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**Crystal Structure of D-Ribulose 5-Phosphate 3-Epimerase in Complex with D-Xylitol 5-Phosphate.** Alexander A. Fedorov, Elena V. Fedorov, Julie Akana\*, John A. Gerlt\*, Steve C. Almo, Dept. of Biochemistry, Albert Einstein College of Medicine, Bronx, NY 10461 \*Dept. of Biochemistry, Univ. of Illinois, at Urbana-Champaign, Urbana, IL 61801.

D-Ribulose 5-Phosphate 3-Epimerase belongs to the "ribulose phosphate binding" superfamily defined by the Structural Classification of proteins (SCOP). The crystal structure of D-Ribulose 5-Phosphate 3-Epimerase from *Streptococcus pyogenes* complexed with D-Xylitol 5-Phosphate and Zn was solved by molecular replacement with EPMR using model derived from the *Synechocystis* RPE hexamer (PDB file 1TQJ). The refinement was carried out using CNS at 1.8 Å resolution to a  $R_{\text{cryst}}=0.224$  and  $R_{\text{free}}=0.256$ . The final structure contains 19748 protein atoms, 12 inhibitor molecules, 12 Zn atoms and 991 water molecules for two hexamers of the complex in the asymmetric unit. Every Zn atom in the structure is coordinated by two oxygens from the inhibitor and by His 34, Asp 36, His 67 and Asp 176 from the enzyme. The functional and structural correlations for D-Ribulose 5-Phosphate 3-Epimerase will be presented.