



**Figure S4. Bayesian analysis of Unk10 (108 aa positions) from marine *Synechococcus*.** For each strain phylogenetic affiliation is mentioned in brackets and the pigment type is indicated by colored circles. The tree is rooted using the sequence from *Crocosphaera watsonii* sp. WH8501. Series of four numbers shown at nodes correspond to Bayesian posterior probabilities (PP, ranging between 0 and 1), bootstrap values for ML analyses, Neighbor-Joining and Parsimony methods, respectively. Bootstraps, represented as a percentage, were obtained through 1,000 repetitions and PP from 1,000,000 generations. Only values higher than 0.60 for PP and 60% for bootstrap values are shown on the phylogenetic tree. The scale bar represents 0.1 substitutions per nucleotide.