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Structure of Phosphatidylglycerophosphatase (Pgpase), A Membrane-Bound Phosphatase, Reveals A Binuclear Metal Binding Site and Channel Formation. Desigan Kumaran, Subramanyam Swaminathan. Biology Dept., Brookhaven National Laboratory, Upton, NY.

Phosphatidylglycerophosphatase (PGPase, T1493, www.nysgsrc.org), an enzyme involved in the lipid metabolism, catalyzes the formation of phosphatidylglycerol from phosphatidylglycerophosphate. Phosphatidylglycerol is a multifunctional and ubiquitous phospholipid in the biological membranes of many organisms. Here we report the crystal structure of PGPase, the first representative structure of this family, from *Listeria monocytogenes* at 1.8 Å resolution. The crystal structure of PGPase containing one selenomet for a possible of 167 amino acids has been phased by the dual wavelength anomalous dispersion method. PGPase, an all-helical molecule, forms a homotetramer with NCS 222 symmetry. Each protomer contains an independent active site with two metal ions, Ca and Mg, forming a hetero-binuclear center located in a hydrophilic cavity near the surface of the molecule. The catalytic mechanism of this enzyme is likely to proceed via binuclear metal activated nucleophilic water. Notably, a long channel with two inter-linked linear water chains termed “proton wires” is observed at the tetrameric interface. The correlation between the binuclear center and this water channel will be discussed.