Project: Protonation and coordination states in protein – nucleic acids interactions

Supervisor: Jan Dohnálek

Project description: The project focuses on the experimental characterization of the protonation states of chemical groups, which play a crucial role in protein-nucleic acid interactions. The methods include atomic resolution X-ray crystallography and neutron crystallography, in combination with specialized computational approaches.

Candidate profile: The Laboratory of Structure and Function of Biomolecules at the Institute of Biotechnology, Czech Academy of Sciences, is looking for a highly motivated and enthusiastic Ph.D. student. The ideal candidate should hold a master's degree in biochemistry, structural biology, biophysics, macromolecular physics, or a related field. Basic knowledge and skills in the structural analysis of biological molecules are expected. Previous experience in biophysics, crystal structure analysis, or biophysical chemistry will be considered an advantage. The candidate should have a keen interest in experimental and computational structural biology and be eager to work in an interdisciplinary and international research environment. Proficiency in English is required.

We offer a collaborative and stimulating research environment at a cutting-edge institution, providing access to state-of-the-art methodologies and computational tools.

Suggested reading:

1. Adámková K, Kovaľ T, Østergaard LH, et al. (2022) Atomic resolution studies of S1 nuclease complexes reveal details of RNA interaction with the enzyme despite multiple lattice-translocation defects. Acta Crystallogr D78, 10, 1194-1209.
2. Blakeley MP (2016) Neutron crystallography aids in drug design. IUCrJ 3, 296–297.
3. Blakeley MP, Hasnain SS, Antonyuk SV (2015) Sub-atomic resolution X-ray crystallography and neutron crystallography: promise, challenges and potential. IUCrJ 2, 464-474.
4. Kovaľ T, Østergaard LH, Lehmbeck J, et al. (2016) Structural and Catalytic Properties of S1 Nuclease from Aspergillus oryzae Responsible for Substrate Recognition, Cleavage, Non-specificity, and Inhibition. PLOS One 11, 12, e0168832.