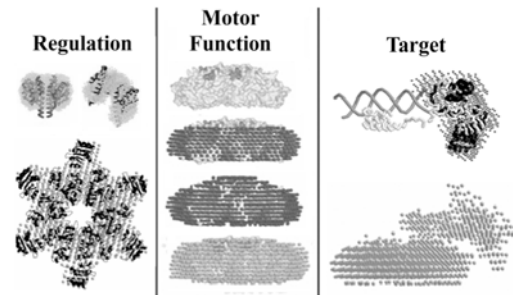


## W0061

**SAXS/WAXS Studies of  $\sigma 54$ -Dependent AAA+ ATPases: Insights about Signal Transduction and Motor Function.** B.T. Nixon,<sup>1</sup> B. Chen,<sup>1</sup> M. Callahan,<sup>2</sup> T.R. Hoover,<sup>3</sup> E. Kondrashkina,<sup>4</sup> <sup>1</sup>Biochemistry and Molecular Biology, Penn State Univ., University Park, PA 16802, <sup>2</sup>Chemistry, Univ. of California, Berkeley, CA, <sup>3</sup>Microbiology, Univ. of Georgia, Athens, GA, <sup>4</sup>BioCAT at APS/Argonne National Lab, Illinois Inst. of Technology, 9700 South Cass Ave, Argonne, IL 60439.

AAA+ ATPases are important molecular motors in all kingdoms of life. We are still learning how their actions are controlled and how they perform mechanical work. *Ab initio* solution structures provide us insight into both questions for AAA+ ATPases that regulate transcription of genes by the  $\sigma 54$ -form of bacterial RNA polymerase. In one case, a regulatory domain adopts two homo-dimeric forms, alternately repressing or derepressing motor assembly by adjacent ATPase domains; in another case, regulatory and ATPase domains cooperate to stabilize the assembled motor. Structures of ATPase in the presence of nucleotide analogs show subdomain reorientations that are coupled with conformational changes in the 'second region of homology' and pore region of the ring shaped motors to mediate interaction with the target protein,  $\sigma 54$ . Scattering data also yield preliminary models to explain how  $\sigma 54$  binds tightly to the activator in the transition state for ATP hydrolysis.



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