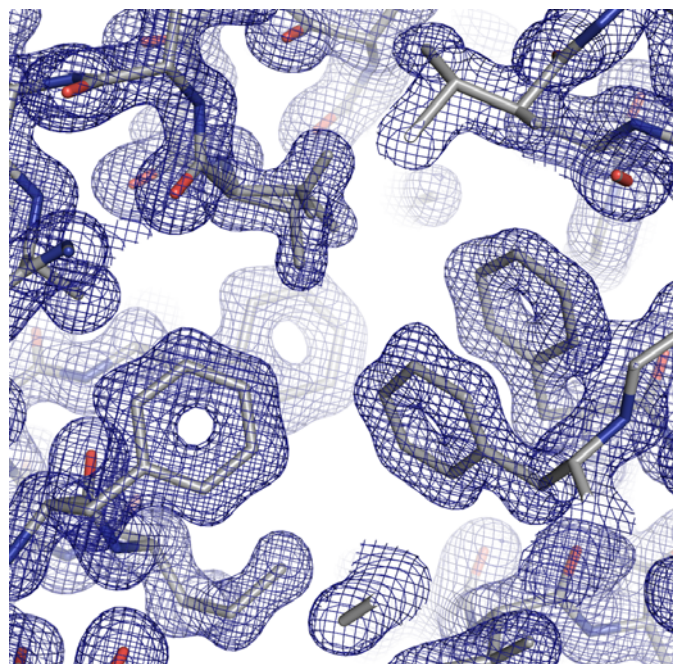
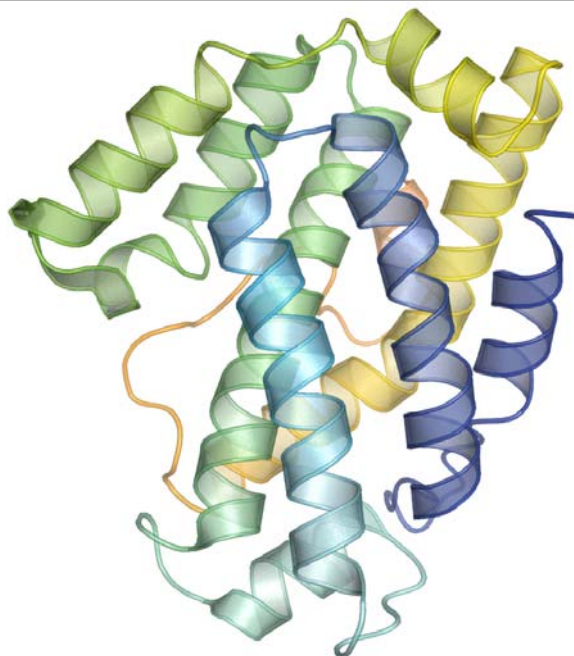


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.80017	
<b>Source Organism</b>	<i>Galdieria sulphuraria</i>	
<b>Target Name</b>	c503_101305g25.t1	
<b>PDB Entry</b>	2I3F	Deposition: 18-Aug-2006
<b>Function</b>	glycolipid transfer-like protein (FF/Refine: 2Q52)	
<b>Produced From</b>	<i>E. coli</i> B834 pRARE2	
<b>Structure by X-ray</b>	Resolution: 1.38Å	R-value (R-free): 18.2% (21.3%)
	No. of Residues/ASU: 448 (430)	Monomers/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source 22-ID 04-Aug-2006	
<b>Authors</b>	J.G. McCoy, G.E. Wesenberg, G.N. Phillips, Jr., E. Bitto, C.A. Bingman	



### Structural Features

The protein product of gene c503\_101305g25.t1 from *Galdieria sulphuraria* shows limited homology to a number of annotated glycolipid transfer proteins. The most similar structure in the Protein Data Bank is bovine glycolipid transfer protein which shares 27% identity to the *Galdieria* protein. The protein also shares 26% identity with the HET-C2 protein from the fungus *Podospora anserina*, which was shown to specifically bind glycosphingolipids *in vitro*. The structure is characterized by two layers of helices. The channel formed at the intersection of the two helices is strongly hydrophobic.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	27% (1SX6)
<b>Pfam Cluster</b>	Saposin (?)
<b>Sequence Cluster Size : Structures in PDB</b>	138 NR at e<0.1 : 2

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