongatus PCC 7942]
 TGTATCCGTTGCTACC
 >Synpcc7942_2107(cynA) Score=4.4 Pos=-67 [Synechococcus elongatus PCC 7942]
 TGTAACGACGGCTACA
 >Synpcc7942_2156(glnA) Score=4.8 Pos=-194 [Synechococcus elongatus PCC 7942]
 TGTATCAGCTGTTACA
 >Synpcc7942_0321(glnB) Score=4.8 Pos=-103 [Synechococcus elongatus PCC 7942]
 TGTAGCAGTAACTACA
 >Synpcc7942_1240(nirA) Score=4.9 Pos=-220 [Synechococcus elongatus PCC 7942]
 TGTAGCAATTGCTACT
 >Synpcc7942_1240(nirA) Score=4.3 Pos=-149 [Synechococcus elongatus PCC 7942]
 AGTATCAATGATTACT
 >Synpcc7942_1240(nirA) Score=4.4 Pos=-80 [Synechococcus elongatus PCC 7942]
 TGTAGTTTCTGTTACC
 >Synpcc7942_0127(ntcA) Score=4.7 Pos=-157 [Synechococcus elongatus PCC 7942]
 AGTAGCAGTTGCTACA
 >Synpcc7942_1241(nirB) Score=4.3 Pos=-153 [Synechococcus elongatus PCC 7942]
 AGTAATCATTGATACT
 >Synpcc7942_1241(nirB) Score=4.9 Pos=-82 [Synechococcus elongatus PCC 7942]
 AGTAGCAATTGCTACA
 >Synpcc7942_1845(SYNPCC7002_A2101) Score=4.3 Pos=-27 [Synechococcus elongatus PCC 7942]
 TGTATCCGTTGCTACC

>Synpcc7942_2158(apcF) Score=4.8 Pos=-214 [Synechococcus elongatus PCC 7942]
 TGTAACAGCTGATACA
 >PMT1853(amt1) Score=3.8 Pos=-160 [Prochlorococcus marinus str. MIT 9313]
 TGTAACAAAATGAACT
 >PMT0601(glnA) Score=4.2 Pos=-79 [Prochlorococcus marinus str. MIT 9313]
 GGTACCTGTTGCTACA
 >PMT2229(urtA) Score=4 Pos=-146 [Prochlorococcus marinus str. MIT 9313]
 TGTTGCAACAGCTACC
 >PMT2229(urtA) Score=4.7 Pos=-95 [Prochlorococcus marinus str. MIT 9313]
 TGTATCATTCACCTACA
 >CYA_0030(fur) Score=3.6 Pos=-66 [Synechococcus sp. JA-3-3Ab]
 GCTATTATCAATTACA
 >CYA_0570(SYNPCC7002_A2395) Score=3.9 Pos=-139 [Synechococcus sp. JA-3-3Ab]
 GGTAAGATAAAAATACA
 >CYA_0570(SYNPCC7002_A2395) Score=4.2 Pos=-81 [Synechococcus sp. JA-3-3Ab]
 CGTATCAAAGGCTACT
 >CYA_1363(glnA) Score=4.3 Pos=-138 [Synechococcus sp. JA-3-3Ab]
 CGTATCAGAACTACA
 >CYA_1508(glnB) Score=4.5 Pos=-74 [Synechococcus sp. JA-3-3Ab]
 TGTATCCGTTTTTACA
 >CYA_0612(nirA) Score=3.9 Pos=-72 [Synechococcus sp. JA-3-3Ab]
 TGTAAGTCCAATACC
 >CYA_1799(ntcA) Score=4.7 Pos=-181 [Synechococcus sp. JA-3-3Ab]
 TGTAGCTCCTGCTACA
 >CYA_0984(ntcB) Score=4.2 Pos=-89 [Synechococcus sp. JA-3-3Ab]
 TGTAACGGTGTTTACA
 >CYA_1920(urtE) Score=3.9 Pos=-248 [Synechococcus sp. JA-3-3Ab]
 AGAAACAGAAGCTACA
 >CYA_1924(urtA) Score=3.7 Pos=-272 [Synechococcus sp. JA-3-3Ab]
 GGTATCCCGCGATACA
 >SYNW0253(amt1) Score=4.2 Pos=-100 [Synechococcus sp. WH 8102]
 TGTATCAATTAACACA
 >SYNW0246(SYNPCC7002_A1954) Score=4.1 Pos=-143 [Synechococcus sp. WH 8102]
 TGTAACTTTGGTTGCA
 >SYNW2487(cynA) Score=4.1 Pos=-103 [Synechococcus sp. WH 8102]
 TGTAGCAAGTGAGACA
 >SYNW2487(cynA) Score=4.5 Pos=-66 [Synechococcus sp. WH 8102]
 AGTATCACCTGATACA
 >SYNW2442(urtA) Score=4 Pos=-118 [Synechococcus sp. WH 8102]
 TGTTGCAACAGCTACC
 >gvip146(glnA) Score=4 Pos=-116 [Gloeobacter violaceus PCC 7421]
 CGTATCTCAGACTACA
 >gvip212(nirA) Score=4 Pos=-146 [Gloeobacter violaceus PCC 7421]
 TGTATCTGGGGTTACG
 >gvip454(ntcA) Score=3.9 Pos=-77 [Gloeobacter violaceus PCC 7421]
 AGTAGTCCCTAATACA
 >gvip213(ntcB) Score=4 Pos=-46 [Gloeobacter violaceus PCC 7421]
 CGTAACCCAGATACA
 >glr3304(fur) Score=3.9 Pos=-116 [Gloeobacter violaceus PCC 7421]
 TGTAACAAATTGTAGA
 >gl10880(trxA) Score=3.6 Pos=-379 [Gloeobacter violaceus PCC 7421]
 TGTATCTAGAACTAGC
 >null(gifB) Score=4.4 Pos=-175 [Thermosynechococcus elongatus BP-1]
 TGTTAAATTAGATACA
 >amt1(amt1) Score=4.4 Pos=-190 [Thermosynechococcus elongatus BP-1]

TGTATAACGTGATACA
 >tsr2448(SYNPCC7002_A0076) Score=4.1 Pos=-63 [Thermosynechococcus elongatus BP-1]
 AGTATTGGATATTACA
 >tlr1468(SYNPCC7002_A2395) Score=4.3 Pos=-85 [Thermosynechococcus elongatus BP-1]
 TGTAGTTGAGTTTACA
 >tlr0194(tlr0194) Score=4.2 Pos=-111 [Thermosynechococcus elongatus BP-1]
 TGTAACCTATCTTACA
 >tlr0591(glnB) Score=5.1 Pos=-80 [Thermosynechococcus elongatus BP-1]
 TGTAGCTATTGCTACA
 >tlr1349(nirA) Score=4.6 Pos=-82 [Thermosynechococcus elongatus BP-1]
 AGTAGCAAAATTTACA
 >tlr1330(nrrA) Score=4 Pos=-138 [Thermosynechococcus elongatus BP-1]
 AGTATTATTCGTTACG
 >null(ntcB) Score=3.9 Pos=-122 [Thermosynechococcus elongatus BP-1]
 TGTATCAATCAACACA
 >tlr1120(urtA) Score=4 Pos=-81 [Thermosynechococcus elongatus BP-1]
 TGTAGCCTAGCATACA
 >tlr2286(trxQ) Score=4 Pos=-130 [Thermosynechococcus elongatus BP-1]
 AGTAGCAATGACAACA
 >null(isiA) Score=3.8 Pos=-195 [Thermosynechococcus elongatus BP-1]
 AGTTTCTGGAAATACA
 >null(ndhF) Score=3.6 Pos=-220 [Thermosynechococcus elongatus BP-1]
 GGTAACTTTTGCTATG
 >null(gifB) Score=4.4 Pos=-146 [Thermosynechococcus elongatus BP-1]
 TGTTAAATTAGATACA

Supplementary position frequency matrix (PFM 1) for PHO boxes in cyanobacteria:

A: 20	10	4	61	66	21	14	23	0	0	0	7
	18	3	43	61	24	4	16	0	0	0	12
	6	2	49	63	17	11	16				
C: 20	1	0	0	1	28	42	8	0	0	0	28
	2	2	0	1	30	38	6	0	0	0	34
	5	3	3	0	36	31	11				
G: 14	1	0	4	4	6	5	2	0	0	0	22
	1	1	2	7	2	7	4	0	0	0	18
	0	0	3	6	6	2	2				
N: 0	0	0	0	0	0	0	0	77	77	77	0
	0	0	0	0	0	0	0	77	77	77	0
	0	0	0	0	0	0	0				
T: 23	65	73	12	6	22	16	44	0	0	0	20
	56	71	32	8	21	28	51	0	0	0	13
	66	72	22	8	18	33	48				

Supplementary position frequency matrix (PFM 2) for Fur boxes in cyanobacteria:

A: 100	29	3	45	101	34	134	129	64	58	92	21
	13	26	11	26	147	127	18				
C: 1	5	1	4	18	9	8	1	6	18	2	18
	0	38	5	63	0	1	30				
G: 22	3	0	67	10	52	2	2	0	7	2	10
	2	10	41	2	4	25	2				
T: 44	130	163	51	38	72	23	35	97	84	71	118
	152	93	110	76	16	14	117				

Supplementary position frequency matrix (PFM 3) for NtcA boxes in cyanobacteria:

A: 47	3	6	201	99	29	108	94	90	88	71	88
	27	225	2	168							
C: 18	2	1	1	2	131	36	18	28	16	6	61
	7	1	211	19							
G: 20	220	1	3	52	1	19	43	21	33	113	8
	2	1	8	12							
T: 143	3	220	23	75	67	65	73	89	91	38	71
	192	1	7	29							

Supplementary Table 2. Pho regulon prediction. PHO boxes sequences, their position in the genome, orientation, the genes that are controlling (the Pho regulon), locus tag from these genes, the distance of the box from the gene and the gen function from single-letter of functional (COGs) are presented.

PHO boxes sequences	Position	Orientation	Pho regulon (genes)	Locus_tag	Distance	COG
GATATCCTTAACATAATTCTAATAAC TT	37692	(+)	AbgT family transporter	PCC7418_RS00155	-342	H
TTTAATTTATCCTAGTTAGGCTTAA GT	41629	(+)	serine hydrolase-HP-ABC transporter ATP-binding protein/permease	PCC7418_RS00180/RS00185/RS00190	-145	V, S, S
AATAAACTTAATTAAAGCCATCTTAAC CT	48034	(+)	PstS family phosphate ABC transporter substrate-binding protein (<i>pstS</i>)	PCC7418_RS00210	-51	P
AAGAAATAATGTGTTAAAGTTAATATA AT	54813	(-)	PAS domain-containing protein response regulator	PCC7418_RS00225/RS00230	-315	T, T
GAGTAAACCAAAGGCTAAATTAACAAT ATT	59558	(-)	thioredoxin	PCC7418_RS00250	-262	O
TCCTAAAGTTACAGTTAATGAAAGATTA TA	61353	(-)	mechanosensitive ion channel	PCC7418_RS00255	-316	M
GAGTTATCGGAAGAAAAAGATGAGTAT AAT	63341	(-)	recombination protein RecR- tetra-tryptophan repeat protein	PCC7418_RS00265/RS00270	-47	S, L
ATTTAATTACTTAGAACTCTGCTTAAC AA	73689	(+)	IS200/IS605 family element transposase accessory protein (<i>tnpB</i>)	PCC7418_RS00335	-175	L
TTTAAACTCAGCATTATCTTTAGATTTG AC	119529	(+)	RMD1 family protein-hypothetical protein (HP)-asparagine synthase	PCC7418_RS00490/RS00495/RS00500	-519	S, S, L, E
TTTAGCCTCTTCTTACCCTTTTTTAAC AA	163587	(+)	universal stress protein	PCC7418_RS00715	-112	T
TTTTGTGTTACTTTAACCTTCCTTTTAG CA	168098	(+)	ABC transporter substrate binding protein	PCC7418_RS00750	+34	G
AATTTAAAATGAAATTATGCAATCAAAA AT	187427	(-)	HP-glycoside hydrolase	PCC7418_RS00830/RS00835	-221	G, S
AATTAAACCTAAAATAGTTTCAAGGATA AT	192110	(-)	transposase	PCC7418_RS00850	-615	S
TCATTAAGTTTTTGTAAAGGAAGGTTA TC	193598	(-)	phosphoribosylformylglycinamide cyclo-ligase	PCC7418_RS00865	-47	F
ATTAAGTTTTTGTAAAGGAAGGTATC AT	193600	(+)	septal ring lytic transglycosylase RlpA family protein	PCC7418_RS00870	-256	M
TTGTAAGGCAGAATCAAAATTCAGTTT ATC	226059	(-)	HP	PCC7418_RS01010	-253	O
CTTAATGTGATTTAAATACCATTTAAG TT	226508	(+)	HP	PCC7418_RS01025	-223	S
TTTAATATTAGTTTAATATTAGTTTAAG TA	227609	(+)	NifH like leader peptide family natural product precursor	PCC7418_RS01030	-115	S

CTTAGCCCCAGCTTTAGTTAATATTAATAC	299142	(+)	archease RtcB family protein-phosphoribosyltransferase	PCC7418_0261/RS01330/RS01335	-274	S, L, S
GTTTACTTAATTTTTATTACAAAATAAGAT	323385	(+)	B12-binding domain-containing radical SAM protein	PCC7418_RS01445	-99	C
AATTTAAGACCTAGTAATCAACACGAAATT	345451	(-)	iron uptake porin	PCC7418_RS01525	-15	M
TTTAGTAATCGCTTAACCTTTTCTTAAC TT	351477	(+)	thylakoid membrane photosystem I accumulation factor	PCC7418_RS01570	-439	CO
GTTTATCAACTTTTTACATAAGATTTAGCA	362063	(+)	NAD(P)H dependent glycerol 3 phosphate dehydrogenase	PCC7418_RS01620	-78	I
AGTCAAAAAAATATTAAATCAATCATTAT	362100	(-)	NUDIX hydrolase	PCC7418_RS01615	-293	F
ATTAACCTTTTTAATATCAGAGTATAATCA	397041	(+)	HP-NblA/ycf18 family protein	PCC7418_RS01780/RS01785	-106	S, S
ATTATTTTAATGTTTTTCAGTCTTTTTAT TT	402390	(+)	3-isopropylmalate dehydrogenase (<i>leuB</i>)	PCC7418_RS01815	-308	CE
AGATTAAGCCAATTTATGAAGAGGTTAAA	435783	(-)	bifunctional aminoglycoside phosphotransferase ATP binding protein	PCC7418_RS01975	-39	S
TTTTATTTATATTTACACTGCCTTTAACGA	440704	(+)	trypsin-like peptidase domain containing protein	PCC7418_RS02005	-238	O
AATTAAGTTATGATAAAAGCGATCTTAA	449261	(-)	SIMPL domain containing protein	PCC7418_RS02035	-714	S
AGGTTAAATATGGTTCAAAAACTATTCAA	449976	(-)	uroporphyrinogen III C-methyltransferase	PCC7418_RS02045	0	H
GTTTAAGTTTCGATAAAATTCGTTATCAT	456308	(+)	phosphomannose isomerase type II C-terminal cupin domain-lecithin retinol acyltransferase family protein	PCC7418_RS02090/RS02095	-115	G, KT
AAATGAAGAAGAAATTATGCTGATGCCAAA	456629	(-)	branched-chain amino acid ABC transporter permease	PCC7418_RS02085	-325	E
AAGTAAAGTCTTTTTAATAAAAAATTTAATA	524155	(-)	response regulator-HP	PCC7418_RS02385/PCC7418_RS19225	-356	T, S
AATTCAACAAAATTATAAGGAGGGGTTAAA	543130	(-)	gas vesicle protein GvpG	PCC7418_RS02455	-185	S
GAATGAATTAAAAGATTAATTTCTTTTAAAC	547534	(-)	gas vesicle structural protein GvpA (<i>gvpA</i>)-HP-gas vesicle protein GvpN/gas vesicle protein (<i>gvpN</i>)-HP-HP-gas vesicle protein K (<i>gvpK</i>)-GvpL /GvpF family gas vesicle protein (<i>gvpL/gvpF</i>)	PCC7418_RS02490/RS02485/RS02480/RS02475/RS02470/RS02465/RS02460	-103	S, S, S, S, S, J, S
AATGAATTAAAGATTAATTTCTTTTAAACT	547535	(+)	GvpL/GvpF family gas vesicle protein (<i>gvpL/gvpF</i>)	PCC7418_RS02495	-196	S
TTATGAAAAAATAATTAACAAAAGATAAAT	550498	(-)	histidine phosphatase family protein-glucokinase	PCC7418_RS02510/RS02505	-11	G, G
GAGTTAGAGGATGGTTATAAACATATAAAG	599343	(-)	(2Fe-2S) binding protein	PCC7418_RS02740	-365	C

ATTAAATCCGATCAATCTAAAAATAAGTT	609687	(+)	ferredoxin nitrite reductase	PCC7418_RS02810	+11	C
TATGATTTTCAATTTAACTGTACCTATCTT	612817	(+)	UDP-N-acetylmuramoyl tripeptide D-alanyl-D-alanine ligase	PCC7418_RS02820	-1	M
TTTTCAATTCTTCTTAAAAACCTGATTAC	641750	(-)	Ig like domain containing protein	PCC7418_RS02875	-148	S
TTTTACTGAATTTTAATTTAAACTTAGAAC	657612	(+)	ABC transporter ATP binding protein	PCC7418_RS02955	-191	V
TAATTTATATCTTTTAAAGGTTATTTTAAG	675681	(-)	CAP domain-containing protein	PCC7418_RS19240	-284	Q
TTTACCTGAATTTGTTTAAACCTTAAGTC	677077	(+)	Uma2 family endonuclease-Uma2 family endonuclease	PCC7418_RS03075/RS03080	-73	S, S
TGGCTATCTTTATGTTATAATGATTTTAC	683216	(-)	Response regulator	PCC7418_RS03100	-432	T
AATTATCTTCAGTTTAGTTACGCTAATCT	728680	(+)	heme oxygenase (biliverdin-producing)	PCC7418_RS03280	-101	C
ATGAAAAACGTTAGATAAAAAACAATTTAAA	739128	(-)	YvcK family protein	PCC7418_RS03330	-60	S
ATTTAATTAAATTTACAATTGATTTAAATT	766012	(+)	CRISPR associated endoribonuclease Cas6-CRISPR associated protein Cas4 type I D-CRISPR associated endonuclease Cas1-CRISPR associated endonuclease Cas2	PCC7418_RS03470/RS03475/RS03480/RS03485	-264	S, L, L, L
CGTAAACTAAGCATAGTTTGATCTTAATCC	787591	(+)	WYL domain containing protein	PCC7418_RS03530	-80	K
AGGCAAGGAGGAGATAAAAGCATGATCAAA	801527	(-)	LD carboxypeptidase	PCC7418_RS03590	-7	V
TTTAATGAGTGGTTTAAATTCAGTTGATTT	805778	(+)	UDP-N-acetylmuramate L-alanine ligase-UDP-N-acetylmuramate dehydrogenase	PCC7418_RS03620/RS03625	-3	M, M
TTTAATACTTGGTTAGTTCAAGATTATCTT	814733	(+)	glutathione S-transferase family protein	PCC7418_RS03660	-664	O
TTTAATAAACTTAAAAATTGTTATTTACAT	826909	(+)	tRNA (uridine(34)/cytosine(34)/5-carboxymethylaminomethyluridine(34)-2'-O) methyltransferase TrmL (<i>trmL</i>)	PCC7418_RS03720	-52	J
TATTAAATAATAGATCAAAATGAATTTTAT	832833	(-)	carotenoid biosynthesis protein	PCC7418_RS03740	-19	S
TGGTTAGTGAGTGATTAAACAATGGTTAGT	890284	(-)	precorrin 8X methylmutase	PCC7418_RS04085	-190	HK
GAATTAAGGAACATTTAACTTTTGTCAA	898154	(-)	FeoA domain-containing protein (<i>feoA</i>)-Fe(2+) transporter permease subunit FeoB (<i>feoB</i>)	PCC7418_RS04115/RS04120	-240	P, P
AAATAATGCTAAGATTATTATAACATAAA	938858	(-)	IS200/IS605 family element transposase accessoryprotein TnpB (<i>mpB</i>)	PCC7418_RS04310	-16	L

GTAAATCAAGTTTTACGAATGATTTAG AT	939282	(+)	MFS transporter	PCC7418_RS04315	-19	G
TTTAATCCCCTGTTTATGGTAACTTTAG AA	953364	(+)	fused MFS/spermidine synthase	PCC7418_RS04390	-35	H
ATTAACATCAATTAATAATAGCATTTGC TC	955972	(+)	methyltransferase domain- containing protein	PCC7418_RS04410	-27	Q
AGGTAAAGGCGAAAAATAAACTCATTCC AAG	957937	(-)	ABC transporter ATP-binding protein	PCC7418_RS04415	-268	P
GAGTAAACGTTAAGCAAAAATCACATT AAT	961001	(-)	ABC transporter substrate binding protein-sugar ABC transporter permease arbohydrate ABC transporter permease	PCC7418_RS04430/RS04425/RS04420	-131	G, P, P
AGCAAAACCATAAGCAATGGGCAAGTT AAA	964557	(-)	ATP-grasp domain containing protein	PCC7418_RS04445	-352	F
GATTACCACTCGTTAAATTGGTAATAAC AC	970920	(+)	membrane protein insertase YidC- nucleic acid binding protein	PCC7418_RS04500/RS04505	-105	S, U
TTTTTAATATAAAATTAATCAATAGTTA AC	1018379	(-)	DNA starvation/stationary phase protection protein	PCC7418_RS04685	-122	P
GAAAGTTAAAAGTTAACCATTCTTAAC TT	1047914	(+)	glycosyltransferase family 4 protein-amylo alpha 1,6-glucosidase	PCC7418_RS04835/RS04840	-439	M, G
ATCTTAAATTAAGGTTTAAATGAATTTT AA	1071732	(-)	solaneyl diphosphate synthase	PCC7418_RS04940	-313	H
CTTAAGATAAGATTAGTCAGTAATTAAT CC	1072305	(+)	uracil-DNA glycosylase	PCC7418_RS04945	-506	L
CTTATACTAATTTTTTCAAAAGTTTATC CT	1132472	(+)	Uma2 family endonuclease	PCC7418_RS05220	-136	S
AGATTATGGGCTGGTTGACAACATATC AAG	1132816	(-)	phycobilisome rod core linker polypeptide	PCC7418_RS05215	-356	G
ATAAATATTATTATAAAATTAACCTCAAA AT	1170761	(+)	circadian clock protein KaiC- polyphosphate kinase I	PCC7418_RS05365/PCC7418_RS05370	-10	F, P
TTTACCATGGCTATGAATTAACCTTAAC CA	1175011	(+)	MogA/MoaB family molybdenum cofactor biosynthesis protein	PCC7418_RS05380	-145	H
AAGTTAAGAGTGACTTGATCGGGGTTT AAA	1196246	(-)	HlyD family type I secretion periplasmic adaptor subunit	PCC7418_RS05475	-191	M
TTTAAATATCTTTTTTATTCTATTTTAA T	1234207	(+)	L-aspartate oxidase (<i>nadB</i>)	PCC7418_RS05635	-202	H
ATTAATCTCCTAATTATCAACACATCAC TA	1249518	(+)	tRNA (adenosine(37)-N6)- threonylcarbamoyltransferase complex transferase subunit (<i>tsaD</i>)	PCC7418_RS05715	-681	J
TGATTGAGGAGAATTTAAATCAATGTC AAT	1261043	(-)	arsenate reductase, glutathione/glutaredoxin type (<i>arsC</i>)-arsenical resistance protein (<i>arsH</i>)	PCC7418_RS05760/RS05755	-346	T, S
ATTAAACTGCTCATAAGGAAACGTAAA TTT	1360953	(+)	acyl-CoA desaturase	PCC7418_RS06160	-88	I
AAATAATGCTAAGATTATTATAACATAA A	1366037	(-)	IS200/IS605 family element transposase accessory protein TnpB (<i>impB</i>)	-	-15	S

AATTAAAAATAGGAATAAACTAAGCT AAT	1371373	(-)	tetratricopeptide repeat protein	PCC7418_RS06205	-12	S
TTAGAAAAAGAGTTAAATTCTCGTTAAA AT	1375855	(+)	TIGR04282 family arsenosugar biosynthesis glycosyltransferase	PCC7418_RS06240	-215	S
GTTATTTTGTTCCTTTGTGGCTGTTAAT CA	1425334	(+)	transposase	PCC7418_RS06495	-115	S
GTTAATCAACTTTTTACATAAGATTAG AA	1439381	(+)	CRISPR associated endonuclease Cas1-CRISPR associated endonuclease Cas2	PCC7418_RS06595/RS06600	-501	L, L
TGATAACAATAGGTAAAGTAAGGACT TAC	1558203	(-)	type I restriction endonuclease subunit R	PCC7418_RS07055	-251	S
GTTATTTTGTTCCTTTGTGGCTGTTAAT CA	1594235	(+)	transposase	PCC7418_RS07215	-108	S
AGCTGATGACTAGGTAAAGGCTTTCTT AAT	1613769	(-)	ABC transporter substrate binding protein	PCC7418_RS07290	-265	E
CTTTTCCACCTTTGACCTGTGTTAAA TT	1623103	(+)	glutathione S-transferase family protein	PCC7418_RS07335	-249	S
AGATTAAGGAAAATTAAACCTCAACTT AAA	1664840	(-)	sodium:proton antiporter	PCC7418_RS07540	-114	P
ATTAACAATATTAAACAAATTTTAC TA	1665092	(+)	ATP-dependent zinc protease	PCC7418_RS07545	-115	O
TATAATCTTCGCTATAGCTCATTTTATG TT	1679832	(+)	response regulator	PCC7418_RS07610	-364	T
TGTTAAAGACGCAGAAAATCTTATTTTA AA	1708354	(-)	site-specific DNA- methyltransferase	PCC7418_RS07755	-130	L
AACTTAATTTCTGAAAAATCAGGGTTA AT	1744927	(-)	sedoheptulose 7-phosphate cyclase	PCC7418_RS07910	-329	E
AAATAAATCCCTGTTAAAGCTCATAAAA AT	1754941	(-)	response regulator-EAL domain containing response regulator- response regulator	PCC7418_RS07930/RS07935/RS07940	-60	T, T, T
AAATTAATGTTTCATAATGAGGTGGATT AA	1766429	(-)	N(2) fixation sustaining protein CowN	PCC7418_RS07995	-601	S
AGATCATGAGTAATAAATAAATAGGTT AAA	1767932	(-)	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D- alanine endopeptidase	PCC7418_RS08000	-120	M
TTCATAATTAATCGTTAATAAATGATTA AG	1794333	(-)	ABC transporter substrate-binding protein	PCC7418_RS08120	-6	E
ATTTTTTGTTTTAAATTATCCCTTGAC TT	1810041	(+)	ATP phosphoribosyltransferase regulatory subunit	PCC7418_RS08205	-314	E
TTTCCCTCACCTTAGATTAAAGTTTAT TA	1811102	(+)	undecaprenyldiphospho- muramoylpentapeptide beta-N- acetylglucosaminyltransferase	PCC7418_RS08210	-449	M
TTCTAAATCATTCGTAAAAAGTTGATTA AC	1871218	(-)	copper-translocating P-type ATPase	PCC7418_RS08475	-151	P
TTTAAGCATGACCTTACCCCTAATTATC CT	1889348	(+)	NAD(P)H-quinone oxidoreductase subunit 4	PCC7418_RS08560	-648	C
TTTAATTGTAAATTTTCTTATTTTTTAG TT	1900730	(+)	glutathione synthase (<i>gshB</i>)	PCC7418_RS08590	-93	H

TGCTTGTGGTAAAGAAAAGGTTATGTT AAA	1919258	(-)	phosphate ABC transporter substrate binding protein PstS (<i>pstS</i>)-phosphate ABC transporter permease subunit PstC (<i>pstC</i>)- phosphate ABC transporter permease PstA (<i>pstA</i>)-phosphate ABC transporter ATP binding protein PstB (<i>pstB</i>)	PCC7418_RS08670/RS08665/ RS08660/RS08655	-256	P, P, P, P
GTTAATCACAGAGAAAATTAATCTTAA TT	1932831	(+)	endonuclease MutS2	PCC7418_RS08735	-136	L
GATTAAGTTTTGATAAAGTCTTGATCT AG	1942813	(-)	cysteine synthase A (<i>cysK</i>)	PCC7418_RS08775	-162	E
ATTTATGTTATAATAATTTTACCATTAT TT	1970080	(+)	IS200/IS605 family element transposase accessoryprotein TnpB (<i>mpB</i>)	PCC7418_RS08950	-40	S
ATTGAACCTTTATTAAACTCGGTTTATC AA	1996480	(+)	response regulator-chemotaxis protein CheW (<i>cheW</i>)	PCC7418_RS09080/RS09085	-696	KT, NT
TTGTAATGGGCGGGTTAGGAATGGTT AAA	2056920	(-)	glycosyltransferase family 2 protein	PCC7418_RS09320	-565	M
GAGCTAAGAAATGATAATGCTGTTCTA AAC	2134623	(-)	cobalt precorrin 8X methylmutase/bifunctional cobalt- precorrin-7 (C(5)) - methyltransferase cobalt precorrin- 6B (C(15)) methyltransferase (<i>cbiE</i>)	PCC7418_RS09630/RS09625	-343	H, T
TTTAAAAAAGTAATTGTCTCCCGTTTTC CA	2186011	(+)	late competence development ComFB family protein	PCC7418_RS09865	-39	S
AGGTAATGACGATATTAATCCCATTATA AA	2244285	(-)	RNA methyltransferase	PCC7418_RS10105	-172	L
CGGTAAACGTAAATTAGCCCCATGTA AAT	2251376	(-)	5-(carboxyamino)imidazole ribonucleotide synthase	PCC7418_RS10145	-205	F
AATAGTCTCATTTTTATTTTAAATTTTT AT	2285162	(+)	alanine:cation symporter family protein	PCC7418_RS10255	-415	U
ATTATTATAGATATTATCTCCGGCTAAA AT	2323958	(+)	serine O-acetyltransferase	PCC7418_RS10410	-391	E
TTAAATTTAATCATTACTTTAGGTTTAA GT	2388578	(+)	class 1 fructose-bisphosphatase	PCC7418_RS10725	-182	G
GATAAAAAGTTAAATCAACTAAAGATA AAT	2403390	(-)	citramalate synthase	PCC7418_RS10785	-453	E
TTTGCCTAAATTTTATTTCTATTAAC CT	2442208	(+)	PAS domain S-box protein	PCC7418_RS19415	-102	T
AGTAAAAACAATCTTTAAATTGAATTAA AA	2467390	(-)	AAA family ATPase	PCC7418_RS11110	-140	O
AATAAAATATTACGTAAACCATAGGCT AAA	2476471	(-)	lipoprotein signal peptidase	PCC7418_RS11185	0	MU
TTTAACTGCAATTTTAATTTTAATTGGC TT	2487840	(+)	glucosylglycerol 3-phosphatase	PCC7418_RS11220	-321	S

GATTTAAATAAAAGATTGCTAAGGTAA AA	2519448	(-)	saccharopine dehydrogenase NADP-binding domain containing protein	PCC7418_RS11355	-19	E
AAATTAAGAAGTTTTAAGATTATA TA	2523201	(-)	cytochrome ubiquinol oxidase subunit I-cytochrome d ubiquinol oxidase subunit II (<i>cydB</i>)	PCC7418_RS11365/PCC7418_RS11370	-66	C, C
TTTTACGAAGAATTAACTCATTTTTAC CG	2523301	(+)	hemerythrin family protein	PCC7418_RS11375	-80	P
TTTAAATTTTTATAACAATTGATTGAT CA	2657664	(+)	EAL domain containing protein	PCC7418_RS19435	-99	T
GTATGAACGTTAATTAAGGCATAATT AAT	2669847	(-)	macrophage migration inhibitory factor family protein	PCC7418_RS12020	-7	S
ATTAATCATTTGCTTACTCAGGATTAAA CT	2686183	(+)	Crp/Fnr family transcriptional regulator	PCC7418_RS12095	-165	K
AATAATGAACTTTTTCTCTCTTTTA CT	2708076	(+)	NADAR family protein	PCC7418_RS12195	-219	O
TTTATTTTTATGTTATAATAATCTTAGC AT	2735781	(+)	IS200/IS605 family element transposase accessoryprotein TnpB (<i>impB</i>)	PCC7418_RS12340	-45	S
ATTAAGAAGAACTTAACGAATCTTAAT TT	2791405	(+)	Crp/Fnr family transcriptional regulator	PCC7418_RS12605	-41	K
TTTAACTTATATTTTTATTTCCCATGAC TT	2871984	(+)	ureidoglycolate lyase	PCC7418_RS13060	-255	F
TTTAACTTTTTGTTTATTGCCACCTTTC CT	2922699	(+)	llutamate cysteine ligase (<i>gshA</i>)	PCC7418_RS13320	-19	S
CACTGAAAAACAAAAAAGGCTAGTTT AAT	2930864	(-)	lysine tRNA ligase	PCC7418_RS13445	-191	J
TGTTCAAACTACGCAATGTGAAAATT AAT	2954730	(-)	ribosome maturation factor RimM (<i>rimM</i>)	PCC7418_RS13700	-97	J
ATTTATATAATGATTAATTGACTTTGTT TT	3006109	(+)	polysaccharide pyruvyl transferase family protein	PCC7418_RS13700	-127	S
AGATTATTTCTGATTAAAACGAATACTA AA	3128024	(-)	translocation/assembly module TamB domain-containing protein	PCC7418_RS14210	-32	U
TACTTAAGTATAGTATAAGATTATAATA T	3138188	(-)	YqhA family protein- DUF202 domain containing protein	PCC7418_RS14255/RS14260	-89	S, S
AGTAAGAGGTGAATTAAGGGGGGATC AAA	3146602	(-)	formylglycine generating enzyme family protein	PCC7418_RS14295	-69	S
TTTAAAAAATAATTAATTTTCTTCCAAC AT	3179396	(+)	DMT family transporter	PCC7418_RS14440	-219	EG
ATTTATCTAAATATAAACTGAATTAAA TA	3191656	(+)	2Fe-2S iron sulfur cluster binding domain containing protein	PCC7418_RS14510	-279	C
ATATAAACTGAATTAATATAATTATA AC	3191666	(-)	M28 family peptidase	PCC7418_RS14505	-8	S
ATTGATGACTTATTAATTATCAATTAAG TT	3224851	(+)	o-succinylbenzoate synthase	PCC7418_RS14660	-11	M
GATAATATCATGATTATTTTTTCTTAT TA	3244402	(+)	glycosyltransferase	PCC7418_RS14775	-254	V

AAGCTAAACGTAGATAGAGTTGAGTAA AAA	3247808	(-)	glycosyltransferase-sulfotransferase	PCC7418_RS14780/RS14785	-94	M, S
CTTTATCTAATTTTGATCACTAGTTTTA TA	3275429	(+)	DNA phosphorothioation system sulfurtransferase DndC (<i>dndC</i>)	PCC7418_RS14930	-56	EH
CTTAGAATTTAGTAAATCTTAACTTAAT T	3309133	(+)	BCCT family transporter	PCC7418_RS15085	-305	M
ATTAGAATCAGTTTAAACTAAGCTCAAT GT	3332712	(+)	nickel-type superoxide dismutase maturation protease	PCC7418_RS15220	0	U
GTTAATTGTTGCTTAAAAATTACGTTTGC AT	3404962	(+)	peptide chain release factor 1 (<i>prfA</i>)	PCC7418_RS15625	-65	J
ATAATAAAGGGTGGTTATATGAAAGTA AAG	3410009	(-)	DNA (cytosine-5-) methyltransferase	PCC7418_RS15640	-359	H
CTCTAAAAAGTAATCTAAAAAAATTTA AT	3427651	(-)	TdeIII family type II restriction endonuclease	PCC7418_RS15720	-49	L
AGGTTAGAAGCAACTAAAGTTTTTCATA AAT	3454152	(-)	phycobilisome linker polypeptide	PCC7418_RS15845	-4	H
AAACAAAAAGAAAGTTAAATTTTTATAA AC	3455723	(-)	phycocyanin subunit beta	PCC7418_RS15855	-246	C
TTTAATTTCTCCTTAATAGGATATTAGT TA	3467427	(+)	translation initiation factor IF-2	PCC7418_RS15920	-123	S
ATTGACTTTTTGTTAGACTGAATTTAGT TT	3484159	(+)	IS200/IS605 family transposase	PCC7418_RS15965	-48	S
TTTTTTGTCAACTTAACCTTCCCTTTAC TT	3516392	(+)	PstS family phosphate ABC transporter substrate binding protein (<i>pstS</i>)-phosphate ABC transporter permease subunit PstC (<i>pstC</i>)- phosphate ABC transporter permease PstA (<i>pstA</i>)-phosphate ABC transporter ATP binding protein PstB (<i>pstB</i>)	PCC7418_RS16135/RS16140/ RS16145/RS16150	-147	P, P, P, P
TCATTAAACATCGAATAAACTTTGATTA AA	3579899	(-)	LmeA family phospholipid binding protein	PCC7418_RS16405	0	S
ATTAAACATCGAATAAACTTTGATTAAA AT	3579901	(+)	rRNA pseudouridine synthase	PCC7418_RS16410	-53	-
ATTTTTTTGAGCATTATTGAGCATTAT TT	3596661	(+)	response regulator-chemotaxis protein CheW (<i>cheW</i>)	PCC7418_RS16505/RS16510	-120	KT, NT
ATTAATTTTTATTAAGATTATGTTTTTT TT	3799356	(+)	class I SAM-dependent methyltransferase	PCC7418_RS17370	-383	H
ATTTATTGATGTATTTTTTTGTCTTAAC CC	3774649	(+)	alkaline phosphatase	PCC7418_RS17240	-76	P
ATTAATCATTCTCTATCCTCCAAATAAC CA	3842069	(+)	pentapeptide repeat-containing protein	PCC7418_RS17560	-59	S
ATTATTATTTTTGTTATTACGCTTAAC CT	3866970	(+)	transposase	PCC7418_RS17665	-417	Q
ATTAACCTTGCAATTATTTATCCCTTGAT C	3887039	(+)	Hemolysin type calcium binding protein	PCC7418_RS17775	-48	S

TTTAGGCTGTAATTAACTGATGTCAAC AA	3896679	(+)	IS200/IS605 family element transposase accessory protein TnpB (<i>tnpB</i>)	PCC7418_RS17810	-155	S
ATTATAAAAAATAATTTAAATGAATATA AA	3944455	(-)	HindVP family restriction endonuclease	PCC7418_RS18040	0	L
TTTTTAAGCGAAATTTATCAAGGAGAA AA	3960433	(+)	glycogen debranching protein GlgX (<i>glgX</i>)	PCC7418_RS18135	-167	G
GTAAATCAGAGTTAACCCATTATTAA TT	3992761	(+)	methyl-accepting chemotaxis sensory transducer	PCC7418_RS18275	-107	NT
TGGATAATAGCATATAAAGACTTAATA AAT	4015538	(-)	NAD(P)-dependent oxidoreductase	PCC7418_RS18405	-406	GM
ATAAAAAAGATTAATAATAGTAAGGTA AAA	4030328	(+)	glycosyltransferase	PCC7418_RS18495	-129	J
GATAAATCTTCTTTTACTCTTCTTTTA CA	4066330	(+)	D-alanyl-D-alanine carboxypeptidase family protein	PCC7418_RS18675	-233	M
TATAACCTATCATTATTGTCAAATAAC CA	4074906	(+)	ABC transporter ATP binding protein-ABC transporter permease	PCC7418_RS18715/RS18720	-61	V
TAGTTAATTTTAATTAATTATTATAATA TT	4087245	(+)	Na-Ca exchanger/integrin-beta4	PCC7418_RS18775	-319	S
AAATCATCAATTCGTTAAATTCAATTTA AT	4115030	(-)	SDR family oxidoreductase	PCC7418_RS18900	-148	IQ
AGTTTAAATTTATAATCAGTTCAGTTTA AT	4163771	(-)	SHOCT domain-containing protein	PCC7418_RS19070	-26	L
GCTAACCTTTTTATTATCTTAACCTAGA TT	4174392	(+)	GNAT family N-acetyltransferase	PCC7418_RS19130	-255	K

Supplementary Table 3. Fur regulon prediction. Fur boxes sequences, their position in the genome, orientation, the genes that are controlling (the Fur regulon), locus tag from these genes, the distance of the box from the gene and the gene function from single-letter of functional (COGs) are presented.

Fur boxes sequences	Position	Orientation	Fur regulon (genes)	Locus_tag	Distance	COG
GTTAATAAAATATTTTAC	1663	(+)	chromosomal replication initiator protein DnaA (<i>dnaA</i>)	PCC7418_RS00025	-472	L
GTTACAAAATATTTAGAAT	50660	(-)	alpha amylase	PCC7418_RS00215	-58	S
ATCTAAAGTTTTATAAAA	54620	(-)	PAS domain containing protein	PCC7418_RS00230	-123	T
AATTCAAGAAATTTTAAAT	63574	(-)	recombination protein RecR	PCC7418_RS00270	-277	L
ATTA AAAACCATTTTTAT	89952	(+)	esterase like activity of phytase family protein	PCC7418_RS20370	-355	F
TTTGTAATTTTTATCATC	104461	(-)	SDR family oxidoreductase	PCC7418_RS00415	-85	G
ATCTAAATAATCATAAT	114408	(-)	ketol-acid reductoisomerase	PCC7418_RS00460	-250	E
AATTTGGATTTTTTAAT	116549	(+)	glycosyltransferase family 2 protein	PCC7418_RS00475	-38	M
ATTTTGATTATATATAAAT	148165	(+)	prepilin-type N-terminal cleavage/methylation domain-containing protein	PCC7418_RS00635	-172	U
ATTTATAAATATTATCAAT	199345	(+)	energy transducer TonB (<i>tonB</i>)	PCC7418_RS00895	-13	M
ATTTATAAATATTATCAAT	199345	(-)	MotA/TolQ/ExbB proton channel family protein	PCC7418_RS00890	-192	U
ATTGCAATTTTTTGAT	200598	(+)	AraC family transcriptional regulator	PCC7418_RS00900	-38	K
ATTTTCTTTTATTTTAAT	247069	(+)	DUF3298/DUF4163 domain containing protein	PCC7418_RS01105	-454	S
ATTAAGTAATATTACAAA	379625	(-)	heavy metal translocating P-type ATPase	PCC7418_RS01685	-283	P
AATATTATATTCTTAAT	510372	(+)	4-alpha-glucanotransferase	PCC7418_RS02325	-227	G
ATAAAAATTAATAATAAT	524171	(-)	response regulator	PCC7418_RS02385	-374	T
ATTGATAATTTTATTAAC	559257	(-)	coenzyme F420 hydrogenase	PCC7418_RS02560	-101	C
TTTTATGATTATTATCAAT	690115	(+)	ShlB/FhaC/HecB family hemolysin secretion/activation protein	PCC7418_RS03120	-17	M
ATTAATAAACTTTTTTAAC	746975	(+)	photosystem I reaction center protein subunit XI-photosystem I reaction center subunit VIII	PCC7418_RS03390	-246	S
ATTTAATTAATTTTACAAT	766012	(+)	CRISPR associated endoribonuclease Cas6	PCC7418_RS03470	-242	S
ATTGACAAAATTCCTAAT	789753	(-)	photosystem II q(b) protein	PCC7418_RS03535	-74	C

ATTGAAAGTCATTCTTATT	898088	(-)	ferrous iron transport protein A-Fe (2+) (<i>feoA</i>)-transporter permease subunit FeoB (<i>feoB</i>)	PCC7418_RS04120/ RS04115	-93	P, P
ATTAGAAATTTTCTAAAA	1004388	(-)	ISAs1 family transposase	PCC7418_RS20420	0	S
AATGTTAAATTTTATAAA	1169323	(+)	KaiA family protein	PCC7418_RS05355	-185	S
ATTTATAACTTTTCTCTAT	1179409	(+)	MFS transporter	PCC7418_RS05400	-207	G
ATTTTGTATAATTATTAAT	1210254	(+)	HP	PCC7418_RS05535	-184	P
GTTGAAATAGATTCTTATT	1244480	(-)	adenylyl-sulfate kinase	PCC7418_RS05670	-147	P
ATTAGAAATTTTCTAAAA	1277716	(-)	ISAs1 family transposase	PCC7418_RS05850	0	S
ATTTAATTTTTTTGTAT	1541282	(+)	HEAT repeat domain-containing protein	PCC7418_RS07010	-88	C
ACTAATATTTTTCTAAAT	1613963	(-)	solute-ABC transporter substrate-binding protein	PCC7418_RS07285	-458	E
ATTAATAATAAATCTAATC	1626439	(-)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	PCC7418_RS07355	-120	I
ATTAACAAATTATAAAATT	1638172	(-)	sensor domain-containing diguanylate cyclase	PCC7418_RS07405	-11	P
TTATAAAATTATTTACAAT	1773346	(-)	2-carboxy-1,4-naphthoquinone phytyltransferase (<i>menA</i>)	PCC7418_RS08020	-216	H
ATTACAAAAGATTCTCAAC	1846361	(-)	ferrous iron transport protein A-Fe (2+) (<i>feoA</i>)-transporter permease subunit FeoB (<i>feoB</i>)	PCC7418_RS08340/ RS08335	-31	P, P
AATTATTAATAATTATTAAT	1978529	(+)	photosystem II protein PsbX (<i>psbX</i>)	PCC7418_RS08985	-145	C
G TTCATAATATTTTATAAT	2010967	(+)	DUF2207 domain-containing protein	PCC7418_RS09130	-396	S
TTTTAGTATATTTCTCATT	2201702	(+)	30S ribosome-binding factor RbfA (<i>rbfA</i>)	PCC7418_RS09935	-165	H
ATTGACAACTATTTTTAGT	2226486	(+)	methyl-accepting chemotaxis protein	PCC7418_RS10065	-669	L
ATTGCAATTAAATTTAAAA	2226728	(-)	ferrous iron transport protein A-Fe (2+) (<i>feoA</i>)-transporter permease subunit FeoB (<i>feoB</i>)	PCC7418_RS10060/ RS10055	-316	P
TTTTGTAAATTTTTGTAAA	2234872	(+)	glutamate-1-semialdehyde-2,1-aminomutase (<i>gsaI</i>)	PCC7418_RS10080	-177	H
TTTGTAAATTTTTGTAAAT	2234873	(+)	magnesium chelatase subunit H (<i>chlH</i>)	PCC7418_RS10075	-214	H
TTTTAAATAAAAAATAAT	2376830	(-)	hydrogenase maturation protease	PCC7418_RS10660	-207	C
ATTGCTATTTATTCATAAT	2425245	(-)	DUF1643 domain-containing protein	PCC7418_RS19410	-256	S

TTTtagAAAAATTTCTAAT	2459685	(+)	ISAs1 family transposase	PCC7418_RS11060	0	S
TTTGTtATTTATTCTTAGT	2584479	(+)	HP	PCC7418_RS11685	-270	S
AATACAAAAATTTGTTAAA	2609963	(-)	ABC transporter ATP-binding protein	PCC7418_RS11810	-546	V
ATTTTtAATTTTTTGTTAA	2785156	(+)	cobalamin biosynthesis protein (<i>cobW</i>)	-	-64	S
ATTGCAATTTTTTTTATT	2791453	(+)	Crp/Fnr family transcriptional regulator	PCC7418_RS12605	0	K
ATTAAGAAAAATTAATATT	2858373	(+)	argininosuccinate synthase	PCC7418_RS13005	0	E
ATTGTtATTTATTATTtGT	2864252	(+)	6-pyruvoyltetrahydropterin synthase	PCC7418_RS13025	-312	H
ACTGGAAAAATtATCAA A	2874763	(-)	methyltransferase domain-containing protein	PCC7418_RS1306	-194	L
ATTGAGATATTTATCGAT	2883764	(+)	transcription-repair coupling factor	PCC7418_RS13105	-64	L
ATTTTGAAcAAATTTCAAT	2933424	(+)	SpoIID/LytB domain-containing protein	PCC7418_RS13340	-50	D
GTTTTAAAAAATAATTAAT	3179394	(-)	photosystem II reaction center protein Ycf12	PCC7418_RS14435	-25	S
ATTAAATATAATTATAACT	3191678	(-)	M28 family peptidase	PCC7418_RS14505	-21	S
GTTGAGATTAATTTTCATT	3379840	(-)	PAS domain-containing protein	PCC7418_RS15425	-46	T
ATTAATAAAgTTTTGCAAA	3441389	(+)	glutamate-5-semialdehyde dehydrogenase	PCC7418_RS15780	-102	E
GTTGCTAATTTTTAGCAAA	3460255	(-)	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (<i>purH</i>)	PCC7418_RS15885	-45	F
AATTGGAAATTTTTTCAGT	3692765	(+)	peptidase S13	PCC7418_RS16905	-39	S
ATTGCAATTAATTTCAAT	3725995	(-)	alpha/beta hydrolase	PCC7418_RS17030	-21	S
ATTGTCAATTTTTTGTAAT	3727770	(+)	HU family DNA binding protein	PCC7418_RS17045	-245	L
ATTATAAAAACTATTAAC	3774691	(+)	alkaline phosphatase	PCC7418_RS17240	-45	S
GTTAATTTTAATTTTAAT	3840660	(+)	sensor protein	PCC7418_RS17555	-1	S
ATTGCAAAAGATATTCAAT	3885410	(-)	chlorophyll a/b binding light-harvesting protein-chlorophyll a/b binding light-harvesting protein	PCC7418_RS17760	-16	S
TTTGAAATTAACtTGCAAT	3887033	(+)	hemolysin type calcium binding protein	PCC7418_RS17775	-54	V

TATAAAAAATAATTTAAAAT	3944457	(-)	HindVP family restriction endonuclease	PCC7418_RS18040	0	V
GATAAAAAAGATTAATAAT	4030327	(-)	glycosyltransferase family 2 protein	PCC7418_RS18475	-127	M
ATTGAAATAAATTGTCAAC	4047761	(+)	uracil phosphoribosyltransferase	PCC7418_RS18570	-188	F
ATTGAAATAAATTGTCAAC	4047761	(-)	carotene isomerase	PCC7418_RS18565	-141	F
ATTTAGCAAAATTATTAAT	4072511	(+)	magnesium-protoporphyrin IX monomethyl ester anaerobic oxidative cyclase	PCC7418_RS18705	-77	H
TTTGAGAATATTTCTTTTT	4095529	(+)	PadR family transcriptional regulator (<i>padR</i>)	PCC7418_RS18830	-139	K

Supplementary Table 4. NtcA regulon prediction. NtcA boxes sequences, their position in the genome, orientation, the genes that are controlling (the NtcA regulon), locus tag from these genes, the distance of the box from the gene and the gen function from single-letter of functional (COGs) are presented.

NtcA boxes sequences	Position	Orientation	NtcA regulon (genes)	Locus_tag	Distance	COG
TGTAATATTTGTTAAA	193565	(-)	phosphoribosylformylglycinamide cyclo-ligase (<i>purM</i>)	PCC7418_RS00865	-14	F
TGTAACATTCGATACA	433503	(+)	DUF4278 domain-containing protein	PCC7418_RS01970	-53	P
TGTAAATTTTGATACC	435747	(+)	PstS phosphate ABC transporter substrate-binding protein (<i>pstS</i>)	PCC7418_RS01980	-166	P
TGTAAATTTTGATACC	435748	(-)	adenylyl-sulfate kinase (<i>cysC</i>)	PCC7418_RS01975	-3	S
CGTATATTATGATACA	609571	(+)	ferredoxin--nitrite reductase (<i>nirA</i>)	PCC7418_RS02810	-89	C
TGTAATAGTAAATAGA	676478	(+)	Uma2 family endonuclease	PCC7418_RS03075	-18	S
TGTATCTATTGTTACA	857460	(-)	DUF4278 domain-containing protein	PCC7418_RS03870	-116	S
TGTATCAAATATTACT	1222068	(-)	2-oxo acid dehydrogenase subunit E2	PCC7418_RS05590	-159	C
TGTATCAAATATTACT	1222069	(+)	response regulator	PCC7418_RS05595	-100	T
AGTAAAACTGCTACA	1299552	(+)	hybrid sensor histidine kinase/response regulator	PCC7418_RS05925	-195	T
TGTATTGTTTTCTACA	1331526	(-)	helix turn helix domain-containing protein	PCC7418_RS06050	-183	C
AGTAGTTTTTGTTACA	1381373	(+)	glutamate synthase large subunit (<i>gluB</i>)	PCC7418_RS06265	-342	E
TGTATTTTTCGATACA	1487910	(+)	ammonium transporter (<i>amt</i>)	PCC7418_RS06755	-145	P
TGTATCTTTTATACT	1496086	(+)	Crp/Fnr family transcriptional regulator	PCC7418_RS06790	-54	K
TATAACTTTTTTTACA	1502278	(-)	elongation factor G (<i>fusA</i>)-elongation factor Tu (<i>tuf</i>)	PCC7418_RS06815/ RS06810	-82	J, J
AGTAACAATTGATACA	1504147	(-)	cupin domain-containing protein-iron-sulfur cluster assembly accessory protein	PCC7418_RS06835	-14	G
TGTTTTTCTGATACA	1613632	(-)	solute-ABC transporter substrate-binding protein	PCC7418_RS07290	-120	E

TGTATCATTTGTTACA	1907277	(-)	pyridoxal phosphate-dependent aminotransferase	PCC7418_RS08620	-77	E
TGTAGCGTTTGTACT	1946907	(+)	nitrogenase cofactor biosynthesis protein (<i>nifB</i>)	PCC7418_RS08815	-629	C
AGTATTACTAAATACA	1963729	(+)	molybdate ABC transporter substrate-binding protein (<i>modA</i>)	PCC7418_RS08910	-352	P
TGTATAAATCGCTACA	1981610	(-)	ammonium transporter (<i>amt</i>)	PCC7418_RS08960	-56	P
AGTAACATTAAATACA	2022577	(-)	SulP family inorganic anion transporter	PCC7418_RS09170	-90	P
AGTAACATTAAATACA	2022578	(+)	TIGR03279 family radical SAM protein	PCC7418_RS09175	-78	C
TGTAGTTGCAATTACT	2077841	(-)	sugar transferase	PCC7418_RS09405	-75	M
TGTAGCTGATAATACC	2201041	(-)	orange carotenoid-binding protein	PCC7418_RS09925	-53	S
TCTAACAAAAGTTACA	2260357	(+)	photosystem II chlorophyll-binding protein CP47 (<i>psbB</i>)	PCC7418_RS10180	-161	S
TGTAACTTTAGATACG	2301793	(-)	alanine:cation symporter family protein	PCC7418_RS10335	-68	E
TGTAAC TTGTATTACA	2496434	(+)	phosphodiesterase	PCC7418_RS11260	-145	E
TGTATTTAATGTTACA	2725914	(-)	type I glutamate--ammonia ligase (<i>glnN</i>)	PCC7418_RS12280	-72	E
TGTAGTTGAGGTTACA	2977247	(+)	NINE protein	PCC7418_RS13560	-195	E
AGTAGCAATTATTACA	3197191	(-)	sodium:glutamate symporter (<i>gltS</i>)	PCC7418_RS14540	-106	E
TGTATTTTTTGATACA	3288086	(-)	MinD/ParA family protein	PCC7418_RS14970	-204	D
AGTAAAATAAAATACA	3502170	(-)	rhodopsin	PCC7418_RS16035	-294	S
TGTACAAAATATTACA	3542559	(-)	tetratricopeptide repeat protein	PCC7418_RS16280	-70	S
TGTTATTTACGATACA	3690483	(-)	[acyl-carrier-protein] S-malonyltransferase (<i>fabD</i>)	PCC7418_RS16890	-7	I

TGTATTC ACTAATACA	3817904	(+)	response regulator	PCC7418_RS17455	-61	T
AGTAATT ATTGCTACA	3962735	(+)	transcriptional repressor (<i>fur</i>)	PCC7418_RS16465	-7	T
AGTATCT TTTCGTTACA	4051198	(-)	L-histidine N(alpha)-methyltransferase (<i>egtD</i>)	PCC7418_RS18585	-41	S
CGTATCA AGAGATACA	4130890	(+)	ATP-grasp domain-containing protein	PCC7418_RS18945	-144	S