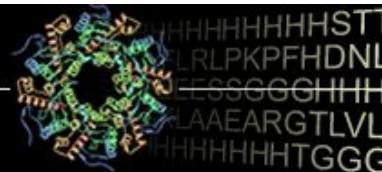


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.35156	
Source Organism	<i>Homo sapiens</i>	
Target Name	BC059385	
PDB Entry	2GOW	Deposition: 14-Apr-2006
BMRB Entry	7095	Deposition: 25-Apr-2006
Function	unknown	
Produced From	Cell-free	
Structure by NMR	Restraints/Residue: 10.8	Subunits/Molecule: 1
	No. of Residues: 116	Molecular Weight: 14.2 kDa
	Backbone RMSD(54-44,56-91): 0.5 Å	All Heavy Atoms RMSD(54-44,56-91): 1.03 Å
Data Collected At	Medical College of Wisconsin	
Authors	Volkman, B.F., de la Cruz, N.B., Lytle, B.L., Peterson, F.C.	



Structural Features

The protein Bc059385, whose solution structure is reported here, is the human representative of a recently identified family of membrane-anchored ubiquitin-fold (MUB) proteins. Analysis of their similarity to ubiquitin indicates that homologous amino acid residues in MUBs form a hydrophobic surface very similar to the recognition patch surrounding Ile-44 in ubiquitin. This suggests that MUBs may interact with proteins containing an alpha-helical motif similar to those of some ubiquitin binding domains. A disordered loop common to MUBs may also provide a second protein interaction site. From the available data, it is probable that this protein is prenylated and associated with the membrane. With <20% identity to ubiquitin, the MUB family further expands the sequence space that maps to the beta-grasp fold, and adds membrane localization to its list of functional roles.

References: (1) de la Cruz, N.B., Peterson, F.C., Lytle, B.L., Volkman, B.F. (2007) Solution structure of a membrane-anchored ubiquitin-fold (MUB) protein from *Homo sapiens*. *Protein Sci* 16(7):1479-84.

Percent Identity with Nearest PDB Structure at Time Solved	100% over 116 aa (1WGH)
Pfam Cluster	None
Protonet Cluster Size : Structures in PDB	26 : 1

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