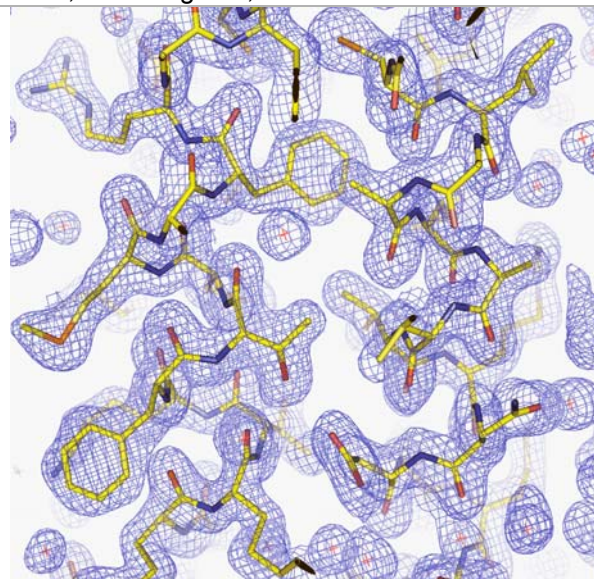
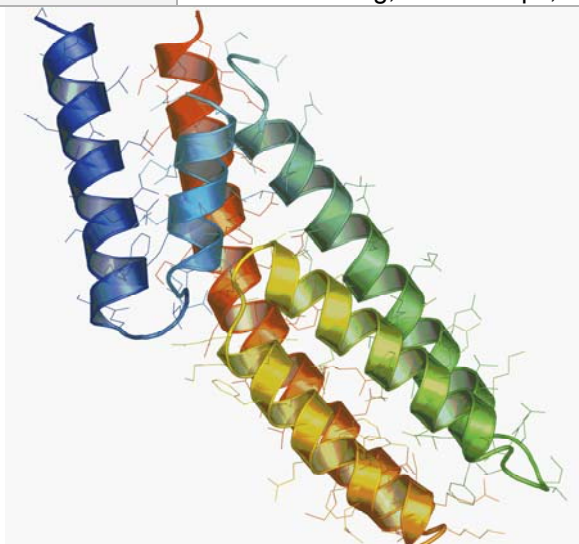




Target ID	GO.33957	
Source Organism	<i>Oryza sativa</i>	
Target Name	AK104879	
PDB Entry	1YVI	Deposition: 15-Feb-2005
Function	phosphotransfer protein (FF/Refine: 2Q4F)	
Produced From	<i>E. coli</i> B834(DE3) p(LACI+RARE) pVP-13	
Structure by X-ray	Resolution: 2.00 Å	R-value (R-free): 17.5% (22.7%)
	No. of Residues/ASU: 276	Monomers/ASU: 2
Data Collected At	Advanced Photon Source 19BM SBC-CAT 16-Dec-2004	
Authors	G.E. Wesenberg, G.N. Phillips, Jr., E.Bitto, C.A. Bingman, S.T.M. Allard	



Structural Features

Ak104879 is a component of the histidine-aspartate phosphorelay, the novel signaling pathway found in bacteria, archaea, amoebae, fungi, and plants, but not in higher eukaryotes. Although originally characterized as two component systems in bacteria, the histidine-aspartate phosphorelay of plants usually consists of three protein elements: a sensory histidine kinase, a histidine containing phosphotransfer protein and a response regulator. Ak104879 functions as the phosphotransfer protein. The fold of this protein is quite similar to the one previously characterized in phosphotransfer proteins in yeast (1), *E. coli*, *Salmonella typhimurium*, and recently elucidated ZmHP2 protein from maize (2). The key histidine residue involved in the phosphate transfer is His80, located in the center of the second helix of central anti-parallel four-helix bundle of the protein. The structure of Ak104879 represents the first example of a phosphotransfer protein of histidine-aspartate phosphorelay system in rice.

References: (1) Song, H.K., Lee, J.Y., Lee, M.G., Moon, J., Min, K., Yang, J.K., Suh, S.W. (1999) Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from *Saccharomyces cerevisiae*. *J Mol Biol* 293(4):753-61; (2) Sugawara, H., Kawano, Y., Hatakeyama, T., Yamaya, T., Kamiya, N., Sakakibara, H. (2005) Crystal structure of the histidine-containing phosphotransfer protein ZmHP2 from maize. *Protein Sci* 14(1):202-8.

Percent Identity with Nearest PDB Structure at Time Solved	88% (1WN0)
Pfam Cluster	Hpt
Sequence Cluster Size	79

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