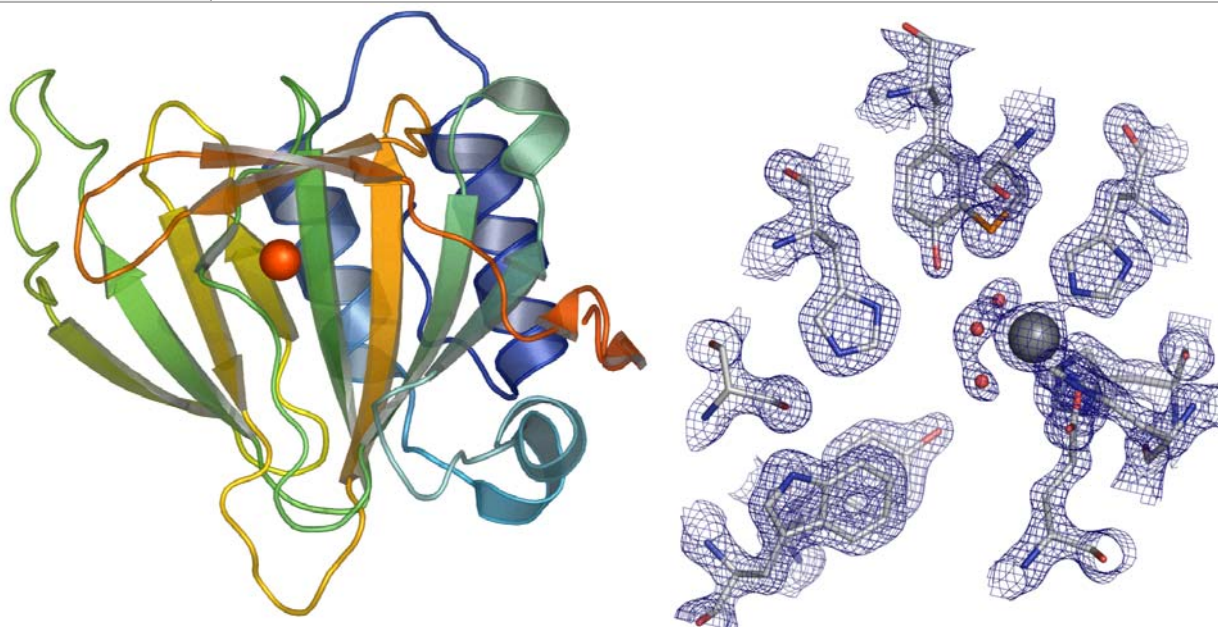


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



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

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

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