FACULTY OF SCIENCE
Charles University

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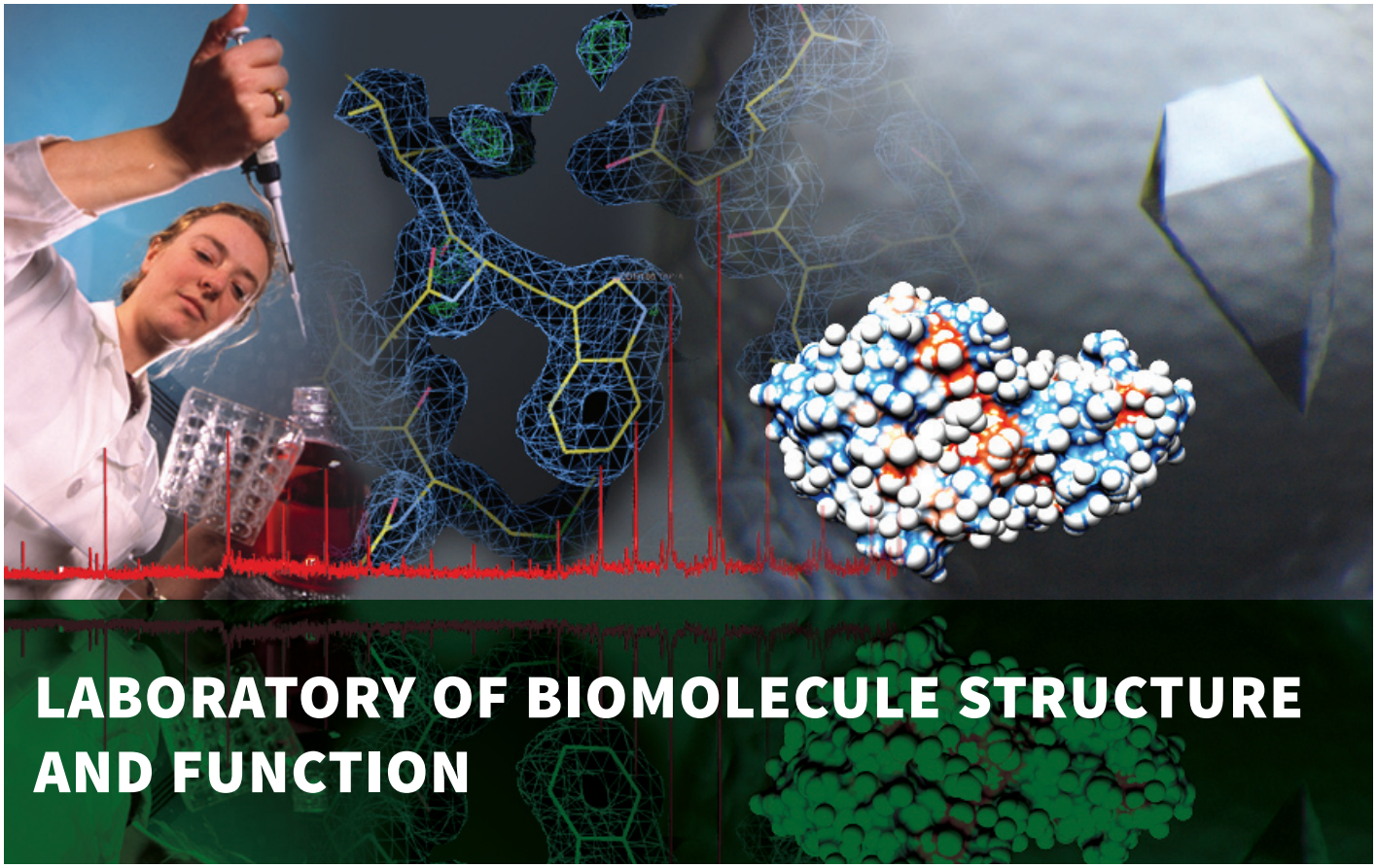

LABORATORY OF BIOMOLECULE STRUCTURE AND FUNCTION

OFFER

We offer our expertise, as well as consultancy or collaboration within a diverse range of issues broadly defined as protein biochemistry and biotechnology, protein structure solution or prediction, mass spectrometry and biomacromolecule analyses, particularly in the fields of:

- Recombinant protein expression and purification (both in bacterial and in mammalian cell line expression systems).
- Protein characterization and binding assessment (by various biochemical and biophysical techniques, e.g. sedimentation analysis in analytical ultracentrifuge, surface plasmon resonance, UV-VIS & CD spectroscopy).
- Protein structure determination (by protein X-ray crystallography or by advanced techniques of mass spectrometry).
- Multi-protein dynamics mapping.
- Molecular dynamic and protein structure modelling.

KNOW-HOW & TECHNOLOGIES

Structure and function relationship of biomacromolecules: target biomolecule identification, isolation and characterization, biotechnologies dealing with recombinant proteins as therapeutic agents.

- Recombinant protein expression and purification.
- Structural biochemistry and biophysical characterization of proteins.
- Structure of ligand-protein and multi-protein complexes.
- Photo-initiated and chemical cross-linking, H/D exchange.
- Mass spectrometry of biochemically interesting macromolecules.
- Molecular modelling of biomolecules.

Development and application of techniques for the structural description of clinical-relevant biomacromolecules and the understanding of their structure-function modulation.

MAIN CAPABILITIES

Consultancy or collaboration within the fields of recombinant protein expression and purification (both in bacterial and in mammalian cell line expression systems) and protein characterization by various biochemical and biophysical techniques, e.g. sedimentation analysis in analytical ultracentrifuge, surface plasmon resonance, UV-VIS & CD spectroscopy, structure solution by protein X-ray crystallography or by advanced techniques of mass spectrometry.

CONTENT OF RESEARCH

The structural and functional characterization of proteins participating in cancer recognition, in xenobiotic biotrans-formation, in the regulation of cell processes, in biocatalysis and immunomodulation in their native conditions. Research of protein structure, protein-protein and protein-ligand/substrate interaction with the use of chemical cross-linking reagents, photo-initiated cross-linking, H/D exchange, photoaffinity labeling protein, determination of disulfide bridges, glycosylation and other post-translational modifi-cations of proteins. Protein identification, structural determination and targeting by advanced techniques of mass spectrometry. Homology modeling, in silico ligand docking, molecular dynamics and interaction energy calculations.

RESEARCH EQUIPMENT

All equipment is operated by responsible persons: M. Šulc, M. Martínková, V. Martínek, P. Novák, P. Man, O. Vaněk, D. Kavan, P. Pompach, P. Jeřábek, T. Ječmen, R. Ptáčková, J. Bláha.

- Analytical ultracentrifuge ProteomeLab XL-I
- Surface plasmon resonance workstation PLASMON-4
- HPLC/UHPLC and FPLC systems
- UV-VIS spectrophotometers, CD spectrophotometer
- Protein sequencer Procise 491
- Two photolysers emitting UV-light with maximum around 254 nm (100W) and 360 nm (500W)
- Bruker Daltonics 15T-Solarix XR FT-ICR mass spectrometer associated with Agilent Technologies 1200 HPLC system
- Bruker qTOF maXis Plus

PARTNERS AND COLLABORATIONS

ACADEMIC PARTNERS

University of Texas, Houston, USA | Technische Universität Berlin, Germany | Institute for Molecular Science, Okazaki, Japan | National Institute of Molecular Studies, Okazaki, Japan | Loyola University, Chicago, USA | Georgetown University, Georgetown, USA

PUBLIC AND PRIVATE SECTOR

Zentiva, a.s. | Apronex, s.r.o.

MAIN PROJECTS

- New ligands for old receptors of human natural killer cells: structure, assembly within the immune synapse and potential for therapy (Czech Science Foundation, 2018–2021).
- Utilization of integrative molecular biophysical approaches for the functional studies of human natural killer cell receptors and formation of their complexes with tumour ligands (INTER--COST MEYS CR, 2017–2020)
- Molecular mechanisms of intraprotein/interdomain signal transduction in model heme sensor proteins (Czech Science Foundation, 2015–2017).
- Harnessing soluble forms of NK cell receptors and their ligands for the generation of novel anticancer immunotherapeutics (Czech Science Foundation, 2015–2017).
- Innovative Technologies for the Identification and Optimization of the New Generation of Anti-Cancer Drugs (Charles University, UNCE 204025/2012, 2012–2017).
- Mammalian microsomal cytochrome P450 interaction with redox partners – topology and structure-function relationships (Czech Science Foundation, 2012–2015).
- Innovation voucher (with Zentiva, a.s., Prague city, 2013–2014).
- Molecular diagnostics of bacterial pathogens (with Apronex, s.r.o., Ministry of Industry and Trade, 2009–2013).

ACHIEVEMENTS

PATENTS

- Czech patent “Soluble form of mouse NK cell receptor NKR-P1A and means of its recombinant preparation” (PV 2010-132).
- Czech utility model “Active form of alfa-N-acetyl-galactosaminidase from filamentous fungi *Aspergillus niger*” (2012-26061).

RECENT PUBLICATIONS

- Stranava M et al.: Coordination and redox state–dependent structural changes of the heme-based oxygen sensor AfGcHK associated with intraprotein signal transduction. J Biol Chem. 292, 20921–935 (2017).
- Kadek A.:Interdomain electron transfer in cellobiose dehydrogenase is governed by surface electrostatics. Biochim Biophys Acta. 1861, 157–167 (2016).
- Vališ K.: Reprogramming of leukemic cell metabolism through the naphthoquinonic compound Quambalarine B. Oncotarget. 8, 103137–153 (2017).
- Bláha J.: High-level expression and purification of soluble form of human natural killer cell receptor NKR-P1 in HEK293S GnTI- cells. Protein Expr Purif. 140, 36–43 (2017).
- Škerlová J.: Crystal structure of native β-N-acetylhexosaminidase isolated from *Aspergillus oryzae* sheds light onto its substrate specificity, high stability, and regulation by propeptide. FEBS J. 285, 580–598 (2018).
- Ječmen T.: Photo-initiated crosslinking extends mapping of the protein-protein interface to membrane-embedded portions of cytochromes P450 2B4 and b5. Methods. 89, 128–37 (2015).