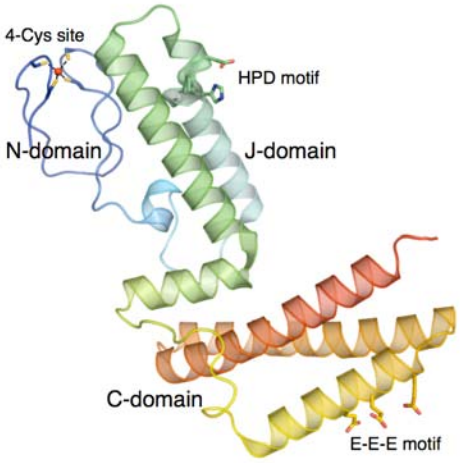
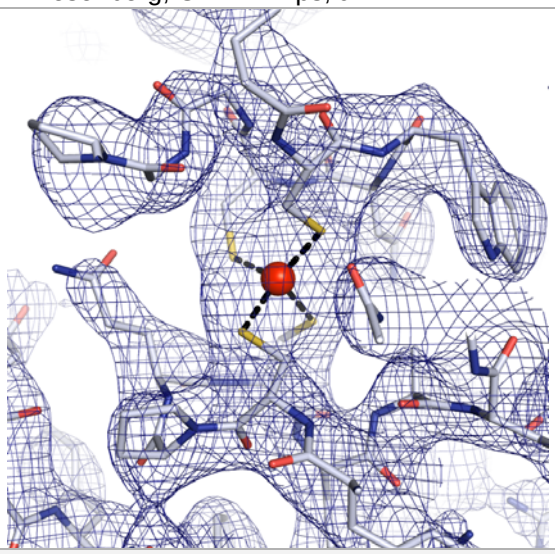
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.91296	
Source Organism	*Homo sapiens*	
Target Name	BC000004-Ndelta29	
PDB Entry	3BVO	Deposition: 07-Jan-2008
Function	co-chaperone protein HscB	
Produced From	*E. coli* B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 3.0 Å	R-value (R-free): 24.0% (28.8 %)
	No. of Residues/ASU: 373	Subunits/ASU: 2
Data Collected At	APS 23-ID-D, 10-Dec-2007	
Authors	E. Bitto, C.A. Bingman, J.G. McCoy, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

Proteins containing iron-sulfur centers are ubiquitous and play essential roles in a wide range of redox, catalytic, and regulatory processes in the cell. They are characterized by the presence of iron-sulfur clusters containing sulfide-linked di-, tri-, and tetrairon centers in variable oxidation states. The Fe/S proteins are best known for their role in the oxidation-reduction reactions of mitochondrial electron transport and photosynthesis. The biogenesis of Fe/S proteins is a complex process that has been the subject of extensive research. The final step of Fe/S protein assembly involves a Fe/S cluster transfer from a cluster-donor protein to cluster-acceptor proteins. This process is facilitated by a specialized chaperone system, which consists of a molecular chaperone from the Hsc70 family and a co-chaperone of J-protein family. In contrast to the prokaryotic assembly pathway, the biosynthesis of Fe/S proteins in eukaryotes is much less understood. The crystal structure of a human HscB J-type co-chaperone solved by CESG represents the first structurally characterized protein from an eukaryotic Fe/S assembly pathway. The overall architecture of human HscB resembles that of its *E. coli* homologue Hsc20. The main difference between the two structures is the presence of a novel metal-binding domain at the N-terminus of the human HscB, which contains a tetra-cysteine coordinated metal and could possibly be involved in Fe/S cluster transfer to an acceptor protein(s). Conserved J- and C-domains of HscB possess a previously described consensus chaperone-binding motif H-P-D (residues 102-104) and an acidic scaffold-protein-binding motif (residues E167, E170, and E174), respectively. We believe that the solution of the crystal structure of human HscB co-chaperone will lead to a better understanding of iron-sulfur proteins biogenesis in eukaryotes.

Percent Identity with Nearest PDB Structure at Time Solved	1FPO (28%)
Pfam Cluster	DnaJ
Sequence Family Size	695

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