BBB Seminar (BMED382)

SCAN ME

Thursday, October 16. 14:30 at the BBB, Auditorium 4

Structural basis for bacterial protein disaggregation and proteolysis

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Protein homeostasis is meticulously maintained across all cells, spanning from archaea to humans. Any deviation from the equilibrium of the proteome, induced by stress or cellular aging, leads to the accumulation of misfolded proteins, contributing to cellular toxicity. A complex proteostasis network actively manages misfolded proteins through processes such as refolding, degradation, or sequestration into intracellular inclusions. Integral to this protein quality control system are ATPases from the AAA+ superfamily (ATPases Associated to a variety of cellular Activities).

These AAA+ proteins, universally present in organisms, share a common structural fold for ATP hydrolysis, but each possesses distinct function-specific domains, enabling specialization in particular cellular activities and interactions with regulatory protein partners.

Our work focuses on the structural investigation of bacterial Hsp100 AAA+ chaperones involved in protein quality control. We aim at understanding their fine-tuned regulation, which is absolutely required by the bacterium to survive harsh environment conditions and useful for us in the effort of killing pathogenic bacterial strains. Using cryo-EM in combination with biochemical functional assays, we can describe the molecular tuning mechanisms used by bacteria to assure the disaggregation or proteolysis of toxic protein species only, while leaving intact functional protein molecules.

Chairperson: Aurora Martinez, Department of Biomedicine