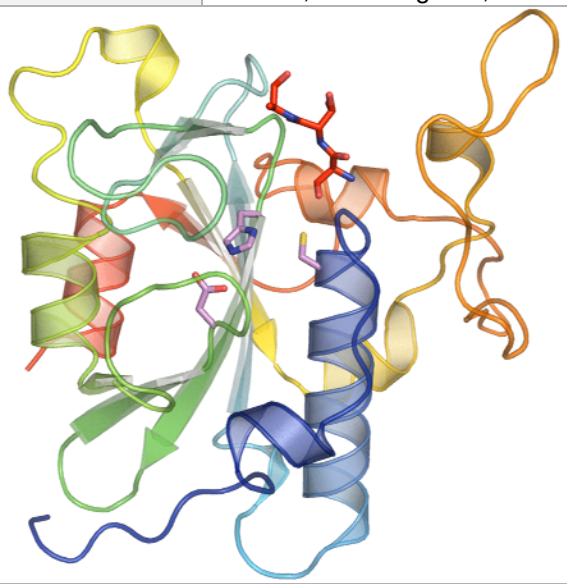
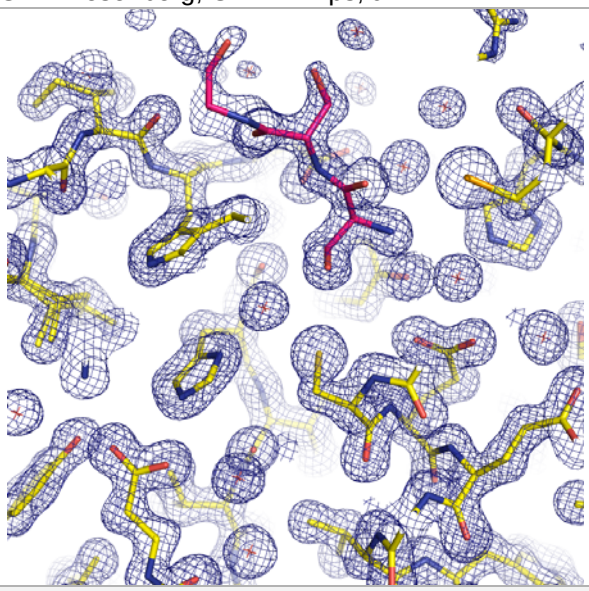
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.39772	
Source Organism	*Homo sapiens*	
Target Name	BC008781	
PDB Entry	3C9Q	Deposition: 18-Feb-2008
Function	uncharacterized protein C8orf32 with bound peptide	
Produced From	*E. coli* B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 1.5 Å	R-value (R-free): 16.2 % (18.0 %)
	No. of Residues/ASU: 195	Subunits/ASU: 1
Data Collected At	APS 23-ID-D, 06-Feb-2008	
Authors	E. Bitto, C.A. Bingman, J.G. McCoy, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

The human protein C8orf32 has been identified as an activator of the cAMP-response element (CRE) pathway, which has been implicated in formation of long-term memories. The protein has not yet been otherwise biochemically characterized. The 1.5 Å structure of C8orf32 solved by CESG reveals a monomeric globular protein of a novel structural fold with alpha-beta-alpha three-layer sandwich architecture. A multiple sequence alignment of homologous proteins from a range of eukaryotic organisms revealed a number of highly conserved residues that cluster in the area with features reminiscent of the active site. Of immediate interest are residues Cys28, His81, and Aps97, which could represent a catalytic triad of a novel cysteine hydrolase (with currently unknown function). The putative active site binds a peptide-like auxilliary molecule with a well resolved N-terminal tripeptide Ser-Thr/Val-Ala in the putative active site and additional disordered residues which reside at the interface of the symmetry related protein molecules in the crystal latice. As the putative catalytic cysteine residue is relatively burried we speculate that C8orf32 could be involved in hydrolytic processes like deacetylation or deformylation of N-termini of the substrate proteins.

Percent Identity with Nearest PDB Structure at Time Solved	1DQN (16%)
Pfam Cluster	
Sequence Family Size	57

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