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Structure of STM3548 Cytoplasmic Protein from *Salmonella typhimurium*. M.E. Cuff, Ry. Wu, T. Petrova, A. Joachimiak, Midwest Center for Structural Genomics and Structural Biology Center, Biosciences, Argonne National Laboratory, 9700 South Cass Ave., Bldg 202, Argonne, IL 60439, USA.

Cytoplasmic protein DUF1355 from *S. typhimurium* forms a striking hexamer exhibiting D3 noncrystallographic symmetry. The monomer is a globular α/β fold with a 5-stranded parallel β -sheet at its core and a β -hairpin. Near the N-terminus is a 23 residue β -hairpin that reaches across the hexamer and H-bonds with the hairpin of the monomer diagonally across from it, forming a 4-stranded anti-parallel β -sheet. Three of these sheets form a triangular center to the hexamer, which may be described as two layers of trimers. Structural homologs can be found to the globular region of DUF1355, but not including the extended hairpin. A SeMet derivative of the 253 amino acid protein was crystallized in space group P2₁2₁2 (a=183.0Å, b=79.5Å, c=115.75Å). The structure was solved with two wavelength MAD data. Structure solution, phasing, and density modification were facilitated with autoSHARP and the model was refined at 2.3Å with Refmac. Sequence, structural comparisons and relationships to members of the glutamine aminotransferase family will be presented.

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