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Crystal Structure of a Novel Tetrahedral-Shaped Protease from *Shigella Flexneri*. Boguslaw Nocek, Andrew Binkowski, Hui Li, Frank Collart, Andrzej Joachimiak, Midwest Center for Structural Genomics and Structural Biology Center, Biosciences, Argonne National Laboratory, Argonne, IL 60439.

Proteins synthesis and degradation are critical processes for living cells. There are several pathways of degradation of proteins in the cell. Proteosomes, large multisubunit assemblies perform most of the intracellular proteolysis in the ATP-dependent manner. Proteosomes break down the polypeptides into 7-9 long amino acid peptides, which are further degraded to amino acids by energy-independent proteases such as: a tricorn protease or recently characterized archeabacterial tetrahedral-shaped dodecameric metalloaminopeptidase. Here we report the crystal structure of a bacterial homologue from *Shigella flexneri* at 2.0 Å resolution. The 37.5 kDa protein (S2589) was described as a hypothetical and shares low sequence similarity with archaeal protease, however it has structural homology with APAP metalloaminopeptidases from *Aeromonas proteolytica*. Protease subunits assemble into 450 kDa homododecamer, that can be described as a tetramer of trimers with $3/2$ symmetry and forms a tetrahedron with an internal cavity. Twelve active sites have been identified inside the cavity with several channels providing access to the bulk solvent. Details of the structure and insights into the possible catalytic mechanism will be presented.

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