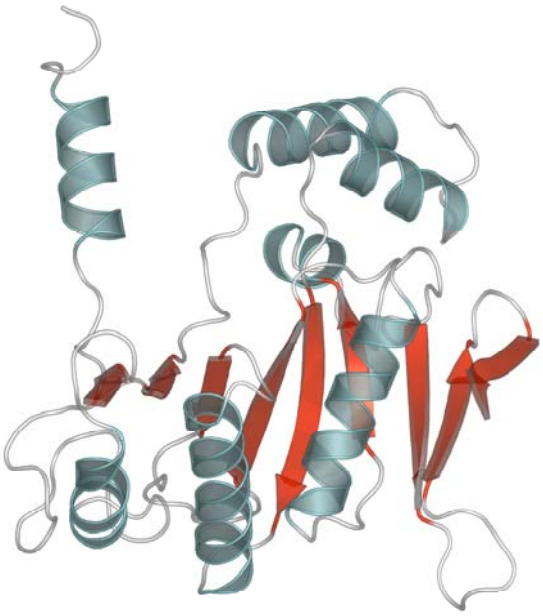
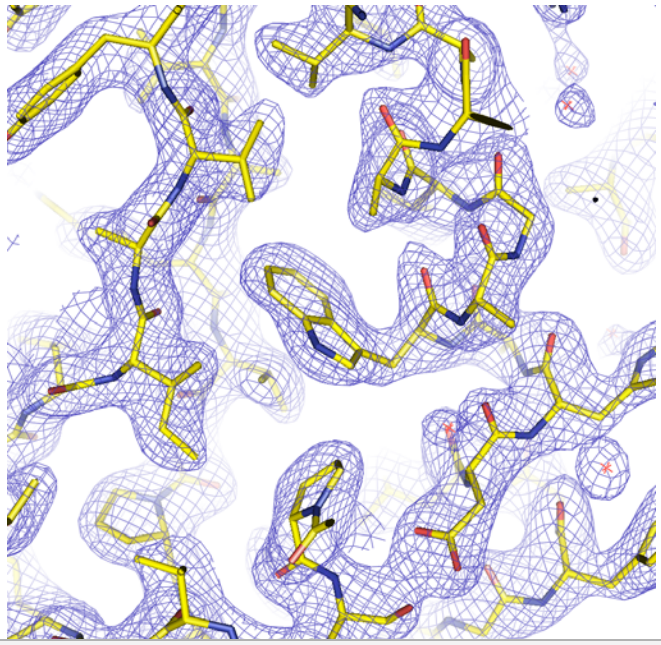
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.36704	
Source Organism	*Homo sapiens*	
Target Name	Hs.433573	
PDB Entry	1ZTP	Deposition: 27-May-2005
Function	basophilic leukemia-expressed protein (BLES03, p5326) (FF/Refine: 2Q4K)	
Produced From	*E. coli* B834, pRARE2, pVP-16	
Structure by X-ray	Resolution: 2.50Å	R-value (R-free): 18.8% (24.5%)
	No. of Residues/ASU: 686 (753)	Complexes/ASU: 3
Data Collected At	Advanced Photon Source NSLS X29A 05-May-2005	
Authors	E. Bitto, C.A. Bingman, H. Robinson, S.T.M. Allard, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

The crystal structure of BLES03 was solved by SeMet SAD using data collected at the mail-in program at NSLS. BLES03 shows no reliable sequence similarity to any functionally characterized proteins. The structure of BLES03 adopts a fold similar to the eukaryotic transcription initiation factor 4E (eIF4E) a protein that binds the mRNA cap structure. In addition to fold similarity, the general features of the electrostatic surface potential of BLES03 and eIF4E are similar. It is proposed that BLES03 is involved in a biochemical process that requires recognition of nucleic acids.

References: (1) Bitto, E., Bingman, C.A., Robinson, H., Allard, S.T.M., Wesenberg, G.E., Phillips, G.N., Jr. (2005) The structure at 2.5Å resolution of human basophilic leukemia-expressed protein BLES03. *Acta Crystallogr Sect F* 61(Pt 9):812-7.

Percent Identity with Nearest PDB Structure at Time Solved	9% (1IPB)
Pfam Cluster	Pfam-B_53833
Sequence Cluster Size : Structures in PDB	18 NR at e<0.1

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