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Structural Determination of the ABC ATPase

J.Chen, Y. Mao, A. Davidson, and F. Quioco (Baylor)

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Introduction: The ATP-binding cassette (ABC) transporters are ubiquitous membrane protein complexes that use the energy generated from ATP binding and hydrolysis to selectively translocate solutes across biological membranes [1]. All ABC transporters are composed of two hydrophobic trans-membrane domains and two hydrophilic nucleotide-binding domains (NBDs). In recent years, enormous progress has been made in structural studies of ABC transporters. Both the monomeric forms [2-4] and the dimeric [5-7] forms of isolated NBDs were determined by X-ray crystallography. Most recently, the first structure of a complete ABC transporter, the bacteria lipid flippase MsbA, was determined to 4.5 angstroms [8]. However, in spite of this progress, our understanding of the ATPase activity regulation is still primitive. This is mainly due to the fact that the crystal structures of the three dimeric NBD revealed three completely different dimer interfaces, each suggesting a different function of the consensus signature motif, or the LSGGQ loop. In these experiments, we plan to resolve the correct subunits interaction between the two NBDs by determining the crystal structure of MalK in the dimeric form.

Methods and Materials: X-ray diffraction data were collected on Se-Met substituted protein crystals of *E.coli*. MalK.

Results: A three-wavelength MAD data set was collected.

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