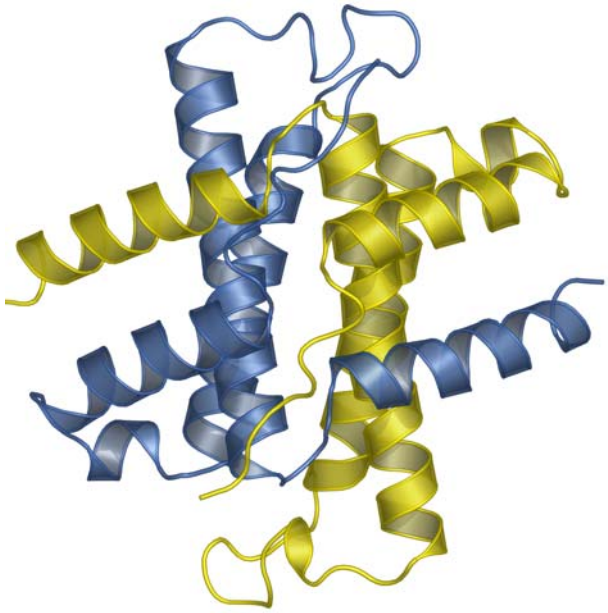
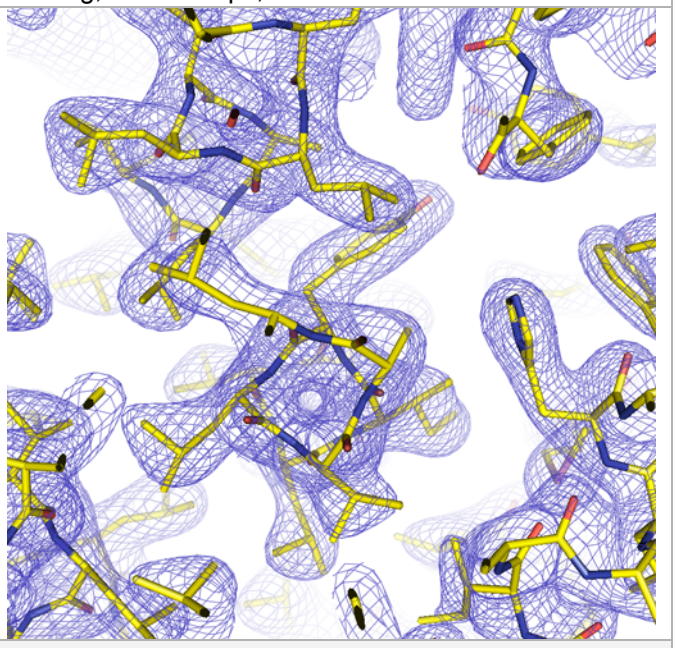
Center for Eukaryotic Structural Genomics

Protein Structure Data Summary

Target ID	GO.34455	
Source Organism	*Mus musculus*	
Target Name	BC004623	
PDB Entry	2A3Q	Deposition: 25-Jun-2005
Function	probable hydrolase (FF/Refine: 2Q4P)	
Produced From	*E. coli* B834, pRARE2, pVP-16	
Structure by X-ray	Resolution: 2.32 Å	R-value (R-free): 21.0% (23.9%)
	No. of Residues/ASU: 224 (340)	Complexes/ASU: 2
Data Collected At	Advanced Photon Source SER-CAT 22-ID 13-Jun-2005	
Authors	E. Bitto, C.A. Bingman, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

This protein shows 75% sequence identity to human XTP3-transactivated protein A (XTP3TPA, Unicode Q9H773) also known as RS21C6 in other species. Recent structure-guided analysis uncovered a relationship between all-alpha NTP pyrophosphohydrolases (dimeric UTPase, NTP pyrophosphorylase MagZ, and RS21C6). Our structure establishes that these proteins share homologous folds and analogous dimeric interfaces. Sequence alignments of these proteins reveals several high conserved negatively charged side chains, which are involved in the coordination of up to three Mg++ ions, and a lysine residue which stablizes the γ-phosphate of NTPs. All these residues (Glu63, Glu66, Glu95, Asp98, and Lys121) are conserved in mouse RS21C6. It has been hypothesized that members of this family may be involved in the housekeeping of non-canonical trinucleotides that could otherwise be incorporated into DNA or RNA. In the case of RS21C6, the protein is hypothesized to act on 5-methyldeoxycytidine.

References: (1) Moroz, O.V., Murzin, A.G., Makarova, K.S., Koonin, E.V., Wilson, K.S., Galperin, M.Y. (2005) Dimeric dUTPases, HisE, and MazG belong to a new superfamily of all-alpha NTP pyrophosphohydrolases with potential "house-cleaning" functions. *J Mol Biol* 347(2):243-55.

Percent Identity with Nearest PDB Structure at Time Solved	25% (1VMG)
Pfam Cluster	Pfam-B_61816,5032,40152,72040
Sequence Cluster Size : Structures in PDB	77 at e<0.1

Center for Eukaryotic Structural Genomics (CESG), University of Wisconsin-Madison Biochemistry Department, 433 Babcock Drive, Madison, WI 53706-1549; phone: 608.263.2183; fax: 608.890.1942; email: cesginfo@biochem.wisc.edu; website: http://www.uwstructuralgenomics.org. This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.