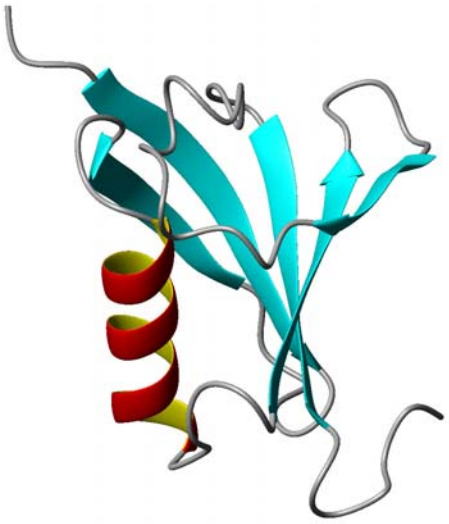
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.33910	
Source Organism	*Caenorhabditis elegans*	
Target Name	Ce5O73/F53F4.3	
PDB Entry	1T0Y (replaced 1SV7)	Deposition: 13-Apr-2004
BMRB Entry	6176	Deposition: 13-Apr-2004
Function	putative tubulin-folding cofactor B	
Produced From	*E. coli* SG13009[pRPEP4]	
Structure by NMR	Restraints/Residue: 14.2	Subunits/Molecule: 1
	No. of Residues: 122	Molecular Weight: 13.6 kDa
	Backbone RMSD(2–88): 0.78 Å	All Heavy Atoms RMSD(2–88): 1.26 Å
Data Collected At	Medical College of Wisconsin, Milwaukee, WI	
Authors	B.L. Lytle, F.C. Peterson, S.H. Qui, M. Luo, B.F. Volkman, J.L. Markley	



Structural Features

This structure is of the N-terminal domain (residues 1–120) of Ce5073, also known as F53F4.3 and tubulin cofactor B (CoB). The most similar structures in the PDB were elongin B, ubiquitin, and a number of other ubiquitin-like domains. Despite very low sequence similarity (< 20%) to ubiquitin and other beta-grasp proteins, the N-terminal domain of CoB adopts the same fold, consisting of a mixed five-stranded beta sheet that partially enfolds an alpha helix. The function of this domain is unknown, although it has been shown to be essential for the function of cofactor B in promoting correct folding of alpha-tubulin monomers and subsequent assembly into tubulin heterodimers. Since it lacks the C-terminal Gly-Gly sequence involved in conjugation, it is unlikely to function as a ubiquitin-like covalent modifier of other target proteins. Instead, we hypothesize that the domain has separate interaction sites for binding α-tubulin and cofactor E. This target aligns to Pfam domain of Pfam-B_9516 over residues 5–119.

References: (1) Lytle, B.L., Peterson, F.C., Qiu, S.H., Luo, M., Zhao, Q., Markley, J.L., Volkman, B.F. (2004) Solution structure of a ubiquitin-like domain from tubulin-binding cofactor B. *J Biol Chem* 279(45):46787-93.

Percent Identity with Nearest PDB Structure at Time Solved	11% over 97 aa (1LM8)
Pfam Cluster	B_9516
Protonet Cluster Size : Structures in PDB	173 : 1

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