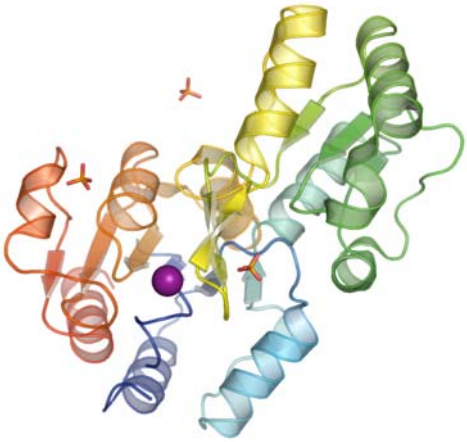
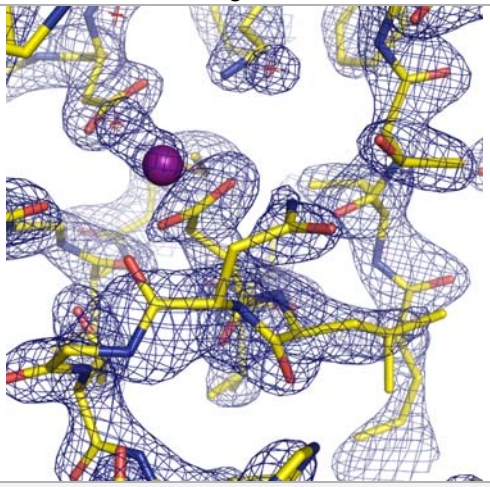
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.34556	
Source Organism	*Mus Musculus*	
Target Name	BC058177	
PDB Entry	2HO4	Deposition: 13-Jul-2006
Function	Haloacid dehalogenase-like	
Produced From	*E. coli* B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 2.20 Å	R-value (R-free): 22.7% (28.2%)
	No. of Residues/ASU: 503	Monomers/ASU: 2
Data Collected At	Advanced Photon Source 23-ID-D 18-Jun-2006	
Authors	J.G. McCoy, G.E. Wesenberg, G.N. Phillips, Jr., E. Bitto, C.A. Bingman	





Structural Features

The product of mouse HDHD2 gene encodes a hypothetical protein of 29 kDa with unknown function (referred to hereafter as Mm29k). The crystal structure of Mm29k revealed that this protein belongs to the α/β class of proteins with Rossmann fold topology. Based on the structure and sequence similarity, Mm29k can be classified as a member of the haloacid dehalogenase (HAD) superfamily of enzymes. The HAD superfamily includes a range of phosphotransferases, nucleotidases, and dehalogenases. The closest structural neighbors of 2HO4 identified by VAST include human pyridoxal 5'-phosphate phosphatase (PDB ID 2CFT) and NagD protein from *E. coli* (PDB ID 2C4N), which has nucleotide phosphatase activity. These structural homologs consist of a conserved core domain capped by an α-helical lid domain that defines the substrate specificity and undergoes a conformational change upon substrate binding. Despite the diverse substrate specificity, all HAD-superfamily enzymes share a common catalytic mechanism involving a conserved aspartate residue from a signature motif DxDx(T/V). The catalytic aspartate (Asp13 in Mm29k) acts as a nucleophile in a group transfer reaction. The second aspartate residue in the motif is involved in coordination of Mg2+ and acts as a general acid/base residue in several HAD-superfamily phosphatases. This residue is replaced by Asn15 in Mm29k structure; therefore it is unlikely that Mm29k possesses phosphatase activity. Several additional active site residues involved in Mg2+ coordination, substrate binding, and catalysis are also conserved in Mm29k (Thr46, Lys179, Asp204, Asp209). Interestingly, a conserved Lys227 is located in the vicinity of the active site of Mm29k. This residue might be structurally equivalent to a conserved arginine that functions as a halogen extraction residue in haloacid dehalogenases. This observation along with the absence of general acid/base residue in the active site of Mm29k suggests that catalytic mechanism of this putative enzyme is more similar to that of dehalogenases than phosphatases of the HAD superfamily.

Percent Identity with Nearest PDB Structure at Time Solved	27% (1ZJJ)
Pfam Cluster	Hydrolase
Sequence Cluster Size	562

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