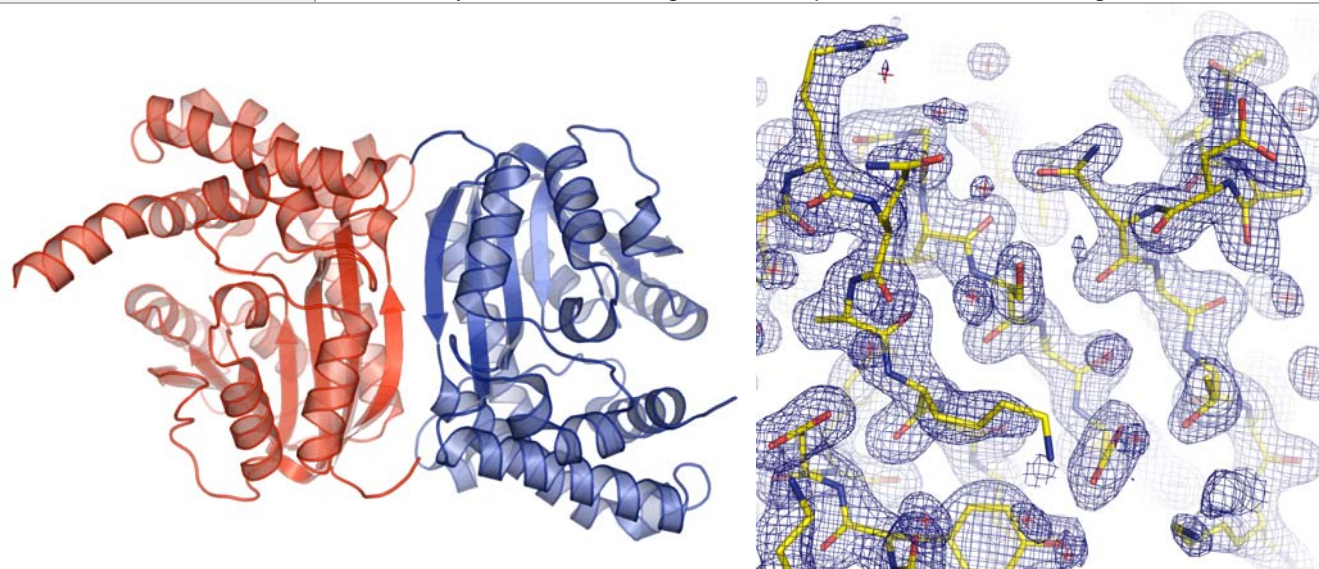


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>CESG ORF No.</b>	80048	
<b>Organism</b>	<i>Galdieria sulphuraria</i>	
<b>Gene Designator</b>	C1006_101305g20.t1	
<b>PDB Entry</b>	2O57	Deposition: 05-Dec-2006
<b>Function</b>	Sarcosine dimethylglycine methyltransferase	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(RARE2) pVP-16	
<b>Structure by X-ray</b>	Resolution: 1.95 Å	R-value (R-free): 16.8% (22.1%)
	No. of Residues/ASU: 1097 (1188)	Subunits/Molecule: 4
<b>Data Collected At</b>	Advanced Photon Source GMCA-CAT 23-ID-D	
<b>Authors</b>	J.G. McCoy, G.E. Wesenberg, G.N. Phillips Jr., E. Bitto, C.A. Bingman	



### Structural Features

This protein from *G. sulphuraria* shares approximately 40 % sequence identity to a number of sarcosine dimethylglycine methyltransferases found in halophilic bacteria. Kinetic analysis confirms that the enzyme catalyzes the transfer of a methyl group from S-adenosyl methionine to the amino group of either sarcosine or dimethylglycine. The final product of this reaction, betaine, plays a significant role in osmoregulation of the organism. In many plants and in bacteria, betaine helps maintain cellular turgor and stabilizes the structure and function of macromolecules during stress conditions such as exposure to high salt concentration or low temperature. This enzyme is not a component of the standard pathway for betaine synthesis, in which the precursor choline is converted to betaine aldehyde either by choline dehydrogenase or by choline monooxygenase, which is in turn converted to betaine by betaine aldehyde dehydrogenase.

The structure of this enzyme is more similar to mycolic acid synthases than to the better-characterized glycine methyltransferases. The core of the protein monomer is a seven-stranded mixed  $\beta$ -sheet sandwiched between two layers of helices. The dimer is generated through the formation of an inter-subunit  $\beta$ -sheet.

*References:* McCoy J.G., et al. Discovery of sarcosine dimethylglycine methyltransferase from *Galdieria sulphuraria*. *Submitted*.

<b>Percent Identity with Nearest PDB Structure at Time Selected/Solved</b>	2fk7 14% (297aa)
<b>Pfam Domain</b>	Methyltransferase-domain
<b>Sequence Family Size</b>	1007

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