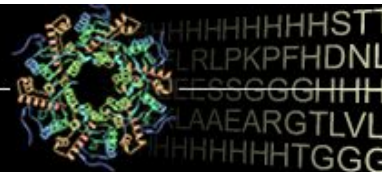
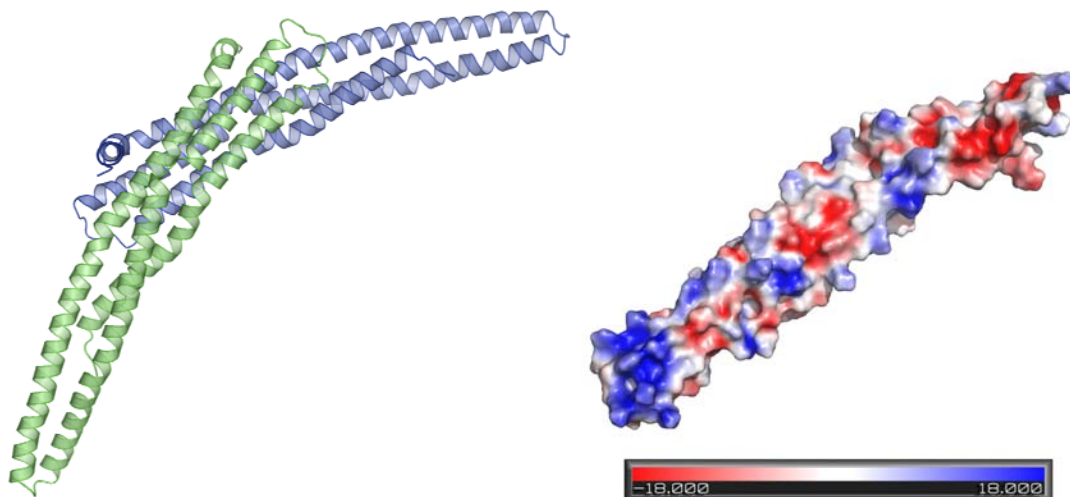


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.80055	
<b>Source Organism</b>	<i>Galdieria sulphuraria</i>	
<b>Target Name</b>	C501_101305G3.T1	
<b>PDB Entry</b>	3CAZ	3CAZ
<b>Function</b>	BAR domain protein	
<b>Produced From</b>	<i>E. coli</i> B834 pRARE2 pVP56K	
<b>Structure by X-ray</b>	Resolution: 3.34 Å	Resolution: 3.34 Å
	No. of Residues/ASU: 588 (415)	No. of Residues/ASU: 588 (415)
<b>Data Collected At</b>	Advanced Photon Source 23-ID-D 18-Aug-2007	
<b>Authors</b>	J.G. McCoy, E. Bitto, C.A. Bingman, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

The protein product of c501\_101305g3.t1 shows weak sequence similarity to a number of BAR domain proteins including amphiphysin and arfaptin. The quaternary structure of the enzyme also corresponds to that of previous BAR domain proteins, consisting of a homodimer of which the individual monomers are composed of three long parallel helices arranged so that the homodimer has a distinct curvature. BAR domains can be further divided into BAR domains, F-BAR domains, and I-BAR domains based on the degree of curvature of the protein. The 80055 protein is structurally analogous with the BAR domain proteins. BAR domain proteins have been associated with a number of cellular processes including apoptosis, endocytosis, regulation of the actin cytoskeleton, secretory vesicle fusion, tissue differentiation, and ion flux across membranes. In general, BAR domains are believed to be involved in binding membranes. This proteins has a series of strong electropositive patches along its concave surface that may be involved in this function. Like many other BAR domain proteins the 80055 protein has an additional C-terminal domain. However, the sequence of the C-terminal region did not demonstrate homology with any known functional domains and the electron density map was insufficient to build in this portion of the protein. BAR domain proteins have so far only been identified in eukaryotes.

*References:* (1) Ren, G., Vajjhala, P., Lee, J.S., Winsor, B., Munn, A.L.. The BAR domain proteins: molding membranes in fission, fusion, and phagy. *Microbiology and Molecular Biology Reviews* 70(1):37-120.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	14% of 205 aa (1149)
<b>Pfam Cluster</b>	No reliable hits
<b>Sequence Family Size</b>	2

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