

SUPPLEMENTARY MATERIAL

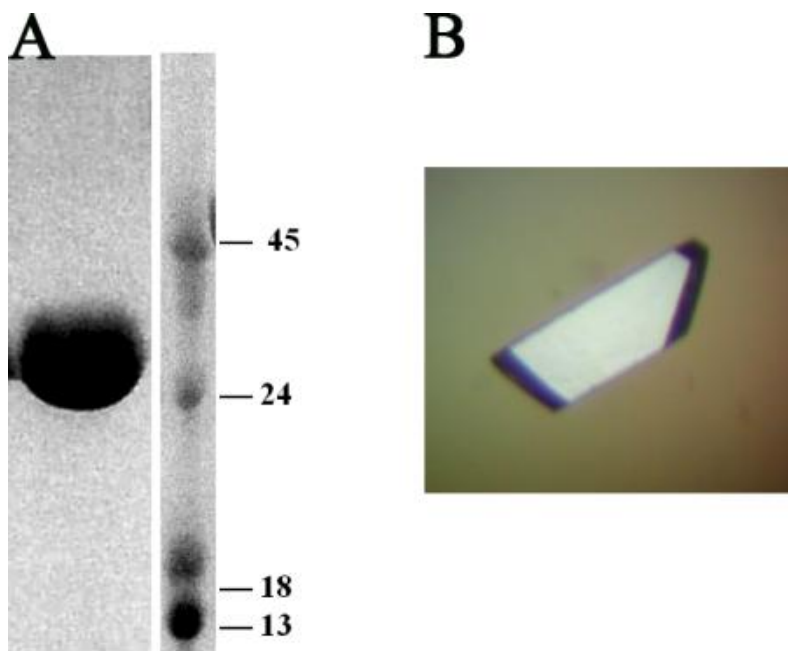


Figure S1. SDS-PAGE gel and crystal picture. (A). SDS/PAGE (12%) gel of purified *A. pernix* fibrillar protein. The protein behaves as a monomer as determined by size exclusion chromatography and SEC-MALS. (B). Protein crystal of *A. pernix* fibrillar protein was crystallized in 20 mM Tris·HCl, pH 7.0, 5% isopropanol, 10% PEG 4000 containing solution. The approximate dimensions of the crystals were 0.4 mm × 1 mm.

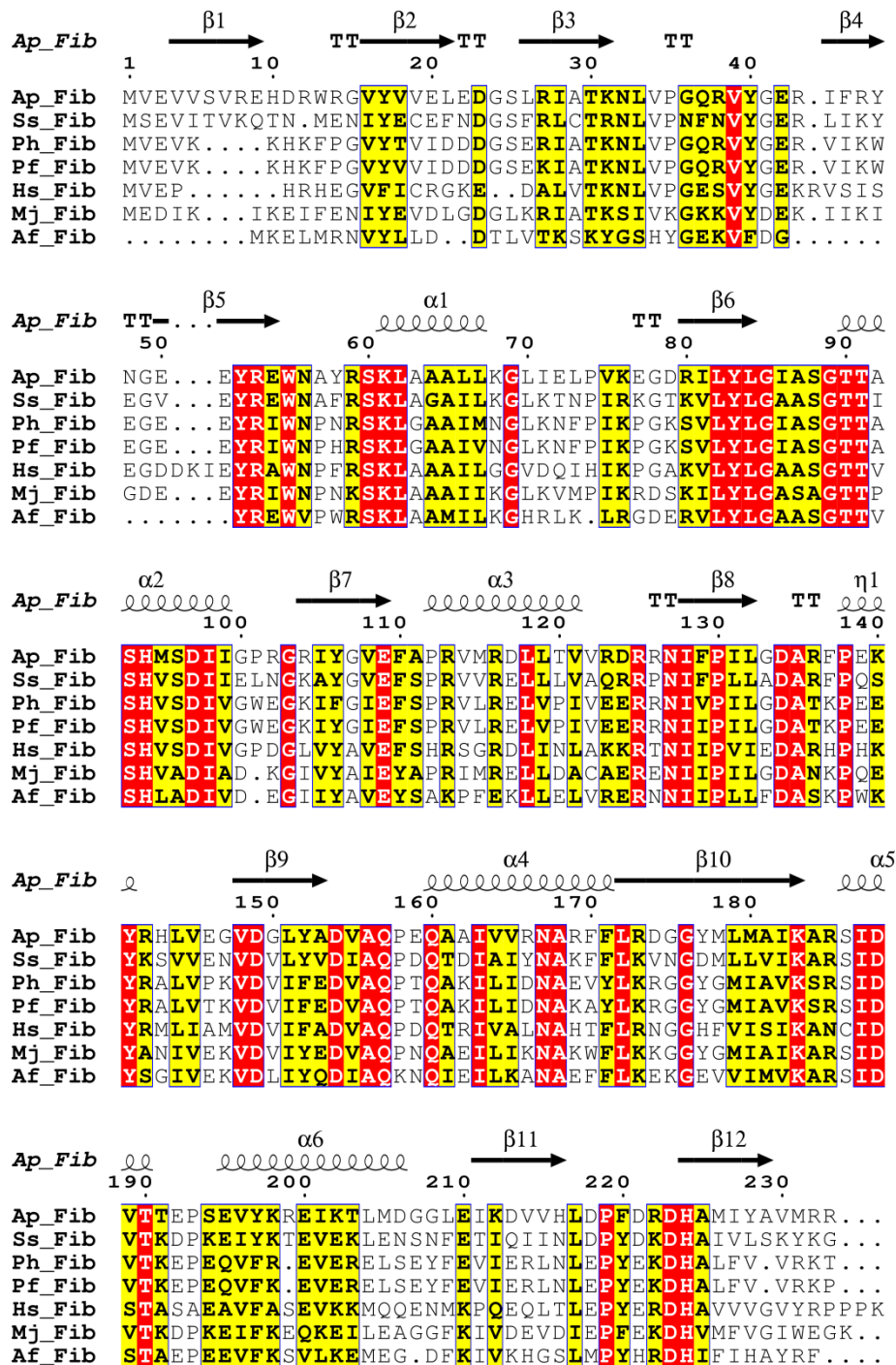


Figure S2. Sequence alignment of *A. pernix* fibrillarlin with fibrillarlin homologues. Sequence alignment *A. pernix* fibrillarlin with fibrillarlin structural homologues. Secondary structure details are from *A. pernix* fibrillarlin. Conserved residues are highlighted in yellow and highly conserved residues are highlighted in red. Residues that interact with SAM are marked with arrows (\blacktriangle). *Ap_Fib*, *Aeropyrum pernix*; *Ss_Fib*, *Sulfolobus solfataricus*; *Ph_Fib*, *Pyrococcus horikoshii*; *Pf_Fib*, *Pyrococcus furiosus*; *Hs_Fib*, *Homo sapiens*; *Mj_Fib*, *Methanococcus jannaschii*; *Af_Fib*, *Archaeoglobus fulgidus*.

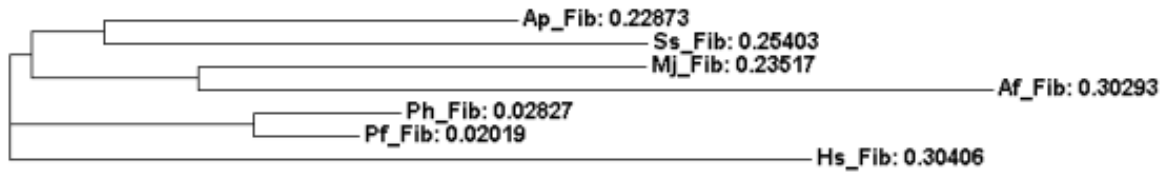


Figure S3.Phylogram. A phylogram of *A. pernix* fibrillarins and its published structural homologues. *A. pernix* fibrillarins are closely related in sequence to the Ss_Fib fibrillarins ortholog with 51% identical residues. Orthologs such as *Pyrococcus furiosus* fibrillarins have diverged significantly from *A. pernix* fibrillarins as shown in the phylogram, yet maintained the methylase function. The values represent the inferred evolutionary change between each branch. The branch-lengths are proportional to the amount of inferred evolutionary change. Ap_Fib, *Aeropyrum pernix*; Ss_Fib, *Sulfolobus solfataricus*; Mj_Fib, *Methanococcus jannaschii*; Af_Fib, *Archaeoglobus fulgidus*; Ph_Fib, *Pyrococcus horikoshii*; Pf_Fib, *Pyrococcus furiosus*; Hs_Fib, *Homo sapiens*.