References:

1. Stach, L. & Freemont, P. S. The AAA+ ATPase p97, a cellular multitool. Biochem. J. 474, 2953–2976 (2017).
2. Hänzelmann, P. & Schindelin, H. The Interplay of Cofactor Interactions and Post-translational Modifications in the Regulation of the AAA+ ATPase p97. Front. Mol. Biosci. 4, 1–22 (2017).
3. Arumughan, A. et al. Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nat. Commun. 7, 13047 (2016).
4. Kernstock, S. et al. Lysine methylation of VCP by a member of a novel human protein methyltransferase family. Nat. Commun. 3, (2012).
5. Thiele, W. et al. Discovery of a novel tumour metastasis-promoting gene, NVM-1. J. Pathol. 225, 96–105 (2011).
6. Cloutier, P. et al. A Newly Uncovered Group of Distantly Related Lysine Methyltransferases Preferentially Interact with Molecular Chaperones to Regulate Their Activity. PLoS Genet. 9, (2013).

Keywords: p97 regulation, reassembly, methylation

MS06-P03

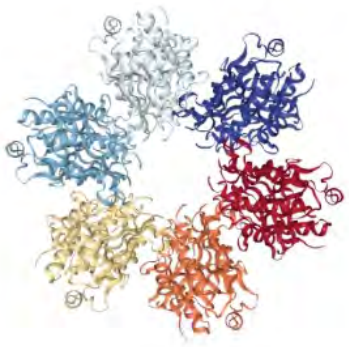
Structure-functional studies of protein P4 from bacteriophage φ8

Barbora Kaščáková[1], Zdenek Franta[2], Tatyana Prudniková[2],Michal Kutý[2], Roman Tuma[3], Ivana Kutá Smatanová[2]

1. University of South Bohemia in České Budejovice, Institute of Chemistry and Biochemistry, České Budějovice, Czech Republic
2. University of South Bohemia, Faculty of Science, Branisovska 1760, CZ-37005 Ceske Budejovice, Czech Republic, České Budějovice, Czech Republic
3. University of Leeds, School of Chemistry, The Astbury Centre for Structural Molecular Biology, Leeds LS2 9JT, UK, Leeds, United Kingdom

email: baja227@azet.sk

The dsRNA bacteriophages of *Cystoviridae* family infect gram-negative *Pseudomonas* species bacteria [1]. The bacteriophages package their genome into empty capsid – procapsid, which protects the genome from degradation inside as well as outside host cell. The genome packaging is performed by a molecular motor - P4 proteins, which are components of procapsid [1, 2]. The P4s possess an NTPase activity that converts the chemical energy from ATP hydrolysis to a mechanical movement of packaging ssRNA precursors into a procapsid, where the replication and transcription of dsRNA occurs [1, 3]. The P4s are RNA helicases belonging to the Superfamily 4 of helicases with characteristic presence of conserved sequence motifs (H1, H1a, H2, H3 and H4) [2, 3]. The RNA helicases cause the distribution of RNA-protein complexes and carry out RNA unwinding [2]. The P4 assembles into hexameric ring (Fig.1), which has on the outer perimeter NTP-binding sites and the nucleic acid binding sites are located in the central channel. Each P4 monomer consist of N-terminal, core NTPase domain with sequence motif and C-terminal domain. The C-terminal domain is inserted into the central channel of hexamer and its conformational changes regulate ring stability and ATPase activity of P4s [3]. Here we report our crystallization experiment results of the φ8 P4 protein crystals.



References:

[1] El Omari K., Meier C., Kainov D., Sutton G., Grimes J.M., Poranen M.M., Bamford D.H., Tuma R., Stuart D.I. & Mancini E.J.(2013) Nucleic Acids Res., 41, 9396-9410.
[2] Rabhi M., Tuma R. & Boudvillain M. (2010). RNA Biol., 7, 655-666.
[3] Kainov D. E., Tuma R. & Mancini E. J. (2006). Cell Mol Life Sci. 63, 1095-1105.

Keywords: Bacteriophages, Protein P4,