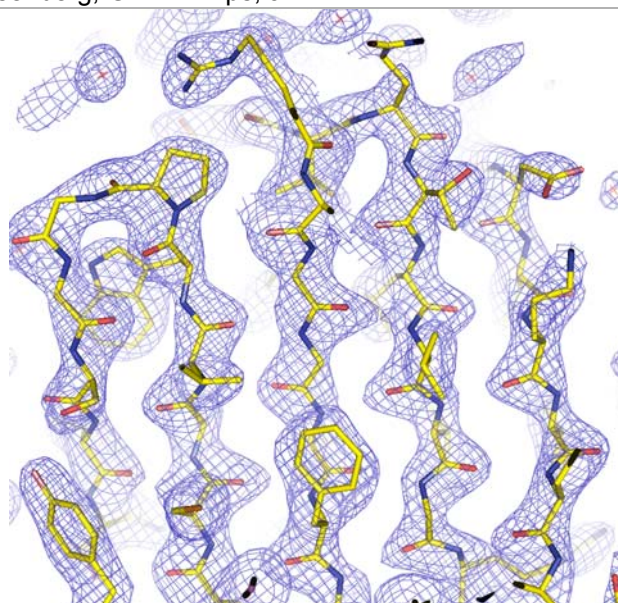
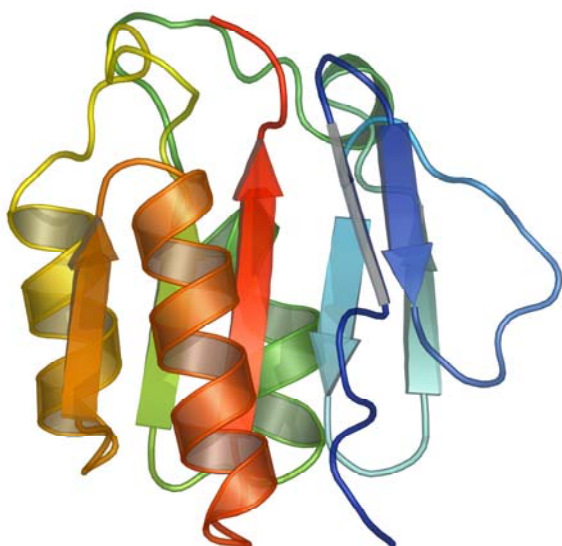




<b>Target ID</b>	GO.33759	
<b>Source Organism</b>	<i>Homo sapiens</i>	
<b>Target Name</b>	BC002752	
<b>PDB Entry</b>	2AB1	Deposition: 14-Jul-2005
<b>Function</b>	hypothetical protein LOC79017 (FF/Refine: 2Q4J, 2Q4Q)	
<b>Produced From</b>	<i>E. coli</i> B834, pRARE2, pVP-16	
<b>Structure by X-ray</b>	Resolution: 2.59Å	R-value (R-free): 19.3% (25.7%)
	No. of Residues/ASU: 234 (244)	Complexes/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source SER-CAT 22-ID 13-Mar-2005	
<b>Authors</b>	E. Bitto, C.A. Bingman, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

The crystal structure of Hs.95870 revealed a fold seen in two other proteins: MTH938 from *Methanobacterium thermoautotrophicum* and PH1505 from *Pyrococcus horikoshii*. Hs.95870 adopts a three layer sandwich architecture with a central mixed 5-stranded beta sheet, a layer of alpha helices, and a 2-stranded beta sheet. Profile-profile alignments of the three structural homologs reveal several conserved residues. Of particular note is a cluster of His45, His119, Cys122, Thr121, Leu75, and Gly70. The first three of these residues appear to be poised to coordinate a metal.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	26% (1IHN)
<b>Pfam Cluster</b>	DUF498 (6-119)
	CoA_trans (56-88)
<b>Sequence Cluster Size : Structures in PDB</b>	28 NR at e<0.1

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