

Poster Presentation

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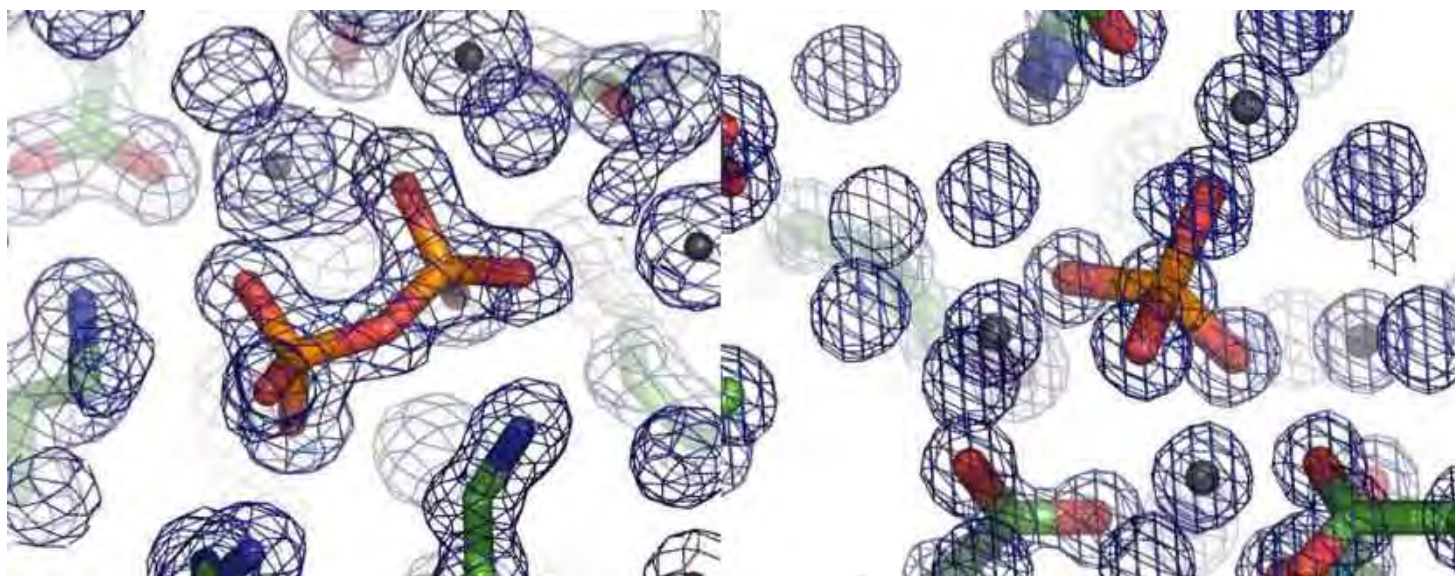
Mechanism of IPPase shown by high resolution Neutron and X-ray crystallography

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Soluble inorganic pyrophosphatase (IPPase) catalyzes the hydrolysis of inorganic pyrophosphate (PPi) to form orthophosphate (Pi). The action of this enzyme shifts the overall equilibrium in favor of synthesis during a number of ATP-dependent cellular processes such as in the polymerization of nucleic acids, production of coenzymes and proteins and sulfate assimilation pathways. Two Neutron crystallographic (2.10-2.50Å) and five high-resolution X-ray (0.99Å-1.92Å) structures of the archaeal IPPase from *Thermococcus thioreducens* have been determined under both cryo and room temperatures. The structures determined include the recombinant IPPase bound to Mg²⁺, Ca²⁺, Br⁻, SO₂²⁻ or PO₄²⁻ involving those with non-hydrolyzed and hydrolyzed pyrophosphate complexes. All the crystallographic structures provide snapshots of the active site corresponding to different stages of the hydrolysis of inorganic pyrophosphate. As a result, a structure-based model of IPPase catalysis is devised showing the enzyme's low-energy conformations, hydration states, movements and nucleophile generation within the active site.

[1] Hughes, R.C., Coates, L., Blakeley, M.P., et al. (2012). Inorganic pyrophosphatase crystals from *Thermococcus thioreducens* for X-ray and neutron diffraction. *Acta Crystallogr Sect F Struct Biol Cryst Commun* 68:1482-1487.



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