

MS07-P16 | STRUCTURAL AND MUTATIONAL INVESTIGATION OF PSYCHROPHILIC ADENYLATE KINASE REVEALS THE IMPORTANCE OF HYDROPHOBIC PACKING IN PROTEIN THERMAL STABILITY

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Protein thermal stability has been of particular interest since thermally stable proteins are desirable in both academic and industrial settings. Information on protein thermal stabilization can be obtained by contrasting homologous proteins from organisms living at distinct temperatures. Here, we report structural and mutational analyses of adenylate kinases (AKs) from psychrophilic *Bacillus globisporus* and mesophilic *Bacillus subtilis*. Comparison of their crystal structures showed suboptimal hydrophobic packing in the central CORE domain of the psychrophilic AK, where a polar side chain makes contacts with hydrophobic neighboring residues. Thermal stability measurement of AK mutants confirmed that optimization of hydrophobic interactions in the CORE domain is important for overall thermal stability. We also determined the crystal structures of AK mutants, which showed the largest thermal stability transition compared to the wild-type AKs. Taken together, our results provide a structural basis of the stability difference between the psychrophilic and mesophilic AK homologues, highlighting the role of hydrophobic interactions in protein thermal stabilization.