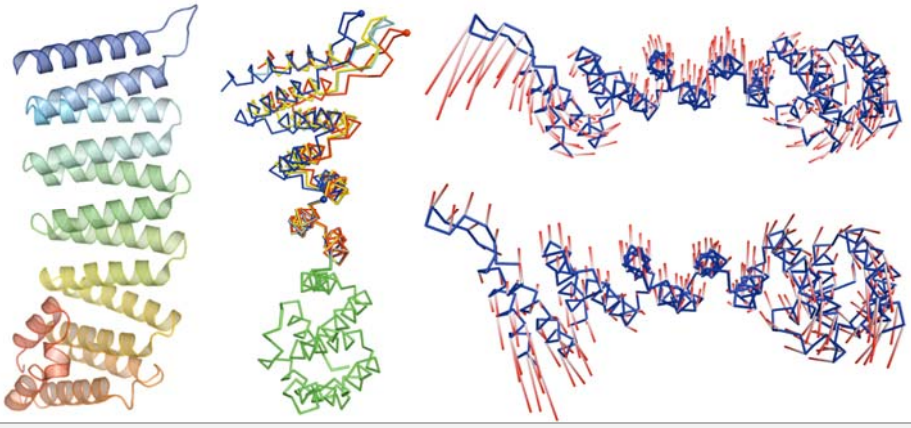
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.79361	
Source Organism	*Brachydanio rerio*	
Target Name	BC091448	
PDB Entry	2IFU	Deposition: 21-Sep-2006
Function	γ-SNAP	
Produced From	*E. coli* B834 p(RARE2) pVP-33K	
Structure by X-ray	Resolution: 2.6 Å	R-value (R-free): 24.0% (26.1%)
	No. of Residues/ASU: 1084	Monomers/ASU: 4
Data Collected At	APS GM/CA-CAT 23-ID-D, 24-Aug-2006; SER-CAT 22-ID 04-Aug-2006	
Authors	E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr., J.G. McCoy, C.A. Bingman	



Structural Features

Soluble N-ethylmaleimide-sensitive factor attachment protein gamma (γ-SNAP) is a member of a eukaryotic protein family involved in intracellular membrane trafficking. γ-SNAP has been found associated with the 20S complex, the cellular machinery involved in the recycling of "addressing" proteins present in the membrane-based complexes formed upon membrane fusion. The minimal 20S complex contains a SNARE (SNAP receptor) bundle coated by three molecules of α-SNAP (soluble NSF attachment protein), and the hexameric ATPase NSF (N-ethylmaleimide-sensitive factor). The X-ray structure of *Brachydanio rerio* γ-SNAP was determined to 2.6 Å and revealed an all-helical protein comprised of an extended twisted-sheet of helical hairpins with a helical-bundle domain at the C-terminus. Structural and conformational differences between multiple conformers of γ-SNAP molecules and Sec17p, an α-SNAP homologue from yeast, were analyzed. Analysis of inter-helical angles by WHATIF revealed that the helical sheet of monomer A of γ-SNAP is twisted by about 20 degrees less than that of Sec17p. Conformational variation in γ-SNAP molecules is matched with great precision by the two lowest frequency normal modes of the structure. Comparison of the lowest-frequency modes from γ-SNAP and Sec17p indicated that the structures share preferred directions of flexibility, corresponding to bending and twisting of the twisted sheet motif. The analysis thus suggests that SNAP proteins are *intrinsically* elastic. This observation may help rationalizing the energy transfer within the 20S complex during its disassembly: ATP hydrolysis by NSF results in a conformational change of NSF that generates the torque that leads to mechanical twisting of elastic adaptors (α-SNAP), subsequent relaxation of which is coupled to the SNARE bundle disruption.

References: (1) Bitto, E., Bingman, C.A., Kondrashov, D.A., McCoy, J.G., Bannen, R.M., Wesenberg, G.E., Phillips, G.N., Jr. (2008) Structure and dynamics of gamma-SNAP: insight into flexibility of proteins from the SNAP family. *Proteins* 70(1):93-104.

Percent Identity with Nearest PDB Structure at Time Solved	33% (1U6H)
Pfam Cluster	NSF
Sequence Cluster Size	173

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