

Supporting Information

Eisenhut *et al.* 10.1073/pnas.0807043105



Fig. S1. Slr0806 represents an enzyme with similarity to glycolate dehydrogenase subunit GlcD. Accordingly, GlcD is termed GlcD1 and Slr0806 GlcD2. (A) Consensus sequence of the flavin-binding site from the enzymes Syn GlcD (*Synechocystis* PCC 6803, SII0404), Eco GlcD (*Escherichia coli*, AAB02530), and Syn Slr0806 (*Synechocystis* PCC 6803, Slr0806). Arrows indicate highly conserved glycine (G) residues. (B) Phylogenetic tree of GlcD1, GlcD2, and GlcE. The tree was constructed from an alignment of GlcD1, putative GlcD2, and GlcE amino acid sequences with the program TreeView 1.5.0. Glucose-6-phosphate dehydrogenase from *E. coli* (G6PD, AAC74922) was defined as outgroup. Following sequences were used for comparison: Ana GlcD (*Anabaena* PCC 7120, Alr5269), Bru GlcD (*Brucella abortus*, AAX75619), Eco GlcD (*E. coli*, AAB02530), Mic GlcD (*Microcystis aeruginosa*, MAE52600), Nit GlcD (*Nitrosomonas europaea*, NP_840754), Pse GlcD (*Pseudomonas aeruginosa*, AAG08740), Syc GlcD (*Synechococcus* PCC 6301, Syc1237 d), Syn GlcD (*Synechocystis* PCC 6803, SII0404), Ana All14443 (*Anabaena* PCC 7120, All14443), Mic Mae300070 (*Microcystis aeruginosa*, MAE30070), Syc Syc0955 (*Synechococcus* PCC 6301, Syc0955 d), Syn Slr0806 (*Synechocystis* PCC 6803, Slr0806), Ana GlcE (*Anabaena* PCC 7120, All0624), Bru GlcE (*Brucella abortus*, YP_222981), Eco GlcE (*E. coli*, P52073), Mic GlcE (*M. aeruginosa*, MAE44320), Nit GlcE (*N. europaea*, CAD84585), Pse GlcE (*P. aeruginosa*, AAG08739), Syc GlcE (*Synechococcus* PCC 6301, Syc2373 d), and Syn GlcE (*Synechocystis* PCC 6803, SII1189).

Table S1. Strains and primers used in this work

Strain or primer	Genotype or sequence (5'→3')	Ref.
<i>Synechocystis</i> strains		
Wild type	PCC 6803	1
$\Delta glcD1$	PCC 6803 <i>sll0404::Km</i>	
$\Delta glcD2$	PCC 6803 <i>slr0806::Sp</i>	This work
$\Delta glcD1/\Delta glcD2$	PCC 6803 <i>sll0404::Km/sl0806::Sp</i>	
$\Delta gcv7/\Delta tsr/\Delta odc$	PCC 6803 <i>sll0171::Sp/sl0229::Km/sl1358::Cm</i>	
Primers		
<i>odc</i> (<i>sll1358</i>)	TCA TAG CGC ACC ACA TTG GTC ATG GAA GGC AGA ACC	This work
<i>glcD1</i> (<i>sll0404</i>)	GTC AAC GCC GTT ACC GAT GCC TAG GTT AAG CCG TTG	
<i>glcD2</i> (<i>slr0806</i>)	GGA GTC GCT CTG GGG ATA ACC GGT GAG ATA AAA GAT TGG TTG	

1. Eisenhut M, et al. (2006) The plant-like C2 glycolate cycle and the bacterial-like glycerate pathway cooperate in phosphoglycolate metabolism in cyanobacteria. *Plant Physiol* 142:333–342.