

# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

|                          |  |   |
|--------------------------|--|---|
| <b>Target ID</b>         | GO.20862   |   |
| <b>Source Organism</b>   | <i>Arabidopsis thaliana</i>  |   |
| <b>Target Name</b>       | At5g66040.1  |   |
| <b>PDB Entry</b>         | 1TQ1   | Deposition: 16-Jun-2004                         |
| <b>BMRB Entry</b>        | 6240   | Deposition: 15-Jun-2004                         |
| <b>Function</b>          | putative sulfotransferase/phosphatase  |   |
| <b>Produced From</b>     | Cell-Free (wheat germ extract)   |   |
| <b>Structure by NMR</b>  | Restraints/Residue: 16.5   | Subunits/Molecule: 1                            |
|                          | No. of Residues: 129   | Molecular Weight: 13.8 kDa                      |
|                          | Backbone RMSD: 1.05 Å<br>(16–56, 85–128)   | All Heavy Atoms RMSD: 1.59 Å<br>(16–56, 85–128) |
|                          |  |   |
| <b>Data Collected At</b> | Nuclear Magnetic Resonance Facility at Madison (NMRFAM)  |   |
| <b>Authors</b>           | C. C. Cornilescu, G. Cornilescu, S. Singh, M.S. Lee, E.M. Tyler, M.N. Shahan, D. Vinarov, J.L. Markley |   |



### Structural Features

The most similar structure in the PDB was a prototype sulfotransferase for the single-domain Rhodanese Homology Superfamily GIpE from *Escherichia coli* (1GMX) with 22% sequence identity over 77 residues. The rhodanese homology domain has an alpha beta fold domain duplicated internally in the rhodanese protein. The enzymatically active cysteine containing domain can be found in CDC25 class of phosphatases, sulfide dehydrogenases and stress protein such as senescence specific protein 1 in plants, PspE and GIpE in bacteria and cyanide and arsenate resistance proteins. Additionally, this domain can be found as a single copy in other proteins such as phosphatases and ubiquitin C-terminal hydrolases. Although At5g66040.1 falls within the Rhodanese Superfamily, the true biological function of At5g66040.1 currently is unknown. This target aligns to domains within Pfam trusted matches for rhodanese over residues 13–114.

*References:* (1) Cornilescu, G., Vinarov, D.A., Tyler, E.M., Markley, J.L., Cornilescu, C.C. (2006) Solution structure of a single-domain thiosulfate sulfurtransferase from *Arabidopsis thaliana*. *Protein Sci* 15(12):2836-41.

|   |                       |
|---|-----------------------|
| <b>Percent Identity with Nearest PDB Structure at Time Solved</b> | 22% over 77 aa (1GMX) |
|---|-----------------------|

|                     |           |
|---------------------|-----------|
| <b>Pfam Cluster</b> | Rhodanese |
|---------------------|-----------|

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| <b>Protonet Cluster Size : Structures in PDB</b> | 53 : 0 |
|--|--------|

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