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**Structure of PITP $\beta$  in Complex with Phosphatidylcholine: Comparison to Other PITP Isoforms.** P.B. Vordtriede<sup>1</sup>, C. Doan<sup>1</sup>, J. Tremblay<sup>2</sup>, L.R. Yarbrough<sup>2</sup>, M.D. Yoder<sup>1</sup>, <sup>1</sup>School of Biological Sciences, Univ. of Missouri-Kansas City, Kansas City, MO 64110 USA, <sup>2</sup>Dept. of Biochemistry & Molecular Biology, Univ. of Kansas Medical Center, Kansas City, KS 66160 USA.

Phosphatidylinositol transfer protein (PITP) is a ubiquitous eukaryotic protein which preferentially binds either phosphatidylinositol or phosphatidylcholine and catalyzes the exchange of these lipids between membranes. The biological function of these proteins is believed to involve cell signaling through phosphoinositide phosphorylation and receptor-mediated phospholipase C hydrolysis of phosphoinositides, although the mechanism of membrane binding and phospholipid exchange is not well understood. Mammalian cytosolic PITPs include the ubiquitously expressed PITP $\alpha$  and PITP $\beta$  isoforms (269-271 residues). We previously described the structure of rat PITP $\alpha$  complexed to PtdCho. We report here the structure determination of the  $\beta$  isoform of rat PITP in complex with phosphatidylcholine, determined to 2.1Å using molecular replacement techniques. This report will include the structure determination and comparison to other isoforms and other structures of PITP.