



Supplementary Figure S1

Supplementary Figure S1. Phylogenetic tree of the GlgX protein from 97 sequenced representatives of diverse cyanobacterial species. GlgX protein sequences were obtained from the JGI/IMG microbial database and aligned with ClustalW within MEGA 7. The phylogenetic tree was generated using MEGA 7 (Maximum Likelihood method). *Bacillus subtilis* and *Aeromonas veronii* were used in the analysis as outliers. While *Aeromonas* formed a distinct branch, *Bacillus subtilis* branched with *Synechococcus* 6803, indicating a similar evolutionary pattern of the gene in non-cyanobacterial prokaryotes. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.