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Mass Spectrometry of Proteins and Peptides

This course is designed to offer students an overview of the current status, methodology and practical applications of mass spectrometry based analysis of proteins and peptides as well as their modifications. In the first part will discuss fundamentals of protein and peptide ionization such as Matrix Assisted Laser Desorption Ionization (MALDI) and Electrospray Ionization (ESI) which will include an overview of instrumentation i.e. mass spectrometers and nano-flow liquid chromatography interfaced with various ion traps (IT), quadropole time of flight (qTOF), triple quadropoles (QQQ) analyzers. We will discuss principles of Collision Induced Dissociation (CID), Higher Energy Collision Dissociation (HCD) and Electron Transfer Dissociation (ETD). In the second part we will focus on identification proteins by tandem mass spectrometry - MS/MS-based - peptide identification, peptide mass fingerprint. Application of protein fragmentation, chemical and enzymatic, will be part of this section. Third part will be devoted to identification and analysis of post-translationally modified peptides and protein isoforms. Finally, in the fourth part of this course we will discuss software and bioinformatics tools used for high throughput mass spectrometry data analysis.

Termin	Dzień tygodnia	Godzina	Miejsce
15.04.2013	**Poniedziałek**	**12.15 – 15.00**	**Minicentrum Konferencyjne (Luwr)**
16.04.2013	**Wtorek**	**12.15 – 15.00**	**Minicentrum Konferencyjne (Luwr)**
17.04.2013	**Środa**	**12.15 – 15.00**	**Minicentrum Konferencyjne (Luwr)**
18.04.2013	**Czwartek**	**14.15 – 17.00** **/zmiana/**	**Minicentrum Konferencyjne (Luwr)**
19.04.2013	**Piątek**	**12.15 – 15.00**	**Minicentrum Konferencyjne (Luwr)**