

Abstract Submitted
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Structure of archaeal proteasomal ATPase PAN by single particle cryoEM RENEE ROYAL¹, University of North Carolina Asheville, Department of Physics, YU YADONG², University of California San Francisco Biophysics and Biochemistry Department, YIFAN CHENG³, University of California San Francisco Biophysics Department, CHENG LAB TEAM — ATP dependent protein degradation in eukaryotes by 26S proteasome are essential for many cellular processes including apoptosis, cell cycles and signal transduction. 26S proteasome is composed of a barrel shaped 20S protease core and two regulatory particles capped on each end. The ATPases in the 19S regulatory particles unfold and translocate substrates into 20S for degradation. Archaea has a homologous yet simpler 20S proteasome and a regulatory ATPase, proteasome activating nucleotidase (PAN.) In this study we used single particle cryoEM to study the three dimensional structure of PAN. We obtained a 3D reconstruction of PAN at a resolution of 18 Angstroms. By docking the atomic structure of PAN's N-terminal domain and ATPase domain to the atomic structure determined x-ray crystallography, we generated an atomic model of full length PAN ATPase.

¹University of California San Francisco Biophysics Department, summer internship

²Cheng Lab

³Principle Investigator

Renee Royal
University of North Carolina Asheville, Department of Physics

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