Clinical Proteomics Lab

"Our team attempts to describe molecular mechanisms of human diseases and identify novel diagnostic or prognostic biomarkers."

Offer

- Identification of proteins from gels and solutions (MS and MS / MS)
- Proteomic analyzes of complex samples
- Marking and quantitative proteomic analysis of iTRAQ, SILAC etc.
- Proteomic analysis of cells and tissues of all types using iTRAQ, TMT or SILAC isotope methods
- Proteomic analysis of integral membrane proteins
- Training and service in the field of two-dimensional electrophoresis and other proteomics techniques

Expertise

- The lab is equipped with a Bruker MALDI TOF-TOF AutoFlex Mass Spectrometer.

- The device is primarily used to identify proteins after single-dimensional and two-dimensional electrophoresis, as well as for profiling small proteins and peptides in body fluids.

- In combination with nano-HPLC and the MALDI robotic fraction collector, the mass spectrometer is used for shot-gun proteomic analysis of complex samples, most commonly using quantitative iTRAQ or SILAC labels.

Research Areas

Proteome is defined as the complete set o proteins present at a given time in organism, tissue or cell. Proteomics aim at quantitative and qualitative description of proteomes and their dynamic changes.

Using the most advanced proteomic methods based on effective separation methods and high-resolution mass spectrometry, identification and quantification of up to 10.000 proteins can be accomplished in a single experiment. This opens a new way toward understanding of physiological and pathological processes on molecular level.

Employing proteomic approaches (based on effective protein and peptide separation methods and mass spectrometry) our team attempts to describe molecular mechanisms of human diseases and identify novel diagnostic or prognostic biomarkers.

Current Projects

- Proteomic analysis of myocardial changes in heart failure
- Proteomic analysis of the development of drug resistance in tumors
- Identification of biomarkers of major diseases
- Development of new methods for the analysis of transmembrane proteins

Partners

- IKEM
- Prague Institute of Hematology and BloodTransfusion
- Prague 2 LF UK
- Prague Eunice Kennedy Shriver National Institutes of Child Health and Human Development (NICHD)
- USA ThermoFisherScientific

Most Significant Recent Publications

- Lorkova L, Scigelova M, Arrey TN, Vit O, Pospisilova J, Doktorova E, Klanova M, Alam M, Vockova P, Maswabi B, Klener P Jr, Petrak J.: *Detailed Functional and Proteomic Characterization of Fludarabine Resistance in Mantle Cell Lymphoma Cells*. PLoS One. 2015 Aug 18;10(8):e0135314

- Klanova M, Lorkova L, Vit O, Maswabi B, Molinsky J, Pospisilova J, Vockova P, Mavis C, Lateckova L, Kulvait V, Vejmelkova D, Jaksa R, Hernandez F, Trneny M,Vokurka M, Petrak J, Klener P Jr.: *Downregulation of deoxycytidine kinase in cytarabine-resistant mantle cell lymphoma cells confers cross-resistance to nucleoside analogs gemcitabine, fludarabine and cladribine, but not to other classes of anti-lymphoma agents.*. Mol Cancer. 2014 Jun 27;13:159

- Lorkova L, Pospisilova J, Lacheta J, Leahomschi S, Zivny J, Cibula D, Zivny J, Petrak J.: *Decreased concentrations of retinol- binding protein 4 in sera of epithelial ovarian cancer patients: a potential biomarker identified by proteomics.*. Oncol Rep. 2012 Feb;27(2):318-24.)

- Petrak J, Pospisilova J, Sedinova M, Jedelsky P, Lorkova L, Vit O, Kolar M, Strnad H, Benes J, Sedmera D, Cervenka L, Melenovsky V.: *Proteomic and transcriptomic analysis of heart failure due to volume overload in a rat aorto-caval fistula model provides support for new potential therapeutic targets – monoamine oxidase A and transglutaminase* 2.2011 Nov 11;9(1):69)

Are you interested in this expertise?

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Experts and their Department

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