Proteomic analysis of clinical samples

Course contents for Postgradual of Study students

The content and aim of the course is to get acquainted with the workflow of proteomic analysis of clinical samples, including acquaintance with analytical, physico-chemical and biochemical procedures used in clinical sample processing, nano-HPLC, basic principles of mass spectrometry and bioinformatics data processing.

Within the subject Proteomic analysis of clinical samples, doctoral students focus on:

- Preparation of the samples for proteomic analysis
- Separation methods used for the preparation of clinical samples
- Basic terms and principles of mass spectrometers
- Ionization techniques used in mass spectrometers
- Electron ionization, chemical ionization, atmospheric pressure ionization, atmospheric pressure photoionization, matrix laser ionization, electrospray ionization, choice of ionization technique and recording polarity
- Basic types of mass analyzers, high and low resolution, accuracy of m / z determination, quadrupole analyzer, triple quadrupole analyzer, 3D ion trap, linear ion trap, flight time analyzer (TOF), electrostatic orbital trap- Orbitrap, Fourier transform ion cyclotron resonance (FT-ICR), tandem mass spectrometry (MS / MS)
- Combination of mass spectrometry and separation techniques
- Bioinformatics analysis of proteomic data

Assoc. Prof. Ján Sabo, Ph.D.
Head of Department