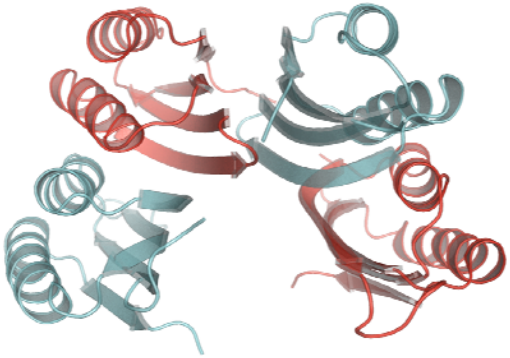
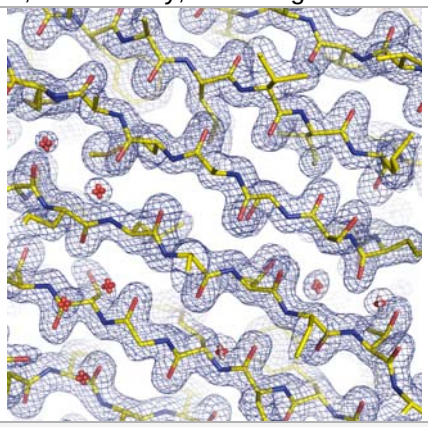
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.80004	
Source Organism	*Galdieria sulphuraria*	
Target Name	C855_101305G34.T1(MSU_GALDI)	
PDB Entry	2NYI	Deposition: 20-Nov-2006
Function	unknown	
Produced From	*E. coli* B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 1.80 Å	R-value (R-free): 17.8% (21.4%)
	No. of Residues/ASU: 341	Monomers/ASU: 2
Data Collected At	Advanced Photon Source 23-ID-D, 08-Nov-2006	
Authors	E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr., J.G. McCoy, C.A. Bingman	





Structural Features

The gene C855_101305G34.T1 of *Galdieria sulphularia* encodes 195-residue long protein of unknown function (hereafter referred to as GsHp21k). GsHp21k crystallizes as a symmetric dimer with horseshoe-like shape. Each monomer consists of two ACT domains connected by a short linker that was not resolved in the crystal structure. The ACT domain is a universal regulatory module that belongs to α/β class of proteins. It has ferredoxin-like topology with four antiparallel β-strands flanked by two α-helices. The ACT domains are found in a wide range of metabolic enzymes that are regulated by amino acid concentration, including aspartokinase (PDB ID 2DTJ), small subunit of acetolactate synthase (PDB ID 2FGC), and D-3-phosphoglycerate dehydrogenase (PDB ID 1YBA). Pairs of ACT domains bind specifically to a particular amino acid leading to allosteric regulation of the multidomain enzymes. The closest structural homolog of GsHp21k is a putative glycine cleavage system transcriptional repressor (PDB ID 1U8S) from *Vibrio cholerae*. The proposed repressor function of the *V. cholerae* protein implies its interaction with DNA. Despite the low sequence identity, GsHp21k and the *V. cholerae* protein have strikingly similar quaternary structure suggesting that GsHp21k might be a DNA-binding protein (possibly a transcriptional regulator). Two structural observations are consistent with this hypothesis: (1) The central opening of the horseshoe-like structure of GsHp21k is large enough to accommodate double stranded DNA; (2) The inner surface of the central cavity is lined with positively charged residues that could compensate the negative charge of DNA. The PSI-BLAST search revealed a distant relationship of GsHp21k to bacterial formyltetrahydrofolate deformylases. These ACT-domain containing enzymes catalyze the conversion of 10-formyltetrahydrofolate to tetrahydrofolate (THF). Interestingly, THF can be used by aminomethyltransferase of glycine cleavage system to make 5,10-methylenetetrahydrofolate, a metabolite essential for thymine synthesis. Taken together, it is intriguing to speculate that GsHp21k may be a regulatory protein of folate metabolism.

Percent Identity with Nearest PDB Structure at Time Solved	28% (1TXE)
Pfam Cluster	ACT
Sequence Cluster Size	140

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