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Asymmetric Hexameric Assembly of the Archaeal Secretion ATPase. A. Yamagata, J.A. Tainer, Dept. of Molecular Biology, The Scripps Research Institute, La Jolla, CA, 92037 USA.

Members of the large family of bacterial and archaeal secretion ATPases play key roles in macromolecular transport, pilin and flagellar assembly systems. The central function of these proteins in facilitating bacterial toxin export and cellular adherence to human cells necessitates further analysis of the poorly understood chemo-mechanical structural mechanisms of secretion ATPases and their role in virulence.

Here, we describe the crystal structure of *Archaeoglobus fulgidus* GspE2, a putative archaeal secretion ATPase, in complex with AMP-PNP. Two subunits in the asymmetric unit exhibit distinct open-closed conformations characterized by rigid-body movement of two defined N- and C- terminal domains. They further form the asymmetric hexameric ring structure along a 3-fold crystallographic axis. AMP-PNP in the open form is bound within C-terminal domain. However, in the closed form, two arginine residues (arginine fingers) from N-terminal domain interact with gamma-phosphate of AMPPNP, suggesting that these interactions are required to maintain the closed conformation. A magnesium ion that is essential for ATP hydrolysis is only observed in closed form, suggesting that the closed form is the catalytically active subunit. Based on these results, we propose the working model how ATP hydrolysis is coupled with the basic mechanism of secretion ATPases.