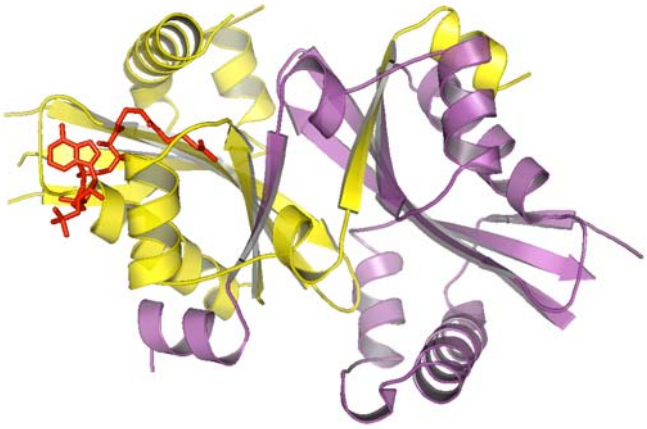
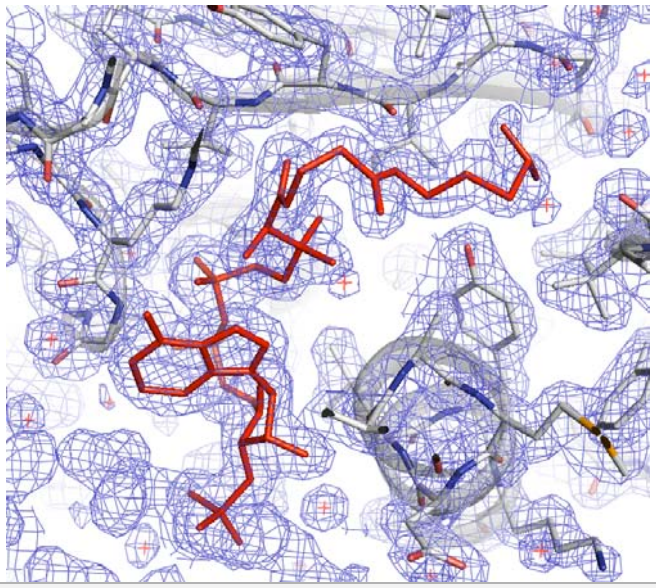
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.36731	
Source Organism	*Homo sapiens*	
Target Name	BC011751	
PDB Entry	2BEI	Deposition: 24-Oct-2005
Function	thialysine N-acetyltransferase (FF/Refine: 2Q4V)	
Produced From	*E. coli* B834, pRARE2, pVP-16	
Structure by X-ray	Resolution: 1.84 Å	R-value (R-free): 20.4% (24.9%)
	No. of Residues/ASU: 318 (338)	Complexes/ASU: 2
Data Collected At	Advanced Photon Source SER-CAT 22-ID 10-Oct-2005	
Authors	B.W. Han, C.A. Bingman, E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

Homo sapiens thialysine N-ε-acetyltransferase has been annotated as Hs spermidine N1-acetyltransferase 2 (HsSSAT2) because of high sequence identity to HsSSAT1. However, recent biochemical studies have shown that this protein fails to perform acetyl transfers to polyamines and that thialysine is a substrate for this enzyme. Thialysine is a structural analog of L-lysine, and is known to play a role as an anti-metabolite by competing with lys for incorporation into polypeptides. A high thialysine to lysine ratio has been shown to block the growth of eukaryotic cells. In addition to this anti-metabolite function, thialysine has been identified in mammalian tissues including brain. Thialysine can be converted into cyclic ketimine and other compounds postulated to serve neurochemical roles. This structure is unique, in that it is the only acetyltransferase in the PDB with acetyl-CoA bound to one subunit of a homodimeric acetyltransferase.

References: (1) Han, B.W., Bingman, C.A., Wesenberg, G.E., Phillips, G.N., Jr. (2006) Crystal structure of *Homo sapiens* thialysine Nepsilon-acetyltransferase (HsSSAT2) in complex with acetyl coenzyme A. *Proteins* 64(1):288-93.

Percent Identity with Nearest PDB Structure at Time Solved	17% (1TIQ)
Pfam Cluster	Acetyltransf_1
Sequence Cluster Size : Structures in PDB	636 proteins 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.