

**P066** Structure of the archaeal Kae1/Bud32 fusion protein MJ1130 (*Methanococcus jannaschii*): a model for the eukaryotic EKC/KEOPS subcomplex involved in transcription and telomere homeostasis  
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The KEOPS complex has been recently described in yeast as essential for telomere elongation and transcription of essential genes. However, its precise biological role and biochemical function still remain unknown. One of these proteins is a universal protein known as Kae1 for Kinase-associated endopeptidase 1 in *S. cerevisiae*. Although this protein is annotated as an endopeptidase in most genomes, we showed that Kae1 protein from the euryarchaeon *Pyrococcus abyssi* has no protease activity, but is an atypical DNA binding protein associated to an AP-lyase activity. More recently, we determined the crystal structure of the Kae1 and Bud32 kinase fusion protein MJ1130 in the euryarchaeon *M. Jannaschii* and use the structure of the archaeal fusion protein to analyze the biochemical function of their homologues in yeast. Analysis of the structure of the bifunctional archaeal protein strongly suggests a direct interaction between yeast Kae1p and Bud32p kinase. Based on structural information from MJ1130 we studied the effect of interfacial mutations in the context of the yeast complex. Mutations that disrupt the Kae1p/Bud32p interaction identified in the archaeal complex have dramatic effects *in vivo* and *in vitro* in yeast, similar to those observed with deletion mutations of the respective components. We show that the direct interaction between Kae1p and Bud32p in yeast is required both for the transcription and the telomere homeostasis function of the KEOPS complex. Our results indicate that MJ1130 fusion protein is a good model for the eukaryotic KEOPS complex.