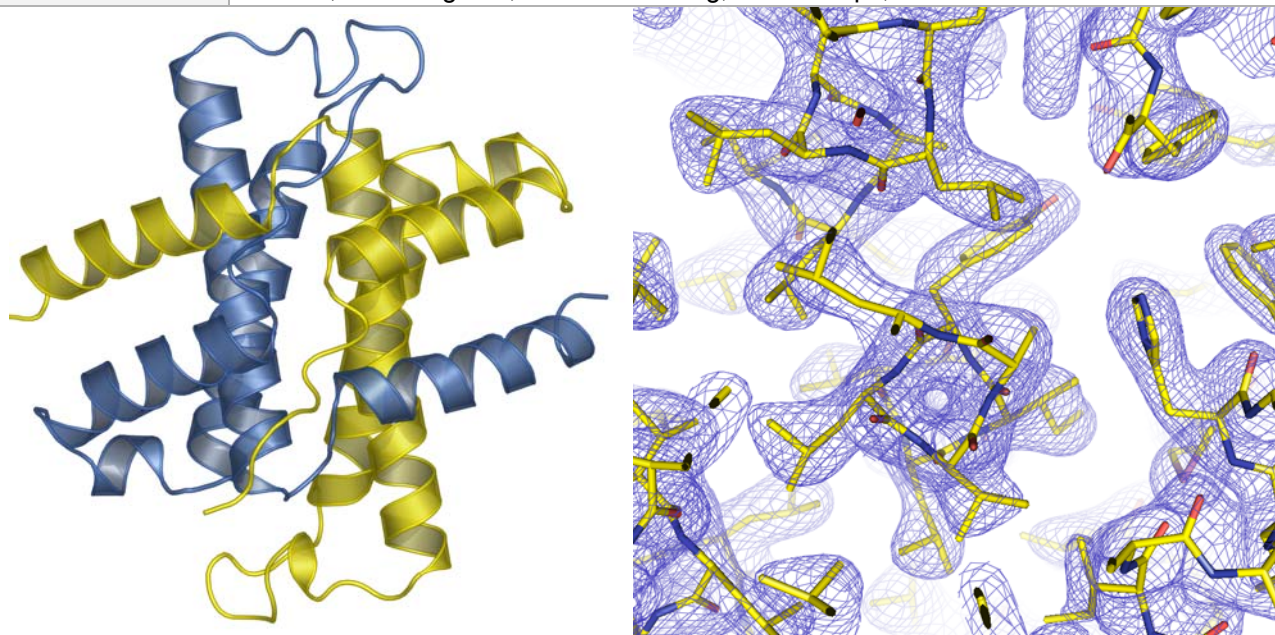


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.34455	
<b>Source Organism</b>	<i>Mus musculus</i>	
<b>Target Name</b>	BC004623	
<b>PDB Entry</b>	2A3Q	Deposition: 25-Jun-2005
<b>Function</b>	probable hydrolase (FF/Refine: 2Q4P)	
<b>Produced From</b>	<i>E. coli</i> B834, pRARE2, pVP-16	
<b>Structure by X-ray</b>	Resolution: 2.32 Å	R-value (R-free): 21.0% (23.9%)
	No. of Residues/ASU: 224 (340)	Complexes/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source SER-CAT 22-ID 13-Jun-2005	
<b>Authors</b>	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<sup>++</sup> ions, and a lysine residue which stabilizes the  $\gamma$ -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.

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

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