

Supplementary Figure 4. Phylogenetic affiliations of predicted complex iron-sulfur molybdoenzyme (CISM) family protein sequences (alpha subunits) derived from single cell DEH-J10 in relation to other relevant alpha subunits from various bacteria and archaea. The phylogenetic analysis presented was performed with Mega5 using Maximum-Likelihood analysis and the Jones-Taylor-Thornton (JTT) substitution model. Phylogenies were also constructed using the Neighbour-Joining method, yet these made no major differences to the overall phylogeny presented. The scale bar represents 20% sequence divergence.

