

## W0346

**A Structural Comparison of CBS Domains.** M. Cuff, R. Zhang, T. Skarina, A. Savchenko, A. Edwards, A. Joachimiak, Biosciences Div. & Structural Biology Center, Argonne National Laboratory, 9700 S. Cass Ave., Argonne, IL 60439, USA.

CBS domains are sequence motifs initially identified in Cystathionine Beta Synthase and are found in organisms as diverse as archaeobacteria and humans. In pairs, they are often a part of larger multidomain proteins such as IMP Dehydrogenase (IMPDH), AMP-activated protein kinase, and CLC chloride channel members. Point mutations to the region cause several hereditary diseases in humans. Recent work has demonstrated that tandem pairs of CBS domains bind adenosine derivatives, perhaps serving as cellular energy status sensors. We determined the crystal structure of a CBS domain protein from *M. thermotrophicus*. A Se-Met derivative of the 125 amino acid protein was crystallized in space group C2 with cell dimensions 58.79 x 48.59 x 56.48 Å,  $\beta=107.8^\circ$ . A three wavelength MAD experiment was conducted at APS Beamline 19ID using inverse beam geometry. Structure solution, density modification, and automatic building were achieved with autoSHARP. The model was refined against 1.4Å data to a final R-factor of 0.19 (R-free=0.20). We compare this structure to the previously determined CBS domain dimer of IMPDH and others encountered in the course of our structural genomics effort at the Midwest Center for Structural Genomics.

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