

Supplementary Materials

Table S1. Cyanobacteria identified in metagenomic and metatranscriptomic.

Samples	Level 1	Function	Closest Species
CT04D	Amino Acids and Derivatives	Proline iminopeptidase (EC 3.4.11.5)	<i>Nostoc punctiforme</i> (strain ATCC 29133/PCC 73102)
	Carbohydrates	Gluconolactonase (EC 3.1.1.17)	<i>Synechococcus</i> sp. CC9311
		Acetate permease ActP (cation/acetate symporter)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
		Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	<i>Synechococcus</i> sp. (strain WH7803)
	Clustering-based subsystems	Phytoene desaturase (EC 1.14.99.-)	<i>Nostoc punctiforme</i> (strain ATCC 29133/PCC 73102)
		Adenylate cyclase	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
	Cofactors, Vitamins, Prosthetic Groups, Pigments	5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)	<i>Synechococcus elongatus</i> PCC 7942
		Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26)	<i>Synechococcus elongatus</i> PCC 7942
	Fatty Acids, Lipids, and Isoprenoids	Phytoene desaturase (EC 1.14.99.-)	<i>Nostoc punctiforme</i> (strain ATCC 29133/PCC 73102)
		Adenylate cyclase (EC 4.6.1.1)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
	Miscellaneous	Serine peptidase (Alpha/beta hydrolase superfamily) fused to N- terminal uncharacterized domain specific to cyanobacteria	<i>Synechococcus</i> sp. CC9311
		Na ⁺ /H ⁺ antiporter	<i>Nostoc punctiforme</i> PCC 73102
	Potassium metabolism	Potassium voltage-gated channel subfamily KQT	<i>Synechococcus</i> sp. RCC307
	Protein Metabolism	Acetate permease ActP (cation/acetate symporter)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
		Selenide,water dikinase (EC 2.7.9.3)	<i>Microcystis aeruginosa</i> (strain NIES-843)
	Regulation and Cell signaling	Adenylate cyclase (EC 4.6.1.1)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
		ATP synthase alpha chain (EC 3.6.3.14)	<i>Crocospaera watsonii</i> WH 8501
	Respiration	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	<i>Prochlorococcus marinus</i> NATL1A
		soluble [2Fe-2S] ferredoxin	<i>Cyanothece</i> sp. (strain PCC 7425/ATCC 29141)
	Virulence, Disease and Defense	Negative regulator of beta-lactamase expression	<i>Synechococcus</i> sp. WH 7805
CT04R	Monosaccharides	Ribokinase (EC 2.7.1.15)	<i>Synechococcus</i> sp. RS9917
	Sugar utilization in Thermotogales	Ribokinase (EC 2.7.1.15)	<i>Synechococcus</i> sp. RS9917

Table S1. Cont.

CT05D	Amino Acids and Derivatives	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	<i>Synechococcus</i> sp. CC9605
	Carbohydrates	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	<i>Synechococcus</i> sp. CC9605
	Carbohydrates	decarboxylase	<i>Prochlorococcus marinus</i> MIT 9313
	Clustering-based subsystems	Adenylosuccinate synthetase (EC 6.3.4.4)	<i>Cyanothece</i> sp. PCC 7425
	Cofactors, Vitamins, Prosthetic Groups, Pigments	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	<i>Synechococcus</i> sp. CC9605
	Miscellaneous	Scaffold protein for [4Fe-4S] cluster assembly, MRP-like, similar to chloroplast-targeted plant protein HCF101	<i>Synechocystis</i> sp. (strain ATCC 27184/PCC 6803/N-1)
	Nucleosides and Nucleotides	Adenylosuccinate synthetase (EC 6.3.4.4)	<i>Cyanothece</i> sp. PCC 7425
	Photosynthesis	photosystem II protein D1 (PsbA)	<i>Synechococcus</i> sp. RCC307
	Protein Metabolism	Arginyl-tRNA synthetase (EC 6.1.1.19)	<i>Synechococcus</i> sp. CC9605
	Protein Metabolism	Chaperone protein HtpG	<i>Synechococcus</i> sp. (strain WH8102)
	Stress Response	Glutamate decarboxylase (EC 4.1.1.15)	<i>Prochlorococcus marinus</i> (strain MIT 9313)
	Amino Acids and Derivatives	Threonine dehydratase, catabolic (EC 4.3.1.19)	<i>Anabaena variabilis</i> (strain ATCC 29413/PCC 7937) <i>Cyanobacteria bacterium</i> Yellowstone
		Urease accessory protein UreG	B-Prime (<i>Synechococcus</i> sp. JA-2-3B'a(2-13))
		Threonine dehydratase, catabolic (EC 4.3.1.19)	<i>Anabaena variabilis</i> (strain ATCC 29413/PCC 7937)
		Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	<i>Cyanothece</i> sp. PCC 7424
		Threonine dehydratase, catabolic (EC 4.3.1.19)	<i>Anabaena variabilis</i> (strain ATCC 29413/PCC 7937)
CT06D	Carbohydrates	Transketolase (EC 2.2.1.1)	<i>Nostoc punctiforme</i> PCC 73102 <i>Cyanothece</i> sp. (strain PCC 7424)
		L-alanine:glyoxylate aminotransferase (EC 2.6.1.44)	(<i>Synechococcus</i> sp. (strain ATCC 29155))
		Transketolase (EC 2.2.1.1)	<i>Nostoc punctiforme</i> PCC 73102
	Carbohydrates	Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	<i>Synechococcus</i> sp. CC9902
		Serine--pyruvate aminotransferase (EC 2.6.1.51)	<i>Cyanothece</i> sp. (strain PCC 7424) (<i>Synechococcus</i> sp. (strain ATCC 29155))
		Transketolase (EC 2.2.1.1)	<i>Nostoc punctiforme</i> PCC 73102

Table S1. Cont.

	Cell Division and Cell Cycle	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	<i>Prochlorococcus marinus</i> MIT 9303
	Cell Wall and Capsule	Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	<i>Synechococcus</i> sp. CC9902
	Clustering-based subsystems	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	<i>Synechococcus elongatus</i> PCC 7942
		Molybdenum cofactor biosynthesis protein MoaD	<i>Thermosynechococcus elongatus</i> (strain BP-1)
Cofactors, Vitamins, Prosthetic Groups, Pigments		Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	<i>Cyanothece</i> sp. PCC 7424
		Flavodoxin	<i>Synechococcus</i> sp. CC9311
		Flavodoxin 1	<i>Synechococcus</i> sp. CC9311
			<i>Cyanobacteria bacterium</i> Yellowstone B-Prime
		Sulfur carrier protein adenylyltransferase ThiF	(<i>Synechococcus</i> sp. JA-2-3B'a(2-13))
	Dormancy and Sporulation	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	<i>Synechococcus elongatus</i> PCC 7942
	Membrane Transport	Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2)	<i>Cyanothece</i> sp. ATCC 51142
	Nitrogen Metabolism	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	<i>Cyanothece</i> sp. PCC 7424
	Nucleosides and Nucleotides	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	<i>Prochlorococcus marinus</i> MIT 9303
	Photosynthesis	Octaprenyl-diphosphate synthase (EC 2.5.1.-)	-
	Protein Metabolism	SSU ribosomal protein S6p	<i>Prochlorococcus marinus</i> SS120 (subsp. <i>marinus</i> CCMP1375)
		Peptidyl-tRNA hydrolase (EC 3.1.1.29)	<i>Synechococcus elongatus</i> PCC 7942
		Prolyl-tRNA synthetase (EC 6.1.1.15)	<i>Synechococcus</i> sp. CC9902
		Chaperone protein DnaJ	<i>Synechococcus</i> sp. WH 7803
			<i>Thermosynechococcus elongatus</i> BP-1
	Stress Response	Urease accessory protein UreG	<i>Cyanobacteria bacterium</i> Yellowstone B-Prime (<i>Synechococcus</i> sp. JA-2-3B'a(2-13))
		Chaperone protein DnaJ	<i>Synechococcus</i> sp. WH 7803
		5-oxoprolinase (EC 3.5.2.9)	<i>Cyanothece</i> sp. (strain ATCC 51142)
CT06R	Photosynthesis	photosystem II protein D1 (PsbA)	<i>Nostoc</i> sp. (strain PCC 7120 / UTEX 2576)

Table S1. Cont.

Amino Acids and Derivatives	Glutamate <i>N</i> -acetyltransferase (EC 2.3.1.35)	<i>Synechococcus</i> sp. JA-2-3B'a(2-13)
	<i>N</i> -acetylglutamate synthase (EC 2.3.1.1)	<i>Synechococcus</i> sp. JA-2-3B'a(2-13)
Carbohydrates	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
Cell Wall and Capsule	Bacillosamine/Legionaminic acid biosynthesis aminotransferase PglE	<i>Prochlorococcus marinus</i> (strain MIT 9303) <i>Cyanothece</i> sp. (strain PCC 7424)
	ADP-heptose synthase (EC 2.7.-.-)	(<i>Synechococcus</i> sp. (strain ATCC 29155)) <i>Cyanothece</i> sp. (strain PCC 7424)
	D-glycero-beta-D-manno-heptose 7-phosphate kinase	(<i>Synechococcus</i> sp. (strain ATCC 29155))
	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)	<i>Microcystis aeruginosa</i> NIES-843
CT12D	Glycosyltransferase	<i>Anabaena variabilis</i> ATCC 29413
	Glycosyltransferase (EC 2.4.1.-)	<i>Anabaena variabilis</i> ATCC 29413
	Translation elongation factor Ts	<i>Prochlorococcus marinus</i> (strain MIT 9303)
	Alanyl-tRNA synthetase (EC 6.1.1.7)	<i>Anabaena variabilis</i> ATCC 29413
	Amino acid permease in hypothetical Actinobacterial gene cluster	<i>Cyanothece</i> sp. (strain PCC 7425/ATCC 29141)
	Helicase PriA essential for oriC/DnaA-independent DNA replication	<i>Cyanothece</i> sp. PCC 7425
	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)	<i>Microcystis aeruginosa</i> NIES-843
	Competence/damage-inducible protein CinA	<i>Synechococcus</i> sp. (strain JA-3-3Ab) (<i>Cyanobacteria</i> <i>bacterium</i> Yellowstone A-Prime)
	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	<i>Prochlorococcus marinus</i> (strain MIT 9215)
	Orotate phosphoribosyltransferase (EC 2.4.2.10)	<i>Synechococcus</i> sp. (strain RCC307)
Cofactors, Vitamins, Prosthetic Groups, Pigments	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	<i>Prochlorococcus marinus</i> (strain MIT 9215)
	Sulfur carrier protein adenylyltransferase ThiF	<i>Cyanothece</i> sp. PCC 8801
DNA Metabolism	Helicase PriA essential for oriC/DnaA-independent DNA replication	<i>Cyanothece</i> sp. PCC 7425

Table S1. Cont.

Miscellaneous	Membrane protein PxcA, involved in light-induced proton extrusion	<i>Synechocystis</i> sp. (strain ATCC 27184/PCC 6803/N-1)27184/PCC 6803/N-1)
	Glutathione S-transferase family protein	<i>Prochlorococcus marinus</i> (strain MIT 9313)
	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)	<i>Microcystis aeruginosa</i> NIES-843
	Glycosyltransferase	<i>Anabaena variabilis</i> ATCC 29413
	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	<i>Prochlorococcus marinus</i> (strain MIT 9215)
	Competence/damage-inducible protein CinA	<i>Synechococcus</i> sp. (strain JA-3-3Ab) (<i>Cyanobacteria bacterium</i> Yellowstone A-Prime)
Nucleosides and Nucleotides	Orotate phosphoribosyltransferase (EC 2.4.2.10)	<i>Synechococcus</i> sp. (strain RCC307)
Phages, Prophages, Transposable elements, Plasmids	Heat shock protein 60 family chaperone GroEL	<i>Prochlorococcus marinus</i> MED4 (subsp. pastoris str. CCMP1378)
Photosynthesis	photosystem II protein D1 (PsbA)	<i>Cyanothece</i> sp. (strain PCC 8802) (<i>Synechococcus</i> sp. (strain RF-2))
Protein Metabolism	Translation elongation factor Ts	<i>Prochlorococcus marinus</i> (strain MIT 9303)
	Translation elongation factor Tu	<i>Cyanobacteria bacterium</i> Yellowstone A-Prime (<i>Synechococcus</i> sp. JA-3-3Ab)
	Alanyl-tRNA synthetase (EC 6.1.1.7)	<i>Anabaena variabilis</i> ATCC 29413
	Valyl-tRNA synthetase (EC 6.1.1.9)	<i>Trichodesmium erythraeum</i> (strain IMS101)
	Prolyl endopeptidase (EC 3.4.21.26)	<i>Gloeobacter violaceus</i> PCC7421
	Heat shock protein 60 family chaperone GroEL	<i>Prochlorococcus marinus</i> MED4 (subsp. pastoris str. CCMP1378)
	4-keto-6-deoxy-N-Acetyl-D-hexosaminy-(Lipid carrier) aminotransferase	<i>Prochlorococcus marinus</i> (strain MIT 9303)
Respiration	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	<i>Anabaena</i> sp. PCC 7120 (<i>Nostoc</i> sp. PCC 7120)
Stress Response	Glutathione S-transferase family protein	<i>Prochlorococcus marinus</i> (strain MIT 9313)
Carbohydrates	Ribokinase (EC 2.7.1.15)	<i>Synechococcus</i> sp. RS9917
Fatty Acids, Lipids, and Isoprenoids	Phytoene desaturase, pro-zeta-carotene producing (EC 1.-.-.-)	<i>Synechococcus elongatus</i> (strain PCC 7942) (<i>Anacystis nidulans</i> R2)
Phosphorus Metabolism	Alkaline phosphatase (EC 3.1.3.1)	<i>Cyanothece</i> sp. CCY0110