

Supplementary

Figure S1. Phylogenetic tree based on 16S rRNA gene sequences of *Pseudanabaena* sp. PD34 and PD35 with *Pseudanabaena* strains information obtained from NCBI. The 16S rRNA sequence of *Synechococcus* sp. was used as an outgroup taxon. The tree was constructed using the neighbor-joining method with the maximum composite likelihood model, employing MEGA10 with 1000 bootstrap replications, and bootstrap values (%) are indicated at nodes.

