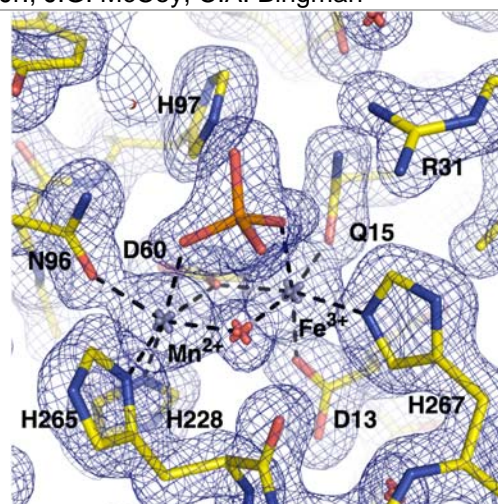
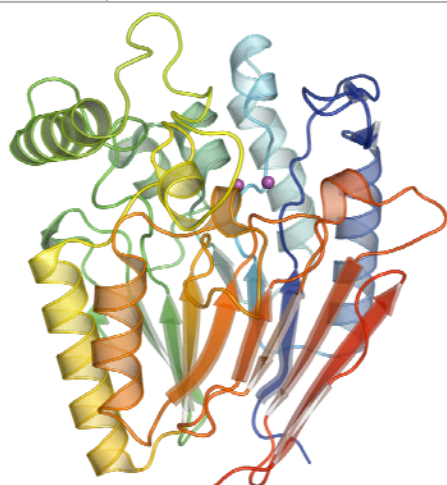


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



| | | |
|---------------------------|--|---------------------------------|
| Target ID | GO.70653 | |
| Source Organism | <i>Danio rerio</i> | |
| Target Name | BC054642 | |
| PDB Entry | 2NXF | Deposition: 17-Nov-2006 |
| Function | Dimetal phosphatase from <i>Danio rerio</i> LOC 393393 | |
| Produced From | <i>E. coli</i> B834 p(RARE2) pVP-16K | |
| Structure by X-ray | Resolution: 1.70 Å | R-value (R-free): 16.2% (18.0%) |
| | No. of Residues/ASU: 314 | Monomers/ASU: 1 |
| Data Collected At | Advanced Photon Source, GM/CA-CAT 23-ID-D, 08-Nov-2006 | |
| Authors | E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr., J.G. McCoy, C.A. Bingman | |



Structural Features

The gene Zgc:64213 of *Danio rerio* encodes a 322-residue long hypothetical protein LOC393393 (hpLOC393393) with a predicted molecular mass of 36.6 kDa. The structure showed that hpLOC393393 belongs to the alpha/beta class of proteins with the 4-layer sandwich architecture and purple acid phosphatase topology (CATH code 3.60.21). The closest structural homologs of hpLOC393393 are purple acid phosphatases from a range of species and several other phosphoesterases including 5'-nucleotidase from *E. coli* (PDB code 1HO5) and cyclic nucleotide phosphodiesterase Rv0805 from *Mycobacterium tuberculosis* (PDB ID 2HYP). All these structures are structurally related to the catalytic subunit of calcineurin A, a calmodulin-dependent serine/threonine protein phosphatase 2B. Calcineurin is a known target of immunosuppressant drugs cyclosporine A and FK506. The close sequence homologs of hpLOC393393 were found in a wide range of mammalian, plant, and bacterial species. None of the proteins homologous to hpLOC393393 have been previously characterized biochemically. The active site of the protein is located above the central beta-sheet sandwich and contains a dimetal center. Both of the metal ions show octahedral coordination. The inductively coupled plasma metal analysis of the protein sample used in this study revealed presence of 1.3 mol iron and 0.23 mol of manganese ions per mol of protein. Residue corresponding to His97 has been proposed to act as general acid/base in the catalytic mechanisms of multiple phosphatases and phosphoesterases. The guanidinium group of Arg31 is located in the vicinity of bound phosphate and may be involved in the neutralization of the charge of the phosphate group of the physiological substrate and/or the transition state species along the catalytic path.

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|---|--------------------|
| Percent Identity with Nearest PDB Structure at Time Solved | 27% (1QFC) |
| Pfam Cluster | Metallophosphatase |
| Sequence Cluster Size | 75 |

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