

**W0346**

**Structural and Biochemical Analysis of Nucleotide Binding in *B. subtilis* SecA.** D. Kim., J.F. Hunt, Dept. of Biological Sciences, Columbia Univ., New York, NY 10027 USA.

Protein translocation through the cytoplasmic membrane in bacteria is achieved through the Sec system. SecA is a peripheral membrane protein that acts as an ATPase and uses the energy derived from binding and/or hydrolysis of ATP to push the preprotein successively through the SecYEG channel; however, the exact nature of these steps is unclear. ecA in an ATP-bound conformation would provide insight into the fundamental role of nucleotide binding and hydrolysis in the conformational cycle of this mechanoenzyme. Non-hydrolysable ATP analogs do not bind SecA with high affinity and therefore are not useful for this study. Instead, a mutagenesis strategy was employed to engineer proteins that could bind but not hydrolyze nucleotide. Structural and biochemical studies of these mutants are underway.

We thank the NSLS at Brookhaven National Laboratory for access to Beamline X12B. This research is supported by the Biophysics Training Grant GM08281-17.