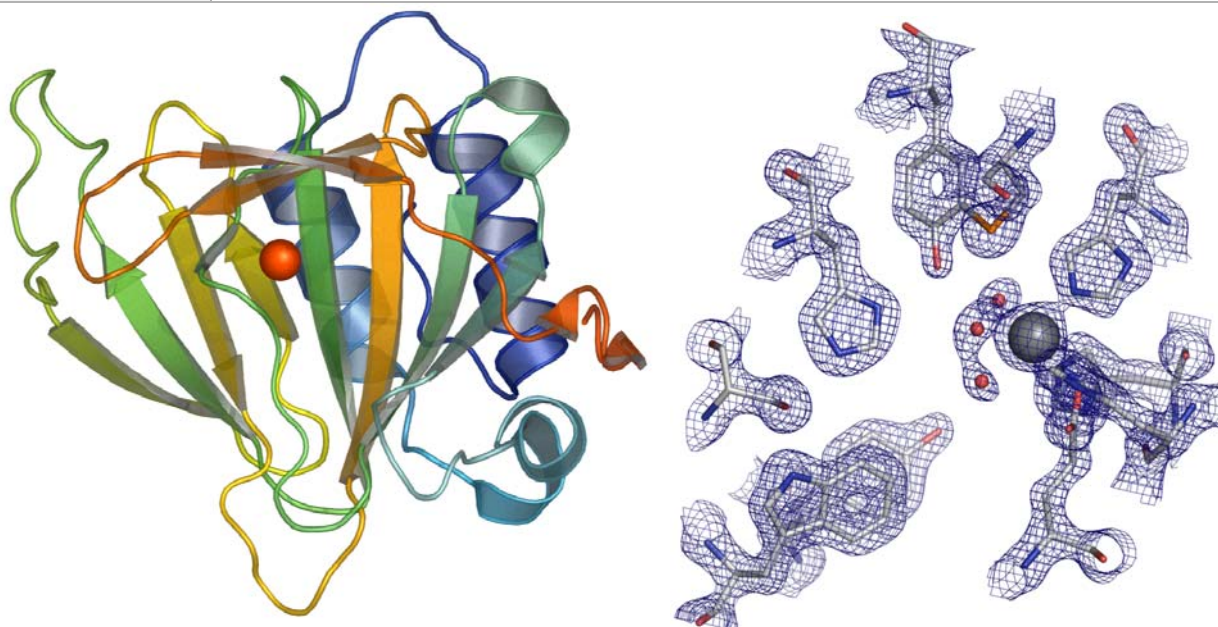


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.35683	
Source Organism	<i>Mus musculus</i>	
Target Name	BC013638	
PDB Entry	2ATF	Deposition: 24-Aug-2005
Function	cysteine dioxygenase (CDO) (FF/Refine: 2Q4S)	
Produced From	<i>E. coli</i> B834, pRARE2, pVP-16	
Structure by X-ray	Resolution: 1.75 Å	R-value (R-free): 17.8% (21.5%)
	No. of Residues/ASU: 199 (200)	Complexes/ASU: 1
Data Collected At	Advanced Photon Source GM/CA-CAT 12-Aug-2005	
Authors	J.G. McCoy, C.A. Bingman, E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr.	



Structural Features

The metalloprotein CDO from mouse is 91% identical to the human homolog. It catalyzes the oxidation of L-cysteine to L-cysteine sulfinic acid, a key intermediate in cys metabolism. This is a branch-point in the pathways to taurine or pyruvate. Reduced activity of this enzyme in humans has been implicated rheumatoid arthritis and systematic lupus erythematosus. An overabundance of cysteine is also associated with Alzheimers and Parkinson's diseases. CDO belongs to the cupin superfamily. In addition to a characteristic protein architecture, cupins contain two conserved sequence motifs that donate three histidines and a glutamate residue to a metal coordination site. The cupins are a functionally divergent superfamily whose members include dioxygenases, isomerases, decarboxylases, nuclear factors and storage proteins. In this structure, the catalytic iron is octahedrally coordinated by three histidines and three water molecules. The structure additionally reveals a rare covalent linkage between the sidechains of Cys93 and Tyr157. Both these residues are conserved in eukaryotic cysteine dioxygenases, with the hydroxyl of Tyr157 located 4.2Å from the iron.

References: (1) McCoy, J.G., Bailey, L.J., Bitto, E., Bingman, C.A., Aceti, D.J., Fox, B.G., Phillips, G.N. Jr. (2006) Structure and mechanism of mouse cysteine dioxygenase. *PNAS* 103(9):3084-9.

Percent Identity with Nearest PDB Structure at Time Solved	12% (1FI2)
Pfam Cluster	CDO_1
Sequence Cluster Size : Structures in PDB	64 at e<0.1

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