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## **Mass Spectrometry of Proteins and Peptides: Post-translational Modifications**

In this edition, the focus of proposed course will be on mass spectrometry based identification and quantification of post-translational modifications (PTMs) of proteins and peptides. During last few decades it has been shown that the human proteome is immensely more complex than the human genome. Such increase in complexity is facilitated by protein PTMs, chemical modifications playing a key role in regulation of activity, localization and interaction with other cellular molecules such as proteins, nucleic acids, lipids, and cofactors. These modifications include but are not limited to phosphorylation, glycosylation, ubiquitination, nitrosylation, methylation, acetylation, lipidation and proteolysis. Identification and quantification of these PTMs is not trivial and in many instances requires a combination of analytical approaches. Therefore, proposed course is designed to offer students systematic and comprehensive overview of the current status, methodology and practical applications of this part of mass spectrometry. In the first introductory part we will discuss fundamentals of ionization and fragmentation of post-translationally modified proteins and peptides. It will include an overview of instrumentation i.e. mass spectrometers and nano-flow liquid chromatography interfaced with various ion traps (IT), quadrupole time of flight (qTOF), triple quadrupoles (QQQ) analyzers. We will also discuss application various techniques of peptide fragmentation such as Collision Induced Dissociation (CID), Higher Energy Collision Dissociation (HCD) and Electron Transfer Dissociation (ETD). Second part will include an overview of major PTMs; phosphorylation, glycosylation, ubiquitination, acetylation and methylation. Students will learn techniques based on metabolic labeling as an experimental approach to investigate dynamics of protein PTMs. Finally, in the last part of this course we will discuss software and bioinformatics tools used for high throughput mass spectrometry data analysis.

<b>Termin</b>	<b>Dzień tygodnia</b>	<b>Godzina</b>	<b>Miejsce</b>
<b>11.05.2015</b>	<b>Poniedziałek</b>	<b>15.15 – 18.00</b>	<b>Minicentrum Konferencyjne (Luwr)</b>
<b>12.05.2015</b>	<b>Wtorek</b>	<b>15.15 – 18.00</b>	<b>Minicentrum Konferencyjne (Luwr)</b>
<b>13.05.2015</b>	<b>Środa</b>	<b>15.15 – 18.00</b>	<b>Minicentrum Konferencyjne (Luwr)</b>
<b>14.05.2015</b>	<b>Czwartek</b>	<b>15.15 – 18.00</b>	<b>Minicentrum Konferencyjne (Luwr)</b>
<b>15.05.2015</b>	<b>Piątek</b>	<b>15.15 – 18.00</b>	<b>Minicentrum Konferencyjne (Luwr)</b>