

## Poster

**Unusual helical crystal packing of potassium-independent L-asparaginase from *Phaseolus vulgaris*.****M. Gilski<sup>1,2</sup>, J. Loch<sup>3</sup>, B. Imiołczyk<sup>2</sup>, I. Pieróg<sup>3,4</sup>, J. Barciszewski<sup>2</sup>, M. Jaskolski<sup>1,2</sup>**<sup>1</sup>*Department of Crystallography, Faculty of Chemistry, Adam Mickiewicz University, Poznan, Poland*<sup>2</sup>*Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland*<sup>3</sup>*Jagiellonian University, Faculty of Chemistry, Krakow, Poland,*<sup>4</sup>*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Krakow, Poland**mirek@amu.edu.pl*

Plant-type (Class 2 in new classification) L-asparaginases are a group of the Ntn-hydrolases, which mature via autoproteolytic cleavage into subunits  $\alpha$  and  $\beta$ , and are further divided into potassium-dependent and potassium-independent enzymes. Ntn-hydrolases utilize an N-terminal nucleophile (Thr in this case) in their catalytic mechanism and share the same  $\alpha\beta\beta\alpha$  sandwich fold. Potassium-dependent L-asparaginase from *Phaseolus vulgaris*, PvAIIIK(+), was characterized previously, including the elucidation of the mechanism of its activation by  $K^+$  ions [1]. However, the potassium independent enzyme PvAIIIK(-), which has a lower affinity for L-Asn, is poorly studied. Here, we present the unique crystal structure of the mature PvAIIIK(-) enzyme, fully cleaved into subunits  $\alpha$  and  $\beta$ , with eight independent  $(\alpha\beta)_2$  dimers in the asymmetric unit. The structure is intriguing from the crystallographic point of view. The PvAIIIK(-) crystals show a complicated fourfold twinning in combination with structural pseudosymmetry. The crystals have the rare *P2* symmetry, with pseudosymmetric 4<sub>1</sub>-like helical packing. The eight dimers are segregated into two helical arrangements. Within each helical assembly, the huge 18-stranded central molecular  $\beta$ -sheet of each dimer is extended in both directions by similar  $\beta$ -sheets of its neighbors. In this fashion, an infinite  $\beta$ -sheet helix is generated along [001] throughout the entire crystal. Each “protein helix” (parallel to [001]) is then complemented by its antiparallel copy generated by the crystallographic twofold axis. In almost all PvAIIIK(-) molecules, the flexible linker, dangling at the C-terminus of subunit  $\alpha$  after autoproteolytic cleavage, is not visible, exception for two chains, where nine and three linker residues can be modeled. A linker from one chain forms a molecular bridge to the complementary chain in the protein “double helix”, thus additionally stabilizing the crystal packing.

[1] Bejger M. et al. (2014). Acta Cryst. D70, 1854-1872.

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