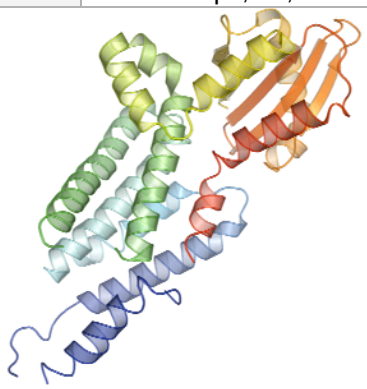
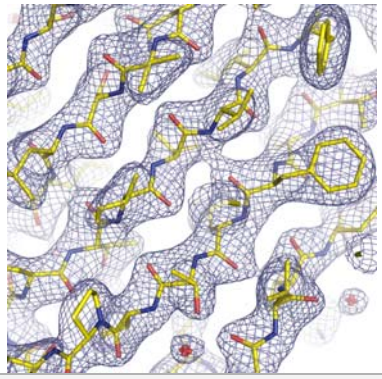
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.34351	
Source Organism	*Mus musculus*	
Target Name	BC065058	
PDB Entry	2GNX	Deposition: 11-Apr-2006
Function	hypothetical protein from Mouse Mm.209172	
Produced From	*E. coli* B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 2.45 Å	R-value (R-free): 28.1% (32.2%)
	No. of Residues/ASU: 288	Monomers/ASU: 1
Data Collected At	Advanced Photon Source 22-ID 10-Jul-2005	
Authors	G.N. Phillips, Jr., J.G. McCoy, E. Bitto, G.E. Wesenberg, C.A. Bingman	





Structural Features

Mouse gene MM209172 encodes 39 kDa protein of unknown function (Mm39k). The truncated N-terminal domain of mM39k (residues 101-235) consists of six parallel α-helices connected by flexible loops that are unresolved in the crystal structure. The C-terminal domain is made of a central five-stranded antiparallel β-sheet flanked by two α-helices on one side and one helix on the other side. The small C-terminal helix is inserted between α-2 and α-6, completing the α-helical bundle. Based on structural homology, the C-terminal domain of Mm39k belongs to GAF domain family. GAF domain is a ubiquitous regulatory module found in a wide range of signaling and sensory proteins in both prokaryotes and eukaryotes. Many GAF domains bind small molecule cofactors/activators that modulate the activity of GAF-domain-containing proteins. The closest structural homologues of Mm39k include the yeast GAF domain protein YKG9, regulatory segments of mouse cyclic nucleotide phosphodiesterase and bacterial adenylate cyclase and transcriptional regulators of IclR family. Despite very low sequence similarity and broad functional diversity, the 3-D structure of GAF domain is well conserved among these homologues. GAF domains of cyclic nucleotide diesterase/adenylate cyclase family contain a conserved NKFDE motif implicated in stabilization of bound cGMP/cAMP. They also harbor several conserved residues involved in binding of ribose and phosphate group of cyclic nucleotide. None of these features is conserved in Mm39k suggesting a different function of this protein. Several closest structural neighbors of Mm39k belong the IclR family of transcriptional activators. They consist of two domains: the N-terminal DNA binding domain, and the C-terminal GAF domain that is likely involved in binding of signal molecule. The α-helical N-terminal domain of Mm39k is reminiscent of the DNA binding modules in these proteins. However, the nature of the putative cofactor as well as the biochemical function of Mm39k remain speculative since the surface of Mm39k lacks any obvious binding site cavity and none of the core residues in its GAF domain are strictly conserved among the eukaryotic sequence homologues of Mm39k.

Percent Identity with Nearest PDB Structure at Time Solved	none
Pfam Cluster	DUF2003
Sequence Cluster Size	33

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