

W0153

**The Refined Structure of Hypothetical Protein Pf0725 from *P. furiosus* Confirms its function as a CoA Binding Protein.** M. Zhao, J. Chang, J. Habel, H. Xu, L. Chen, D. Lee, D. Nguyen, S.H. Chang, P. Horanyi, Q. Florence, W. Tempel, W. Zhou, D. Lin, H. Zhang, J. Praissman, F.E. Jenney Jr., M.W.W. Adams, Z.J. Liu, J.P. Rose, B.C. Wang, Dept. of Biochemistry and Molecular Biology, Univ. of Georgia, Athens, GA 30602 USA.

As part of an ongoing structural genomics study we have determined the structure of hypothetical protein Pf0725 by Se-SAS to 1.70Å resolution.

The selenomet protein was crystallized from a solution containing 0.3M sodium thiocyanate and 35% PEG 3350 by the microbatch method at 291K. The crystals belong to space group  $P6_2$  with  $a = 79\text{Å}$  and  $c = 36\text{Å}$ . The structure was determined on-site at SER-CAT from a single SAS dataset collected at the selenium edge on 22ID using the SCA2Structure pipeline. Total time for data collection and structure determination was under 12 hours. The refined structure ( $R=22.3\%$ ,  $R\text{ free}=24.5\%$ ) has been deposited in the Protein Data Bank, entry 1Y81. Analysis of the electron density maps revealed the presence of bound Coenzyme A (CoA). The presence of CoA together the structure's similarity to the *T. thermophilus* CoA binding protein TT1466 suggests that Pf0725 is a CoA-binding protein.

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