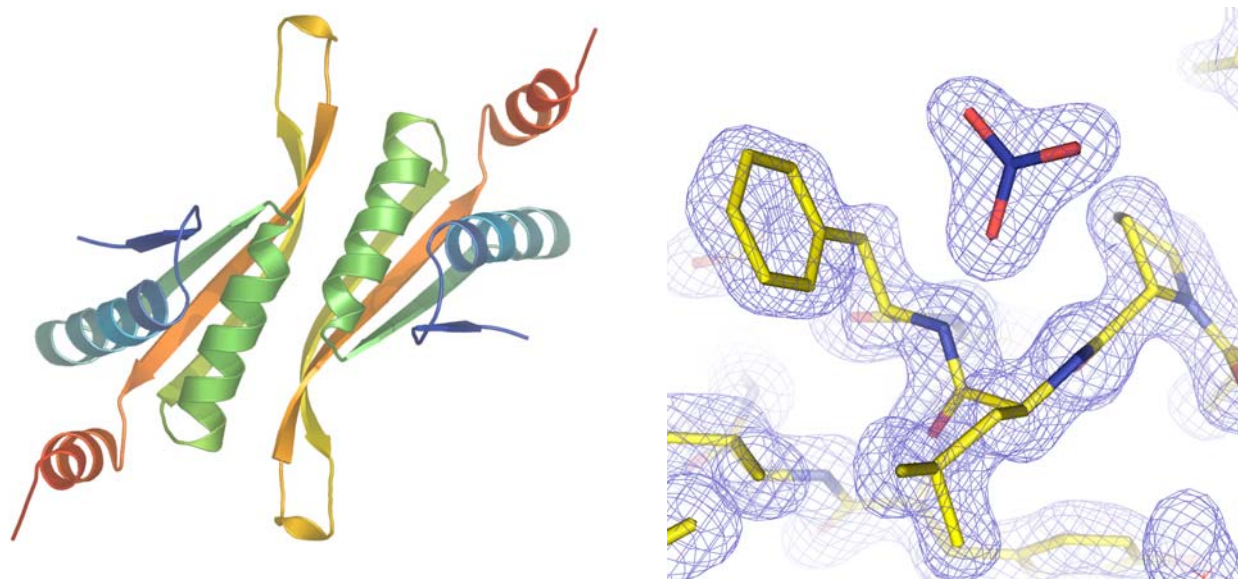


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.8793	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At2g34160.1	
<b>PDB Entry</b>	1VM0	Deposition: 24-Aug-2004
<b>Function</b>	DNA binding, alba-like protein (FF/Refine: 2Q3V)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
<b>Structure by X-ray</b>	Resolution: 1.80 Å	R-value (R-free): 17.7% (22.1%)
	No. of Residues: 130	Subunits/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source COM-CAT 32-ID-B 03-Apr-2004	
<b>Authors</b>	S.T.M. Allard, E. Bitto, C.A. Bingman, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

Sequence searches against the PDB indicate that At2g34160.1 is most similar to the prokaryotic DNA-binding protein Alba (1NH9). The overall level of similarity is significant ( $E=0.12$ ) over 81 amino acids. Blast searches against Genbank show two different length classes of Alba-like proteins. Alba is of the shorter class. At2g34160.1 is the only known structural example of the larger class of Alba-like proteins, with the additional C-terminal helix (the final red helix in the ribbon diagram above). This portion of the protein matches Pfam-B domain 26912. The amino-terminal 18 residues of At2g34160.1 are disordered in the crystal and contain a number of positively charged side-chains that may be involved in embracing nucleic acids. There is spatial similarity between the position of bound nitrates in the dimer-dimer interface in this crystal (above) and positions of phosphates in models of Alba-nucleic acid complexes.

*References:* (1) Wardleworth, B.N., Russell, R.J.M., Bell, S.D., Taylor, G.L., White, M.F. (2002) Structure of Alba: an archaeal chromatin protein modulated by acetylation. *EMBO J* 21(17):4654-62; (2) Aravind, L., Lakshminarayanan, I. M., and Anantharaman, V. (2003) The two faces of Alba: the evolutionary connection between proteins participating in chromatin structure and RNA metabolism. *Genome Biol* 4(10):R64.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	34.6% over 81 aa (1NH9)
<b>Pfam Cluster</b>	Alba, Pfam-B_26912
<b>Protonet Cluster Size : Structures in PDB</b>	10 : 0

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