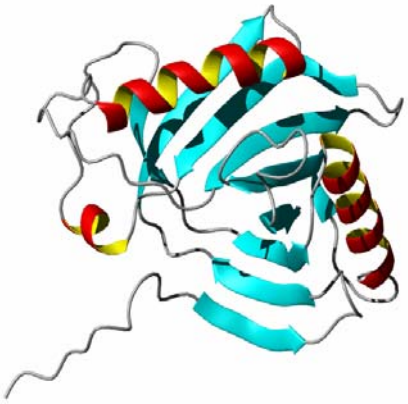
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.79130	
Source Organism	*Mus musculus*	
Target Name	NM_013546	
PDB Entry	2GOV	Deposition: 14-Apr-2006
BMRB Entry	6620	Deposition: 09-May-2006
Function	heme binding (murine p22hbp)	
Produced From	*E. coli*	
Structure by NMR	Restraints/Residue: 12.1	Subunits/Molecule: 1
	No. of Residues: 184	Molecular Weight: 22.8 kDa
	Backbone RMSD(18-171,181-190): 0.82 Å	All Heavy Atoms RMSD(18-171,181-190): 1.28 Å
Data Collected At	Medical College of Wisconsin	
Authors	Volkman, B.F., Dias, J.S., Goodfellow, B.J., Peterson, F.C.	



Structural Features

Murine p22HBP, a 22-kDa monomer originally identified as a cytosolic heme-binding protein ubiquitously expressed in various tissues, has 27% sequence identity to murine SOUL, a heme-binding hexamer specifically expressed in the retina. In contrast to murine SOUL, which binds one heme per subunit via coordination of the Fe(III)-heme to a histidine, murine p22HBP binds one heme molecule per subunit with no specific axial ligand coordination of the Fe(III)-heme. Using intrinsic protein fluorescence quenching, the values for the dissociation constants of p22HBP for hemin and protoporphyrin-IX were determined to be in the low nanomolar range. The three-dimensional structure of murine p22HBP, the first for a protein from the SOUL/HBP family, was determined by NMR methods to consist of a 9-stranded distorted beta-barrel flanked by two long alpha-helices. Although homologous domains have been found in three bacterial proteins, two of which are transcription factors, the fold determined for p22HBP corresponds to a novel alpha plus beta fold in a eukaryotic protein. Chemical shift mapping localized the tetrapyrrole binding site to a hydrophobic cleft formed by residues from helix alphaA and an extended loop. In an attempt to assess the structural basis for tetrapyrrole binding in the SOUL/HBP family, models for the p22HBP-protoporphyrin-IX complex and the SOUL protein were generated by manual docking and automated methods.

References: (1) Dias, J.S., Macedo, A.L., Ferreira, G.C., Peterson, F.C., Volkman, B.F., Goodfellow, B.J. (2006) The first structure from the SOUL/HBP family of heme-binding proteins, murine P22HBP. *J Biol Chem* 281(42):31553-61.

Percent Identity with Nearest PDB Structure at Time Solved	8.6% over 173 aa (1jyh)
Pfam Cluster	PF04832
Protonet Cluster Size : Structures in PDB	7521 : 11

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