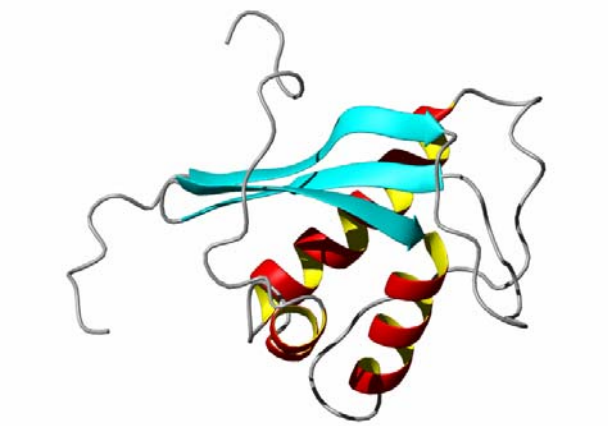
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.33811	
Source Organism	*Homo sapiens*	
Target Name	BC019655	
PDB Entry	2ETT	Deposition: 27-Oct-2005
BMRB Entry	6866	Deposition: 15-Nov-2005
Function	protein transfer	
Produced From	Cell-free	
Structure by NMR	Restraints/Residue: 16.7	Subunits/Molecule: 1
	No. of Residues: 128	Molecular Weight: 14.0 kDa
	Backbone RMSD(10-112): 1.3 Å	All Heavy Atoms RMSD(10-112): 2.0 Å
Data Collected At	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
Authors	Song, J., Zhao, Q., Tyler, R.C., Lee, M.S., Newman, C.L., Markley, J.L.	



Structural Features

The sorting nexins (SNXs) constitute a large group of PX domain-containing proteins that play critical roles in protein trafficking. We report here the solution structure of human sorting nexin 22 (SNX22). Although SNX22 has <30% sequence identity with any PX domain protein of known structure, it was found to contain the alpha/beta fold and compact structural core characteristic of PX domains. Analysis of the backbone dynamics of SNX22 by NMR relaxation measurements revealed that the two walls of the ligand binding cleft undergo internal motions: on the picosecond timescale for the beta1/beta2 loop and on the micro- to millisecond timescale for the loop between the polyproline motif and helix alpha2. Regions of the SNX22 structure that differ from those of other PX domains include the loop connecting strands beta1 and beta2 and the loop connecting helices alpha1 and alpha2, which appear to be more mobile than corresponding loops in other known structures. The interaction of dibutanoyl-phosphatidylinositol-3-phosphate (dibutanoyl-PtdIns(3)P) with SNX22 was investigated by an NMR titration experiment, which identified the binding site in a basic cleft and indicated that ligand binding leads only to a local structural rearrangement as has been found with other PX domains. Because motions in the loops are damped out when dibutanoyl-PtdIns(3)P binds, entropic effects could contribute to the lower affinity of SNX22 for this ligand compared to other PX domains.

References: (1) Song, J., Zhao, Q., Tyler, R.C., Lee, M.S., Newman, C.L., Markley, J.L. (2007) Solution structure of human sorting nexin 22. *Protein Sci* 16(5):807-14.

Percent Identity with Nearest PDB Structure at Time Solved	27% coverage (1OCS)
Pfam Cluster	NA
Sequence Family Size	215

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