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Crystal Structure of a Dodecameric Tetrahedral-shaped Aminopeptidase. Santina Russo, Ulrich Baumann, Dept. of Chemistry and Biochemistry, Univ. of Bern, Switzerland.

Protein turnover is an essential process in living cells. The degradation of cytosolic polypeptides is mainly carried out by the proteasome resulting in 7-9 amino acid long peptides. Further degradation is usually carried out by energy-independent proteases like the tricorn protease from *Thermoplasma acidophilum*. Recently, a novel tetrahedral shaped dodecameric 480 kDa aminopeptidase complex (TET) has been described in *Haloarcula marismortui* which differs from the known ring- or barrel-shaped self-compartmentalizing proteases. This complex is capable of degrading most peptides down to amino acids. We present here the crystal structure of the TET homolog FrvX from *Pyrococcus horikoshii*. The monomer has a typical clan MH fold, as found for example in *Aeromonas proteolytica* aminopeptidase, containing a dinuclear zinc active centre. The quaternary structure is built by dimers with a length of 100 Å which form the edges of the tetrahedron. All twelve active sites are located on the inside of the tetrahedron. Substrate access is granted by pores with a maximal diameter of 10 Å, allowing only small peptides and unfolded proteins access to the active site. FrvX possesses the required properties for degrading the products of the proteasome to amino acids and thus may play a similar role as the tricorn protease.