

<b>Subject name</b>	<b>Introduction to Proteomics</b>	
<b>Subject code</b>	<b>E.1.INTR.SC.ECTIE</b>	
<b>Department</b>	<b>Biochemistry Department, Institute of Plant Biology and Biotechnology</b>	
<b>Faculty</b>	<b>Faculty of Biotechnology and Horticulture</b>	
<b>Subject supervisor/Lecturer</b>	<b>Dr. Pawel Kaszycki / Dr. Pawel Kaszycki, Paulina Supel</b>	
<b>General information</b>	<b>Teaching period</b>	<b>1 semester / winter or summer semester</b>
	<b>ECTS credit</b>	<b>4</b>
	<b>Assessment method</b>	<b>written examination – test; classes: written reports on lab results</b>
	<b>Lectures total</b>	<b>15</b>
	<b>Classes total</b>	<b>15</b>
<b>Objective and general description</b>	<p>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, 2 D 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.</p>	
<b>Lectures</b> (hour by hour)	<p>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.</p> <p>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</p> <p>5. Expression vs. functional proteomics. Basic elements of proteome analysis – step by step procedures.</p> <p>6. 7. <i>Tools of proteomics</i>: electrophoretic methods – basic principles of selected techniques, especially 2DE; data acquisition and visualization, elaboration of 2D-protein maps, construction of databases.</p> <p>8. 9. <i>Tools of proteomics</i>: mass spectrometry (MS) – theoretical background and practical performance; applicability for proteome analyses.</p> <p>10. High-throughput proteomic analyses – automatation, robotization, application of bioinformatics to elaborate and use internet databases, exanples of automated proteomic systems.</p>	

	<p>11. 12. <i>Tools of proteomics</i>: methods for protein isolation, fractionation and characterization: tissue homogenization, ultracentrifugation, ultrafiltration, salting out, precipitation; liquid chromatography (LC): FPLC, HPLC techniques;</p> <p>13. 14. Selected methods to study the structure and properties of proteins: X-ray diffraction, protein structure modeling, spectrometric and spectroscopic techniques.</p> <p>15. New trends in proteomics: - development of bioinformatics, novel protein identification techniques: <i>recognition chips</i>, <i>protein arrays</i>, <i>lab-on-a-chip</i>; nanomethods for ultrasensitive protein detection. Examples of proteome analysis in plant science and microbiology.</p>
<p><b>Classes</b></p>	<p>Elements of functional proteomics – analysis of inducible enzymes under environmental stress: detection of methanol utilization pathway enzymes of non-conventional methylotrophic yeasts.</p> <p>1. Yeast cell culture: inoculum preparation and cultivation in fully automated laboratory-scale fermentor (5h).</p> <p>2. Optimization of fermentor bioprocess conditions, biomass turbidimetric determination; obtainment of cell-free protein extracts: biomass harvest (centrifugation), cell suspension homogenization <i>via</i> ultrasonication, protein determination (3h).</p> <p>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).</p>
<p><b>References</b></p>	<ol style="list-style-type: none"> <li>1. Campbell, A. M., Heyer, L. J. <i>Discovering Genomics, Proteomics, and Bioinformatics</i>. Benjamin Cummings, 2002.</li> <li>2. Dunn M. J. (Ed.) <i>Proteomics Reviews 2001</i>. John Wiley &amp; Sons, 2001.</li> <li>3. Liebler, D. C. <i>Introduction to Proteomics: Tools for the New Biology</i>. Humana Press, 2002.</li> <li>4. Marshak, D.R., Kadonaga J.T., Burgess R.R., Knuth M.W., Breenan Jr. W.A., Lin S.-H. <i>Strategies for protein purification and characterization. A laboratory course manual</i>. Cold Spring Harbor Lab. Press, 1996.</li> <li>5. Pennington S. <i>Proteomics: From Protein Sequence to Function</i>. Dunn M. J. (Ed.) Springer-Verlag New York, Inc., 2000.</li> <li>6. Sibirny A.A., Titorenko V.I., Gonchar M.V., Ubiyvovk V.M. , Ksheminskaya G. P., Vitvitskaya O.P.: Genetic control of methanol utilization in yeasts. <i>J. Basic Microbiol.</i> 28: 293-319, 1988.</li> <li>7. Westermeier R. Naven T. <i>Proteomics in Practice: A Laboratory Manual of Proteome Analysis</i>. John Wiley &amp; Sons, 2002.</li> </ol>