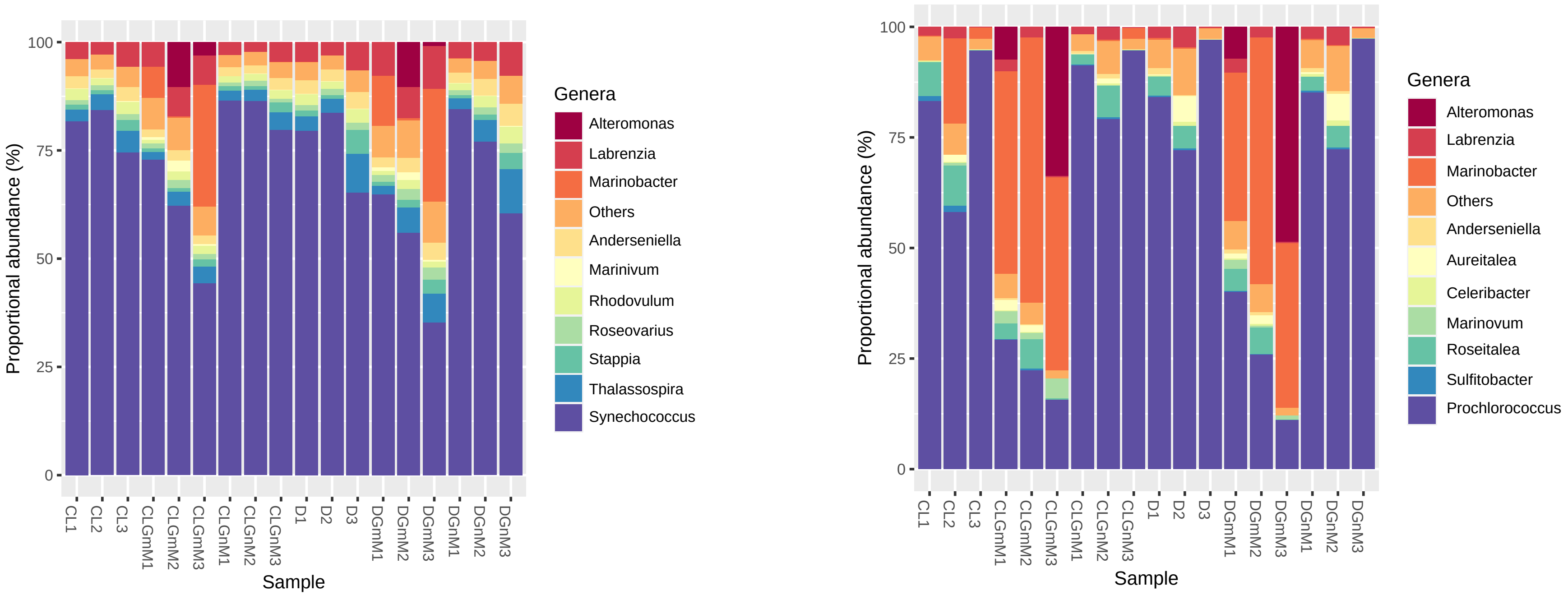
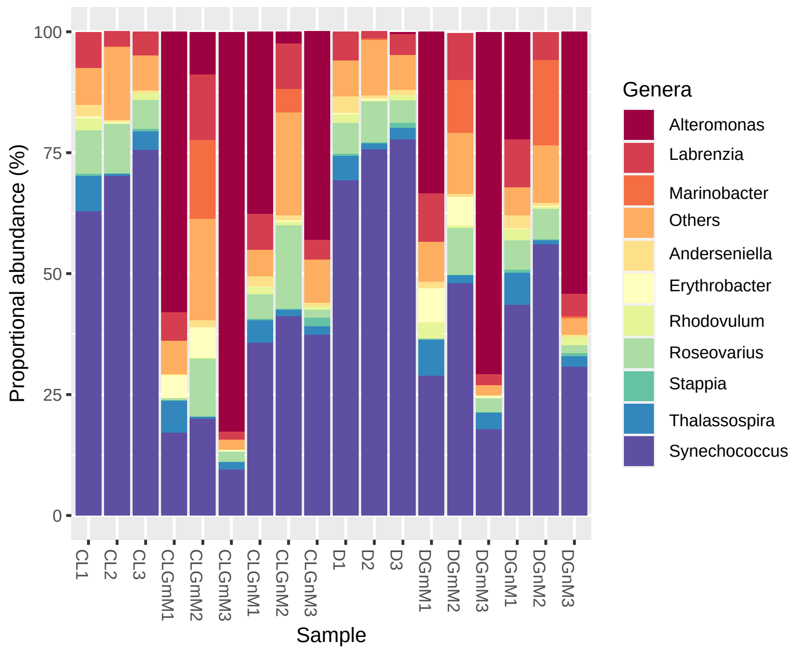
A. Synechococcus sp. WH7803

C. Prochlorococcus sp. MED4

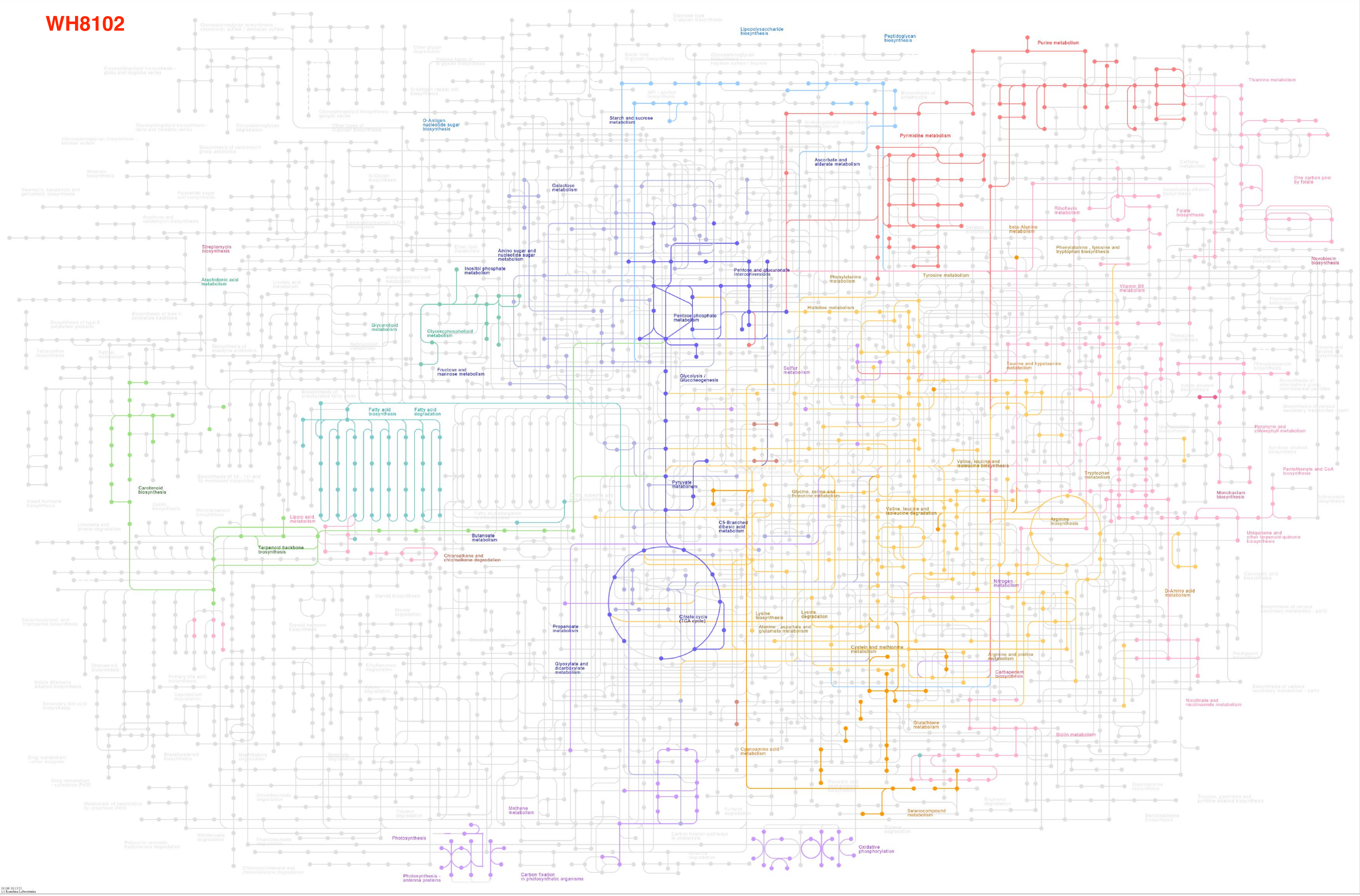


B. Synechococcus sp. BL107



Supplementary Figure 1: Proportional abundance of different genera in cultures from *Synechococcus* and *Prochlorococcus*. Panel A shows results from *Synechococcus* sp WH7803 cultures. Panel B shows the results from *Synechococcus* sp BL107 cultures. Panel C showns the results from *Prochlorococcus* sp MED4 cultures. Proportional abundance was calculated based on total protein intensity per genera obtained by relative label-free abundance using Peaks X (Bioinformatics sol.) divided by total protein intensity per sample. Each column represent a sample. CL=control light, D=Darkess, GmM= glucose addition 5 mM, GnM= glucose addition 100 nM. Three biological replicates were prepared per condition (1,2,3).

WH8102


Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate
Mannose type O-glycan biosynthesis
Lipopolysaccharide biosynthesis
Peptidoglycan biosynthesis
Purine metabolism
Other glycan degradation
Various types of N-glycan biosynthesis
Mucin type O-glycan biosynthesis
Glycosaminoglycan biosynthesis - heparan sulfate / heparin
Thiamine metabolism
Glycosphingolipid biosynthesis - globo and isoglobo series
O-Antigen repeat unit biosynthesis
GPI - anchor biosynthesis
Biosynthesis of siderophore
Glycosphingolipid biosynthesis - ganglio series
Starch and sucrose metabolism
O-Antigen nucleotide sugar biosynthesis
Glycosphingolipid biosynthesis - lacto and neolacto series
Glycosaminoglycan degradation
Other types of O-glycan biosynthesis
Arabinogalactan biosynthesis
Pyrimidine metabolism
Glycosaminoglycan biosynthesis - keratan sulfate
Biosynthesis of vancomycin group antibiotics
Ascorbate and aldarate metabolism
Caffeine metabolism
Aflatoxin biosynthesis
N-Glycan biosynthesis
One carbon pool by folate
Neomycin, kanamycin and gentamicin biosynthesis
Polyketide sugar unit biosynthesis
Galactose metabolism
Isoquinoline alkaloid biosynthesis
Riboflavin metabolism
Folate biosynthesis
Acarbose and validamycin biosynthesis
Lipoarabinomannan (LAM) biosynthesis
beta-Alanine metabolism
Betalain biosynthesis
Streptomycin biosynthesis
Ether lipid metabolism
Amino sugar and nucleotide sugar metabolism
Phenylalanine , tyrosine and tryptophan biosynthesis
Novobiocin biosynthesis
Inositol phosphate metabolism
Pentose and glucuronate interconversions
Phenylalanine metabolism
Tyrosine metabolism
Arachidonic acid metabolism
Linoleic acid metabolism
alpha-Linolenic acid metabolism
Vitamin B6 metabolism
Histidine metabolism
Flavonoid biosynthesis
Biosynthesis of type II polyketide backbone
Biosynthesis of type II polyketide products
Glycerolipid metabolism
Pentose phosphate metabolism
Glycerophospholipid metabolism
Sphingolipid metabolism
Tetracycline biosynthesis
Retinol metabolism
Biosynthesis of ansamycins
Fructose and mannose metabolism
Sulfur metabolism
Glycolysis / Gluconeogenesis
Taurine and hypotaurine metabolism
Phenylpropanoid biosynthesis
Indole alkaloid biosynthesis
Biosynthesis of unsaturated fatty acids
Fatty acid biosynthesis
Fatty acid degradation
Porphyrin and chlorophyll metabolism
Biosynthesis of various secondary metabolites - part1
Valine, leucine and isoleucine biosynthesis
Acridone alkaloid biosynthesis
Biosynthesis of 12-, 14- and 16-membered macrolides
Pyruvate metabolism
Glycine, serine and threonine metabolism
Tryptophan metabolism
Pantothenate and CoA biosynthesis
Carotenoid biosynthesis
Insect hormone biosynthesis
Zeatin biosynthesis
Fatty acid elongation
Valine, leucine and isoleucine degradation
Monobactam biosynthesis
Anthocyanin biosynthesis
Monoterpenoid biosynthesis
Lipoic acid metabolism
C5-Branched dibasic acid metabolism
Arginine biosynthesis
Limonene and pinene degradation
Butanoate metabolism
Ubiquinone and other terpenoid-quinone biosynthesis
Terpenoid backbone biosynthesis
Chloroalkane and chloroalkene degradation
Nitrogen metabolism
Clavulanic acid biosynthesis
D-Amino acid metabolism
Steroid biosynthesis
Steroid degradation
Biosynthesis of various secondary metabolites - part2
Sesquiterpenoid and triterpenoid biosynthesis
Steroid hormone biosynthesis
Propanoate metabolism
Citrate cycle (TCA cycle)
Lysine biosynthesis
Lysine degradation
Alanine , aspartate and glutamate metabolism
Cysteine and methionine metabolism
Arginine and proline metabolism
Prodigiosin biosynthesis
Diterpenoid biosynthesis
Ethylbenzene degradation
Glyoxylate and dicarboxylate metabolism
Carbapenem biosynthesis
Isoquinoline alkaloid biosynthesis
Primary bile acid biosynthesis
Caprolactam degradation
Xylene degradation
Biosynthesis of various secondary metabolites - part3
Secondary bile acid biosynthesis
Nicotinate and nicotinamide metabolism
Glutathione metabolism
Biotin metabolism
Drug metabolism - other enzymes
Brassinosteroid biosynthesis
Naphthalene degradation
Benzoate degradation
Cyanoamino acid metabolism
Drug metabolism - cytochrome P450
Penicillin and cephalosporin biosynthesis
Glucosinolate biosynthesis
Tropane, piperidine and pyridine alkaloid biosynthesis
Aminobenzoate degradation
Methane metabolism
Styrene degradation
Furfural degradation
Metabolism of xenobiotics by cytochrome P450
Toluene degradation
Selenocompound metabolism
Benzoxazinoid biosynthesis
Polycyclic aromatic hydrocarbon degradation
Nitrotoluene degradation
Fluorobenzoate degradation
Photosynthesis
Carbon fixation pathways in prokaryotes
Taurine degradation
Oxidative phosphorylation
Atrazine degradation
Chlorocyclohexane and chlorobenzene degradation
Photosynthesis - antenna proteins
Carbon fixation in photosynthetic organisms
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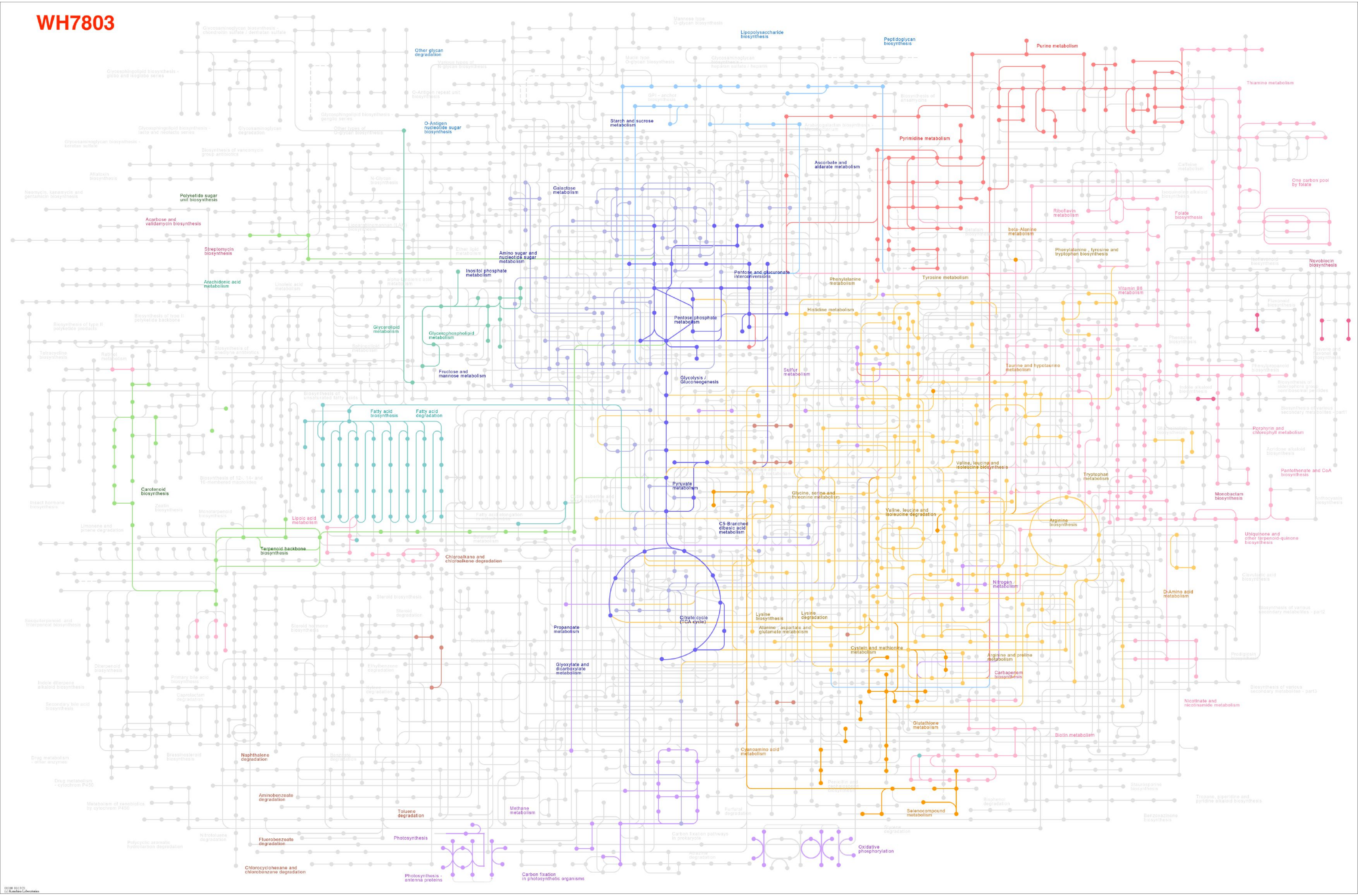
WH7803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Photosynthesis - antenna proteins
Carbon fixation in photosynthetic organisms
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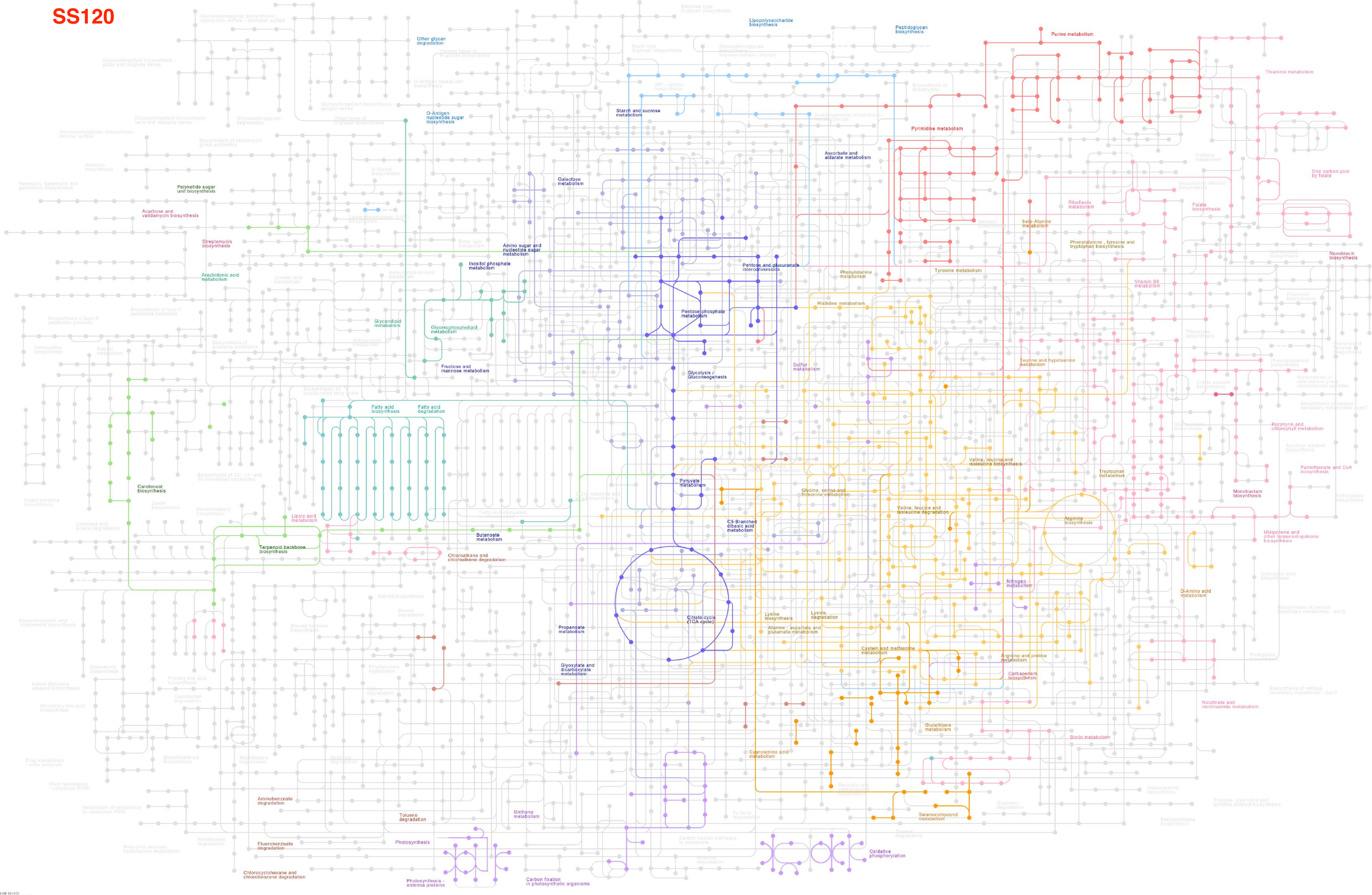
SS120



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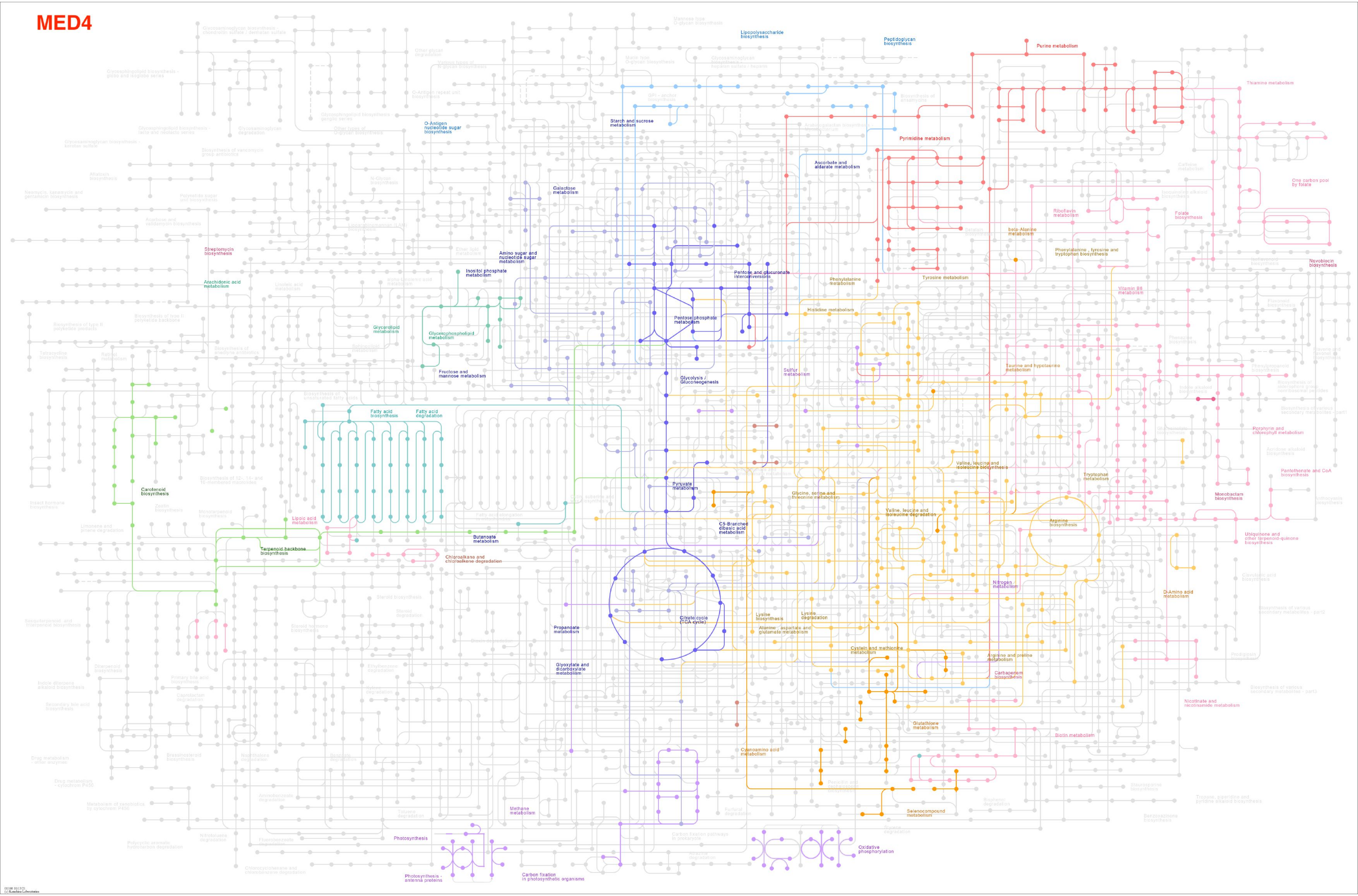
MED4



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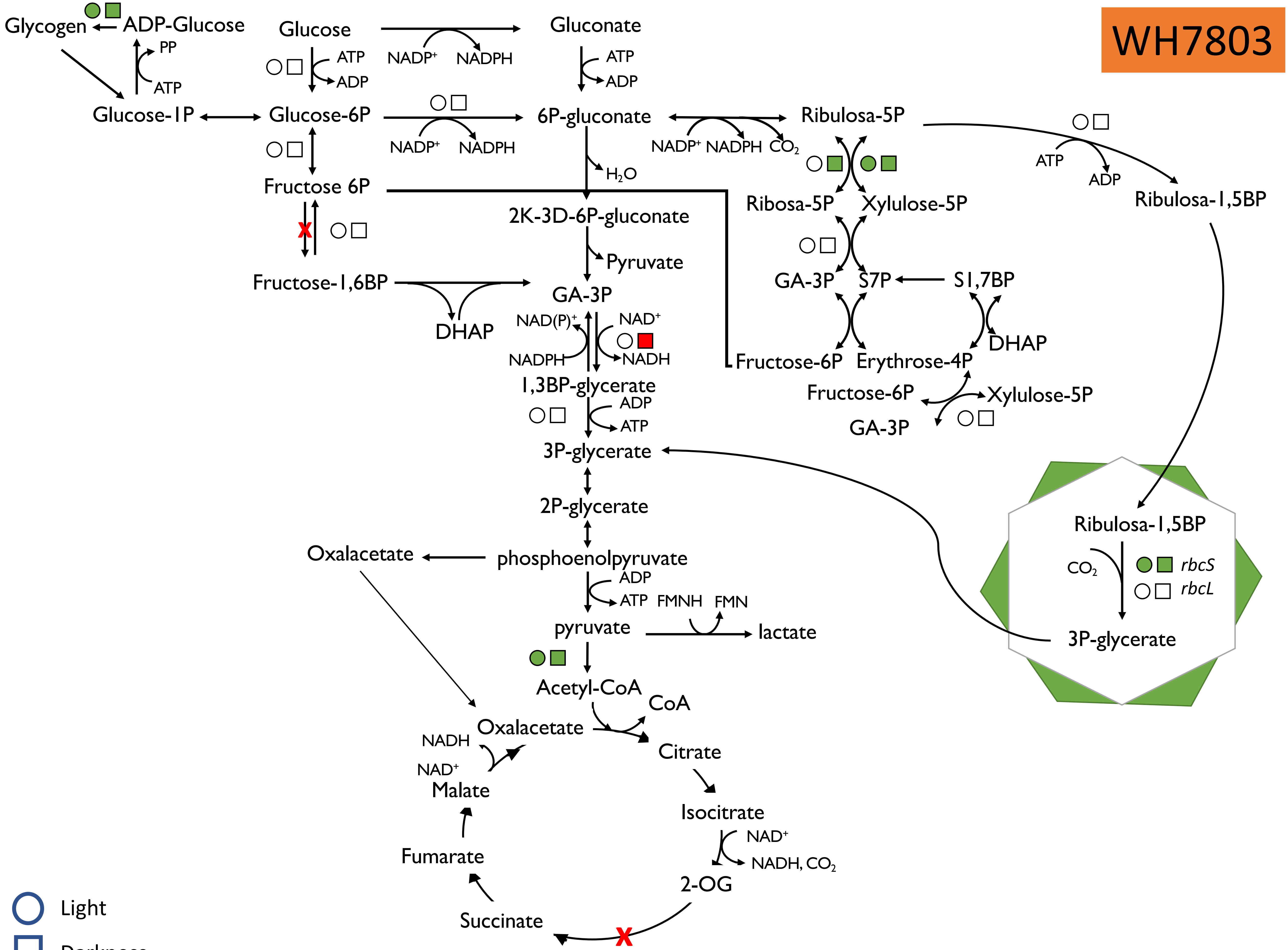
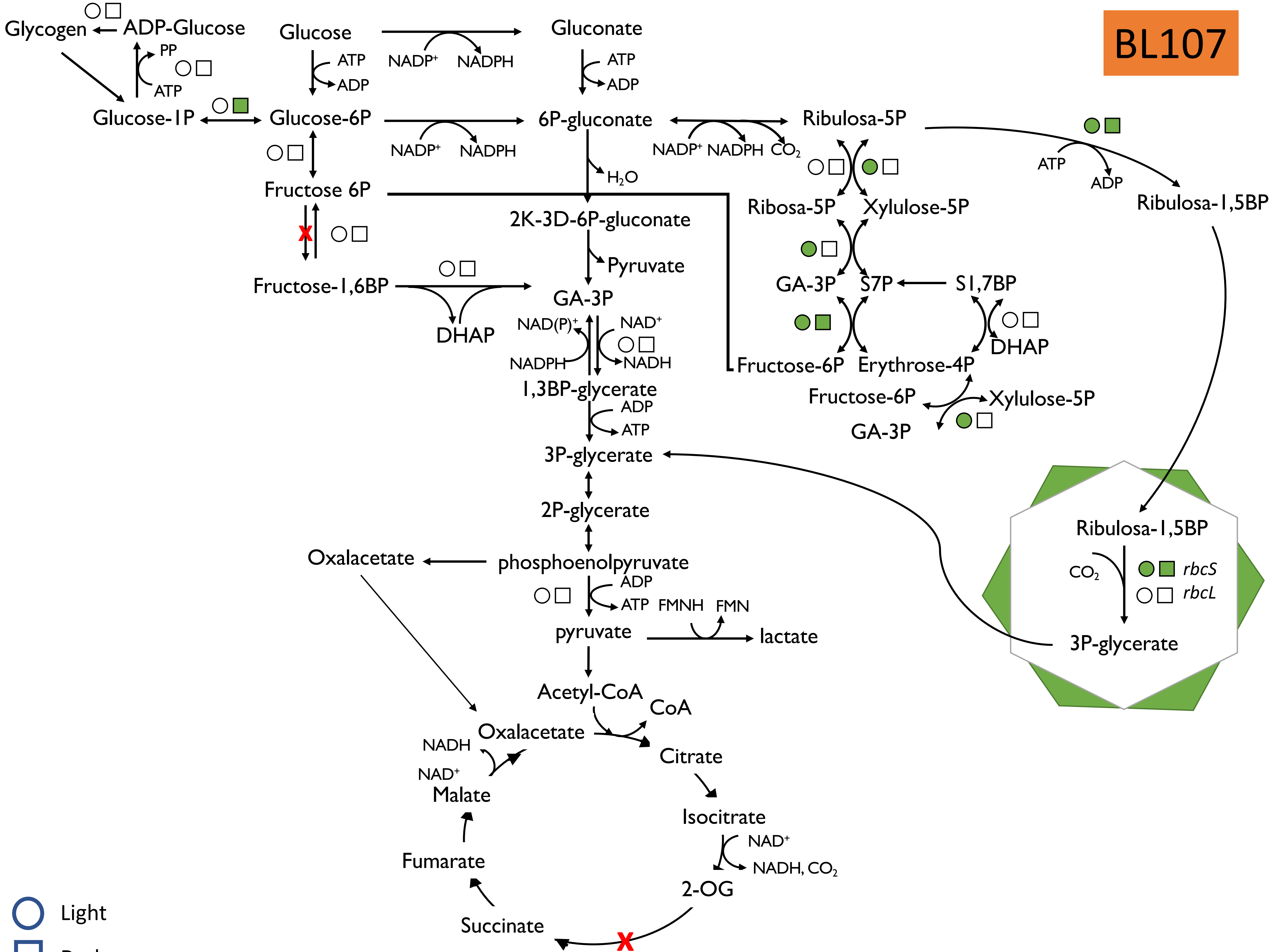
WH7803



○ Light

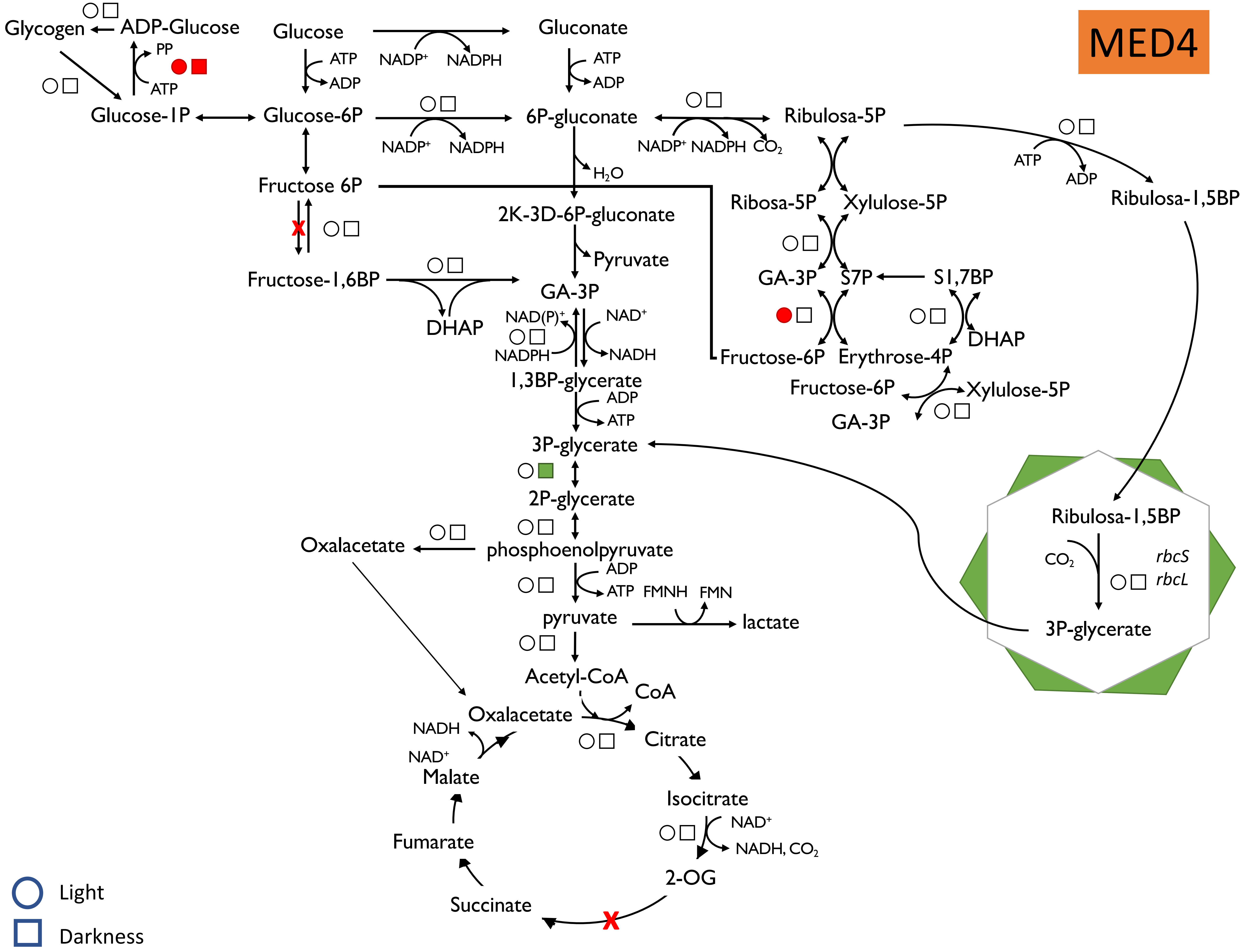
□ Darkness

BL107



○ Light

□ Darkness



MED4

Glycogen

ADP-Glucose

PP

ATP

Glucose-1P

Glucose

ATP

ADP

Glucose-6P

NADP+

NADPH

Gluconate

ATP

ADP

6P-gluconate

NADP+

NADPH

CO_2

Ribulosa-5P

ATP

ADP

Ribulosa-1,5BP

Fructose 6P

Fructose-1,6BP

DHAP

H_2O

2K-3D-6P-gluconate

Pyruvate

GA-3P

NAD(P)+

NADPH

NAD+

NADH

1,3BP-glycerate

ADP

ATP

3P-glycerate

2P-glycerate

Oxalacetate

phosphoenolpyruvate

ADP

ATP

FMNH

FMN

pyruvate

lactate

Acetyl-CoA

CoA

Oxalacetate

Citrate

NADH

NAD+

Malate

Isocitrate

NAD+

NADH, CO_2

Fumarate

2-OG

Succinate

Ribosa-5P

Xylulose-5P

GA-3P

S7P

S1,7BP

DHAP

Fructose-6P

Erythrose-4P

Fructose-6P

Xylulose-5P

GA-3P

Ribulosa-1,5BP

CO_2

rbcS

rbcL

3P-glycerate

○ Light

□ Darkness

Legends for supplementary figures

Supplementary figure 1. Effect of glucose availability on the proportional abundance of genera in cultures from *Synechococcus* and *Prochlorococcus*. A. *Synechococcus* sp. WH7803 cultures. B. *Synechococcus* sp. BL107 cultures. C. *Prochlorococcus* sp. MED4 cultures. Proportional abundance was calculated based on total protein intensity per genera obtained by relative label-free abundance using MarRef v6 as database. Each column represents individual samples. CL=control light, D=Darkness, GmM= glucose 5 mM, GnM= glucose 100 nM. Three biological replicates were prepared per condition (1,2,3).

Supplementary figure 2. Global overview map highlighting quantified proteins in *Synechococcus* sp. strains WH8102 and WH7803, and *Prochlorococcus* sp. strain SS120 and MED4. The pathway map shows all the proteins quantified in the proteomic experiments performed with these cyanobacterial strains. These maps were created in R using the Pathview package (1). KEGG terms were retrieved using the specific tool in UniProt (www.uniprot.com). The *Synechococcus* sp. strain BL107 map is not shown since its genome has not been included yet in KEGG.

Supplementary figure 3. Summary of the proteomics results showing the statistically significant changes in enzymes involved in glucose metabolism in *Synechococcus* sp. strains WH8102 and BL107, and *Prochlorococcus* sp. strain under light and darkness. Circles, light; squares, darkness. Green colour indicates an increase in abundance, and red colour a decrease in abundance. Arrows indicate the metabolic flow upon glucose addition.

Legends for supplementary tables

Supplementary table 1. Compilated quantitation of changes in the proteomes of all studied cyanobacterial strains. Numbers highlighted in light green are statistically significant. TTEST.L.LGnM, Student's t-test of results from cultures in the light vs cultures in the light with 100 nM glucose; FC.L.LGnM, fold-change from control cultures in the light with 100 nM glucose/ cultures in the light ; TTEST.L.LGmM, Student's t-test of results from control cultures in the light vs cultures in the light with 5 mM glucose; FC.L.LGmM, fold-change from control cultures in the light with 5 mM glucose/ cultures in the light ; TTEST.D.DGnM, Student's t-test of results from cultures in darkness vs cultures in darkness with 100 nM glucose; FC.D.DGnM, fold-change results from cultures in darkness with 100 nM glucose/ cultures in darkness ; TTEST.D.DGmM, Student's t-test of results from control cultures in darkness vs cultures in darkness with 5 mM glucose; FC.D.DGmM, fold-change results from cultures in darkness with 5 mM glucose/ cultures in darkness ; TTEST.L.D, Student's t-test of results from cultures in the light vs cultures in darkness; FC.D/L, fold-change results from cultures in darkness / cultures in the light.

Supplementary table 2. Quantitation of changes in the proteomes of all studied cyanobacterial strains. Results for each cyanobacterial strain are shown in a separate tab. Abbreviations of column titles are the same as in Supplementary table 1.

Supplementary table 3. Quantitation of changes in the proteomes of *Alteromonas* from all studied cyanobacterial cultures. Results from each cyanobacterial culture are shown in a separate tab. Abbreviations of column titles are the same as in Supplementary table 1.

Supplementary table 4. **Quantitation of changes in the proteomes of *Marinobacter* from all studied cyanobacterial cultures.** Results from each cyanobacterial culture are shown in a separate tab. Abbreviations of column titles are the same as in Supplementary table 1.

Bibliography

1. Luo W, Brouwer C. 2013. Pathview: an R/Bioconductor package for pathway-based data integration and visualization. Bioinformatics 29:1830-1.