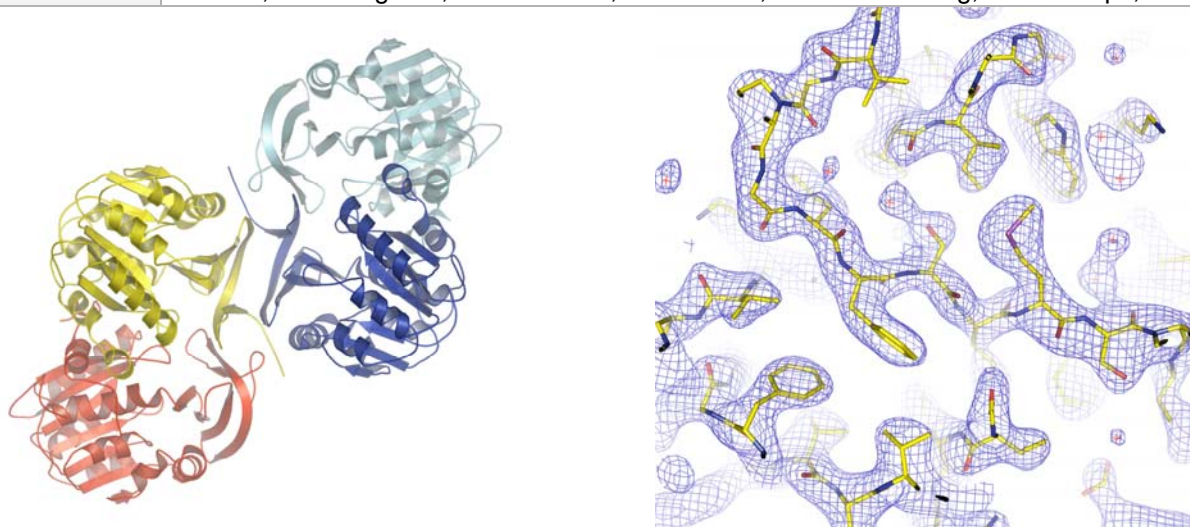


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.3851	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g23820.1	
<b>PDB Entry</b>	1XJ5	Deposition: 22-Sep-2004
<b>Function</b>	spermidine synthase (E.C. 2.5.1.16) SPDS1 (FF/Refine: 2Q41)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(LacI+RARE)	
<b>Structure by X-ray</b>	Resolution: 2.7 Å	R-value (R-free): 18.8% (24.5%)
	No. of Residues:	Subunits/Molecule: 4
<b>Data Collected At</b>	Advanced Photon Source BioCARS 14-ID-B	
<b>Authors</b>	E. Bitto, C.A. Bingman, S.T.M. Allard, D.W. Smith, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

At1g23820.1 protein functions as spermidine synthase. In *Arabidopsis*, there are two closely homologous enzymes with this activity. Spermidine synthase activity of these proteins was confirmed by several biochemical assays (1). At1g23820.1 catalyses synthesis of spermidine from putrescine and decarboxylated S-adenosylmethionine. Spermidine is ubiquitous in all living organisms. In plants, oligo-cation synthesis is highly regulated. If oligo-cation homeostasis is challenged, cells cease to proliferate or undergo apoptosis. Spermidine degradation may serve as an anti-parasitic peroxide generator in plants. At1g23820.1 shows substantial 3D similarity to known spermidine synthases from prokaryotes (1INL, 1IY9, 1MJF). However, At1g23820.1 exists in the crystal as a tetramer in a novel quaternary structure compared to the tetrameric protein from *T. maritima* (1INL). Differences in the N-terminal domains displace the crystallographic dimers by 50 Å relative to 1INL. This tetramer is held together by contact of two monomers, but in 1INL, all monomers contribute to a central 8-stranded antiparallel beta-barrel. Spermidine synthases of many other species exist as dimers.

*References:* (1) Hanzawa, Y., Imai, A., Michael, A.J., Komeda, Y., Takahashi, T. (2002) Characterization of the spermidine synthase-related gene family in *Arabidopsis thaliana*. *FEBS Lett* 527(1-3):176-80; (2) Panicot, M., Minguet, E.G., Ferrando, A., Alcázar, R., Blázquez, M.A., Carbonell, J., Altabella, T., Koncz, C., Tiburcio, A.F. (2002) A polyamine metabolon involving aminopropyl transferase complexes in *Arabidopsis*. *Plant Cell* 14(10):2539-51.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	36.2% over 268 aa (1JQ3)
<b>Pfam Cluster</b>	Spermine_synth
<b>Protonet Cluster Size : Structures in PDB</b>	185 : 3

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