Subject name: Introduction to Proteomics

Subject code: E.1.INTR.SC.ECTIE

Department: Biochemistry Department, Institute of Plant Biology and Biotechnology

Faculty: Faculty of Biotechnology and Horticulture

Subject supervisor/Lecturer: Dr. Pawel Kaszycki / Dr. Pawel Kaszycki, Paulina Supel

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<tr>
<th>General information</th>
<th>Teaching period</th>
<th>1 semester / winter or summer semester</th>
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<tr>
<td>ECTS credit</td>
<td>4</td>
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<tr>
<td>Assessment method</td>
<td>written examination – test; classes: written reports on lab results</td>
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<td>Lectures total</td>
<td>15</td>
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<td>Classes total</td>
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Objective and general description:
Proteomics as a new scientific and practical research approach contributing to the views on modern biology, genetics, biochemistry and environmental sciences. Being the large-scale analysis of proteins, it contributes greatly to the understanding of gene function in the post-genomic era. The tools of proteomics will be presented: mass spectrometry, 2D electrophoresis, protein separation techniques, spectroscopic methods for studying protein structure and function, and bioinformatics. Proteome analysis in biotechnology: achievements of expression and functional proteomics in basic research and applicational practice, supported by several research examples.

Lectures (hour by hour):
1. 2. Basic definitions: genome and genomics as contrasted with proteome and proteomics. Proteomics as a compilation of basic and application research; study strategies and the contribution into contemporary nature-based sciences.
3. 4. Protein life cycle and regulatory mechanisms of protein expression – from biosynthesis to ultimate degradation; proteome definition based on genome analysis; comparison of proteomes of different organisms.
6. 7. Tools of proteomics: electrophoretic methods – basic principles of selected techniques, especially 2DE; data acquisition and visualization, elaboration of 2D-protein maps, construction of databases.
8. 9. Tools of proteomics: mass spectrometry (MS) – theoretical background and practical performance; applicability for proteome analyses.
10. High-throughput proteomic analyses – automatation, robotization, application of bioinformatics to elaborate and use internet databases, examples of automated proteomic systems.
11. 12. **Tools of proteomics**: methods for protein isolation, fractionation and characterization: tissue homogenization, ultracentrifugation, ultrafiltration, salting out, precipitation; liquid chromatography (LC): FPLC, HPLC techniques; 

**Classes**

1. Yeast cell culture: inoculum preparation and cultivation in fully automated laboratory-scale fermentor (5h). 
2. Optimization of fermentor bioprocess conditions, biomass turbidimetric determination; obtainment of cell-free protein extracts: biomass harvest (centrifugation), cell suspension homogenization via ultrasonication, protein determination (3h). 
3. Fractionation and preliminary purification of methylotrophic pathway enzymes – alcohol oxidase and formaldehyde dehydrogenase; protein FPLC chromatography and identification of enzyme activities in the resultant fractions with specific enzymatic assays (7h).

**References**