

1. Genes present in *Synechococcus* sp. BDU 130192 genome

Analysis of the annotated genome [11] revealed that the amino acid and protein metabolism subsystems have the highest number of genes (13% each), followed by the cofactor and vitamins subsystems (12%) and the "stress metabolism" (5%). Other subsystems like membrane transport, DNA metabolism, cell division and cell cycle have relatively lower number of genes compared to *Synechococcus* sp. PCC 7002. Figure 5 shows the distribution of genes among different subsystems. We found genes involved in exopolysaccharide synthesis in the genome. Genes encoding CRISPR-associated helicases Cas1, Cas2 as well as Cas4 were also found. The transporters for branched chain amino acids and cyanate were also seen. The cytochrome-*b6* complex has 7 genes while cytochrome *c* also has 7 genes whereas *Synechococcus* sp. PCC 7002 has 4 genes for cytochrome *b6* complex and 5 for cytochrome *c* oxidase. The circadian clock proteins KaiA, KaiC as well as the circadian oscillation regulator KaiB are present in the genome.

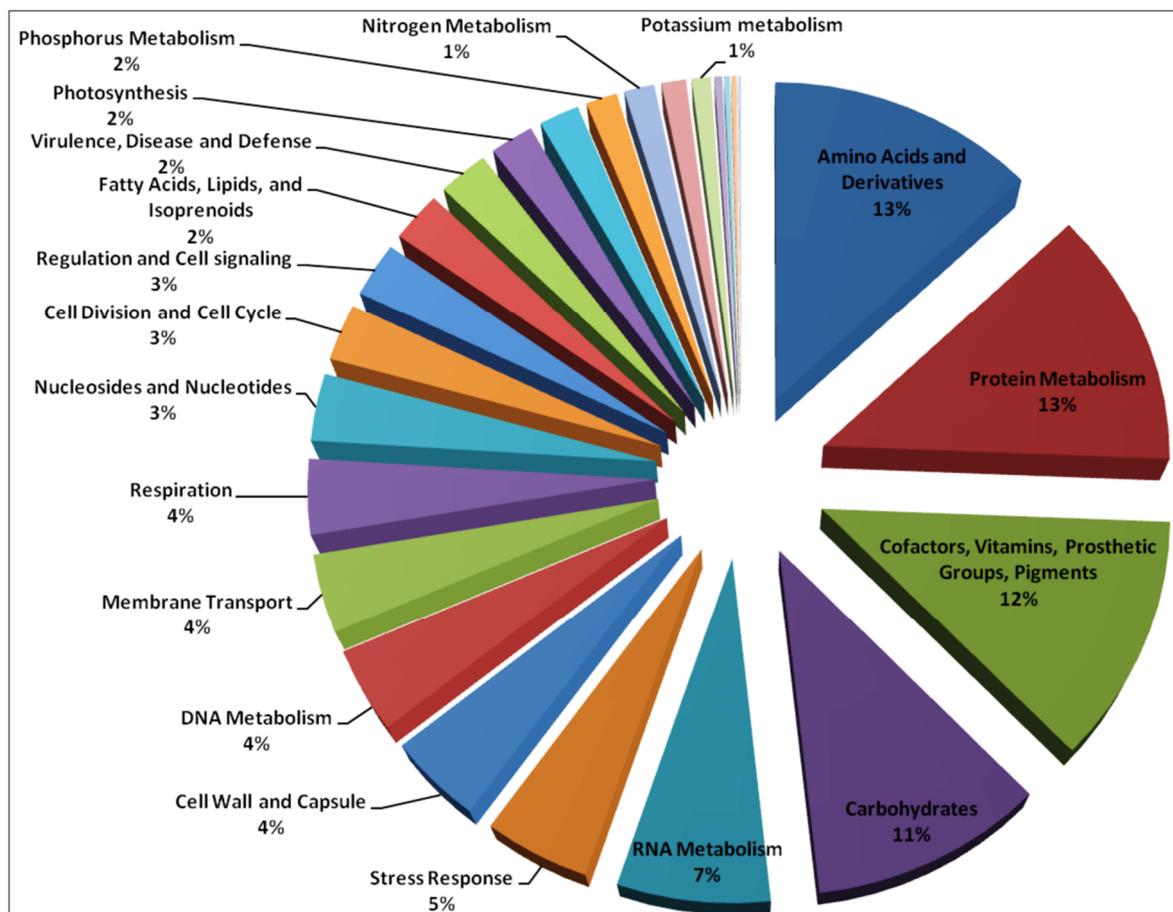


Figure S1. A pie-chart showing distribution of annotated genes among different subsystems.

2. Comparison of our model to the model of *Synechococcus* sp. PCC 7002

The model *iSyn706* is the second-largest in terms of the number of reactions compared to other publically-available models of cyanobacteria (Table 2(a)).

We performed a pathway-wise comparison of *iSyn706* model with the *iSyn708* model. As given in Table 2b, *iSyn706* has 908 reactions while *iSyn708* has 647 reactions. The *iSyn706* model contains 165 reactions while *iSyn708* contains 115 belonging to amino acid metabolism. Further analysis revealed that *iSyn706* has more reactions involving different amino acids compared to *iSyn708*. There are 31 and 6 reactions involved in phenylalanine, tyrosine and tryptophan metabolism in *iSyn706* and *iSyn708* models, respectively. Also, 27 and 12 reactions that are involved in 'cysteine and methionine

metabolism' are present in the *iSyn706* and *iSyp708* models, respectively. There are 10 and 3 reactions involved in histidine metabolism in *iSyn706* and *iSyp708* models, respectively. Only 4 reactions involved in folate metabolism are present in *iSyp708* as against 15 in the *iSyn706* model. In case of riboflavin metabolism, only 2 reactions are present in *iSyp708* against 13 in the *iSyn706* model. There are 81 and 60 reactions involving carbohydrate metabolism present in *iSyn706* and *iSyp708* models, respectively. Also, 85 and 54 reactions involving nucleotide metabolism are present in *iSyn706* and *iSyp708* models, respectively. So, the *iSyn706* model has more alternative routes for synthesis of different biomass components. However, the reactions of alanine, aspartate and glutamate metabolism are slightly more in *iSyp708* than in *iSyn706*, 28 vs. 24, respectively (Table 2(b)).

Table S1. Pathway-wise comparison between *iSyn706* and *iSyp708* models.

	<i>iSyn706</i>	<i>iSyp708</i>
Phenylalanine, Tyrosine and Tryptophan Metabolism	31	6
Cystine and Methionine Metabolism	27	12
Histidine Metabolism	10	3
Alanine, Aspartate and Glutamate Metabolism	24	28
Carbohydrate Metabolism	81	60
Nucleotide Metabolism	85	54
Folate Metabolism	15	4
Riboflavin Metabolism	13	2

3. Photoautotrophic production of industrially-relevant compounds

Table S2. Table showing the maximum theoretical yields of various native and non-native products under photoautotrophic conditions as per the *iSyn706* model.

S. No.	Product	Yield (mol/mol carbon)	No. of added Reactions	Added Genes
Native				
1	Acetate	0.09	0	
2	Succinate	0.05	0	
3	Pyruvate	0.06	0	
4	Citrate	0.03	0	
Non-Native				
5	Acetone	0.06	3	atoB, {atoD or atoA}, adc
6	Phenyl Alcohol	0.02	2	ipdC, adhC
7	Butanol	0.05	6	Thl, Hbd, crt, bcd, adhE2 (adhE2 catalyzes 2 reactions)
8	Propane	0.05	6	Thl, Hbd, crt, bcd, adhE2, ADO
9	PHB	0.05	3	phaA, phaB, phaC
10	Ethanol	0.1	1	adhE

The growth rates were fixed at 80% of the wild type growth rate.

A homolog of alcohol dehydrogenase, which catalyzes the last reaction in ethanol formation, is present in the genome of *Synechococcus* sp. BDU 130192. However, no homolog for acetaldehyde

dehydrogenase was found. Therefore, ethanol synthesis requires only one additional (heterologous) reaction.