**Figure 1S:** Structure-based sequence alignment of PrmA homologues from representatives of 9 different bacterial phyla.

Color coding represents the percentage identity. Secondary structure elements are indicated on top based on the PrmA3 structure. The position of the flexible glycine-rich loop is marked with a green box. Residues comprising the AdoMet binding site are enclosed in red boxes and labeled “A” and residues in the active site are indicated with orange boxes and labeled “S.” Genbank Accession Codes: *Thermus thermophilus* Q84BQ9, *Aquifex aeolicus* NP_214439, *Bacillus subtilis* P54460, *Bacteroides fragilis* YP_211276, *Chlorobium tepidum* Q8KG70, *Cytophaga hutchinsonii* ZP_00309590, *Escherichia coli* K12 NP_417725, *Synechococcus elongates* YP_173195, *Thermotoga maritima* Q9X0G8.