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**Analytical Ultracentrifugation as a Method to Analyze Membrane Protein Homogeneity.** Matthew C. Clifton<sup>†</sup>, Huide Zhang<sup>‡</sup>, John W. Burgner II<sup>†</sup>, Mark A. Hermodson<sup>‡</sup>, Cynthia V. Stauffacher<sup>†</sup>, <sup>†</sup>Dept. of Biological Sciences and <sup>‡</sup>Dept. of Biochemistry, Purdue Univ., West Lafayette, IN 47907.

Energy-dependent transport of molecules across the membrane is essential for the cell and defects in transport have been implicated in a number of diseases. To understand the mechanism of energy-dependent transport, our laboratory has been physically characterizing the ribose import system from *Escherichia coli*. Ribose import in *E. coli* is performed by an ABC transporter which hydrolyzes ATP to transport ribose from the periplasm to the cytoplasm. The intact ribose ABC transporter complex has been thought to include one copy of the nucleotide-binding domain protein RbsA, one copy of the ribose-binding protein RbsB, and two copies of transmembrane protein RbsC. Our laboratory has recently purified the intact ribose transporter RbsABC as well as transport complex assembly intermediates RbsBC and RbsAC. Analytical ultracentrifugation was used as a method to determine sample homogeneity for use in future crystallization experiments as well as to determine the oligomeric state of the protein complexes. Stability of the complexes was analyzed through variations in centrifuge speed and concentration. The RbsABC complex was monodisperse in solution, and crystallization trials are now underway.