Supplemental Figure 1

WU-BLAST was used to identify proteins homologous to Psb29. The proteins identified in the analysis all had E-values<10^{-14}. Protein sequences were aligned using CLUSTAL-W, followed by manual alignment. Three well conserved blocks were identified and used for tree building, consisting of a total of 165 columns. Columns are numbered according to the *Synechocystis* 6803 protein sequence.