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Evolution of Function in the Family of Cyclitol Sugar Phosphatases. Boguslaw Stec¹, Kimberly A. Stieglitz², Mary F. Roberts², ¹Dept. of Chemistry, Univ. of Texas, El Paso, TX, 79968, ²Dept. of Chemistry, Merkert Chemistry Center, Boston College, Chestnut Hill MA 02467.

In 1995, York, J. D., Ponder, J. W., and Majerus, P. W. (*Proc. Natl. Acad. Sci.* 92, 5149-5153) described structural similarities between inositol monophosphatase (IMPase) and Fructose 1,6 bisphosphatase and suggested that they originated from a common ancestor. Since that time this class of proteins with distinct α - β - α - β - α architecture has been enriched by new crystal structures and the class was extended to include inositol polyphosphate phosphatase as well as bis-phosphate nucleotidase. We have contributed to understanding of the relationships in this family by solving number of structures and identifying the dual function enzymes in archaeal organism. Recently, we have further enlarged this class by solving IMPases from *Thermotoga maritima* and *E. coli*. The refined structures suggest the manner in which the divergence of function and specialization of those enzymes is achieved. The IMPase from *E. coli* is monomeric and plays an auxiliary role in gene expression while the tetrameric enzyme from *T. maritima* is one of the most active IMPases known. What is even more interesting that the tetrameric organization is analogous to regulated tetramers of fructose 1,6 bisphosphatases from eukaryotic organisms. We will present the structures of those new IMPases. By comparing the new crystal structures with those already determined we will highlight features responsible for specialization of function and suggested the way the enzymes evolve.

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