When Structures of Unknown Proteins are Determind, What is next?

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As part of Midwest Center for Structural Genomics (MCSG), our current aim is to solve high-resolution protein structures with less than 30% sequence identity to known structures. This approach unavoidably brings the realization that a large fraction of protein targets will be functionally uncharacterized. Three-dimensional structures of such proteins may furnish insight into their function. In the following case study we present recently determined x-ray crystallographic structures of proteins representing this category.

The RBSTP1166 protein from *Bacillus stearothermophilus* consists of 216 amino acids and related sequences appear to occur in a very small range of species. Preliminary structural comparisons suggest the protein may be a glycoside hydrolase.

YfiT, a hypothetical protein from *Bacillus subtilis* is found to have a divalent cation bound by three conserved histidines.The localization of the metal, its coordination geometry, the surrounding residues and the ligands involved suggest that YfiT might function as a peptidase or hydrolase.

An outer surface protein from *Bacillus cereus* has a two-domain structure. The large domain shows (βα)8 barrel motif and the small domain suggests structural similarity to cyclophilin A.

Keywords: structural genomics, high-resolution protein structures, domain structure