



Subject card

Subject name and code	PROTEOMICS, PG_00069555						
Field of study	InfoBioChem						
Date of commencement of studies	February 2026		Academic year of realisation of subject		2026/2027		
Education level	second-cycle studies		Subject group		Obligatory subject group in the field of study Subject group related to scientific research in the field of study		
Mode of study	Full-time studies		Mode of delivery		at the university		
Year of study	1		Language of instruction		Polish Polish		
Semester of study	2		ECTS credits		2.0		
Learning profile	general academic profile		Assessment form		assessment		
Conducting unit	Department of Physical Chemistry -> Faculty of Chemistry -> Faculties of Gdańsk University of Technology						
Name and surname of lecturer (lecturers)	Subject supervisor		prof. dr hab. inż. Jacek Czub				
	Teachers		prof. dr hab. inż. Jacek Czub dr inż. Paweł Wityk				
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	15.0	0.0	0.0	30
	E-learning hours included: 0.0						
	eNauczanie source addresses: Moodle ID: 6947 PROTEOMIKA https://enauczanie.pg.edu.pl/2025/course/view.php?id=6947						
Learning activity and number of study hours	Learning activity	Participation in didactic classes included in study plan		Participation in consultation hours		Self-study	SUM
	Number of study hours	30		2.0		18.0	50
Subject objectives	The aim of the course is to introduce students to untargeted metabolomics and shotgun proteomics using LC-MS/MS techniques. Students learn the principles of sample preparation, data acquisition and quality control, and the identification and quantitative analysis of metabolites and proteins. The course covers metabolomics data processing using MS-DIAL, DIA proteomics data analysis using DIA-NN, the use of the UniProt database for protein identification, annotation, and functional interpretation, and the statistical analysis, visualization, and biological interpretation of results using the MetaboAnalyst platform. Students independently analyze the results, prepare an individual report, and present their findings orally.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[K7_K05] is ready for continuous learning, developing interdisciplinary knowledge, and updating their skills in a dynamically changing scientific and professional environment.	is prepared to systematically expand their knowledge of proteomics and metabolomics, update their skills in the use of bioinformatics tools, and communicate the results of omics analyses reliably and clearly.	[SK1] Assessment of group work skills [SK4] Assessment of communication skills, including language correctness
	[K7_U02] is able to use IT tools for operations on nucleotide and protein sequences.	is able to use bioinformatics tools and protein sequence databases for protein identification and quantification, particularly by processing DIA proteomics data using DIA-NN, Uniprot.	[SU1] Assessment of task fulfilment [SU2] Assessment of ability to analyse information [SU3] Assessment of ability to use knowledge gained from the subject [SU4] Assessment of ability to use methods and tools [SU5] Assessment of ability to present the results of task
	[K7_U04] is able to accurately select and apply research methods and tools appropriate to the curriculum in the field of biological, medical, and chemical sciences, including molecular, systems, and medical biology, biotechnology, and bioinformatics.	is able to select and apply appropriate methods for analyzing data from untargeted metabolomics and shotgun proteomics experiments using MS-DIAL, DIA-NN, and the MetaboAnalyst platform, interprets the results, prepares an individual report, and presents the findings orally.	[SU1] Assessment of task fulfilment [SU2] Assessment of ability to analyse information [SU3] Assessment of ability to use knowledge gained from the subject [SU4] Assessment of ability to use methods and tools [SU5] Assessment of ability to present the results of task
	[K7_W03] knows and understands methods for statistical analysis of biological phenomena, biotechnological or chemical processes, and specialized bioinformatics tools.	knows and understands the principles of data processing, quality control, and statistical analysis in untargeted metabolomics and shotgun proteomics, as well as the use of MS-DIAL, DIA-NN, and the MetaboAnalyst platform.	[SW3] Assessment of knowledge contained in written work and projects [SW1] Assessment of factual knowledge

Subject contents	Course content – lecture 1. Introduction to omics sciences: proteomics and metabolomics and their applications in biological and biomedical research – 1 hour. 2. Design of omics experiments, sample preparation, randomization, control samples, and quality control – 2 hours. 3. Fundamentals of liquid chromatography and tandem mass spectrometry (LC-MS/MS) – 2 hours. 4. Untargeted metabolomics: feature detection, deconvolution, signal alignment, normalization, metabolite identification, and annotation – 2 hours. 5. Metabolomics data processing using MS-DIAL – 2 hours. 6. Shotgun proteomics: enzymatic protein digestion, peptide and protein identification, quantitative proteome analysis, and DDA and DIA acquisition strategies – 2 hours. 7. DIA proteomics data analysis using DIA-NN and the use of UniProt for protein identification, annotation, and functional interpretation – 2 hours. 8. Statistical analysis and visualization of omics data, multivariate analysis, biological interpretation using MetaboAnalyst, and principles of reporting results – 2 hours.		
	Course content – laboratory 1. Organization of metabolomics and proteomics experiments, preparation of metadata, data quality assessment, and introduction to mass spectrometry data file structures – 3 hours. 2. Untargeted metabolomics data processing using MS-DIAL: feature detection, deconvolution, alignment, filtering, normalization, and metabolite annotation – 3 hours. 3. Analysis of DIA shotgun proteomics data using DIA-NN: peptide and protein identification, FDR control, and quantitative analysis – 3 hours. 4. Retrieval of protein information from UniProt and functional annotation and biological interpretation of proteins – 2 hours. 5. Statistical analysis and data visualization using MetaboAnalyst: normalization, PCA, cluster analysis, heat maps, and analysis of differences between groups – 2 hours. 6. Biological interpretation of results, preparation of an individual report, and oral presentation of the analysis results – 2 hours.		
Prerequisites and co-requisites	Basic knowledge of biochemistry, molecular biology, analytical chemistry, and statistics. Knowledge of protein structure and function and the fundamentals of cellular metabolism. Basic computer skills, including the use of spreadsheets and the interpretation of biological data.		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	ocena prezentacji	60.0%	40.0%
	ocena raportu	60.0%	60.0%

Recommended reading	Basic literature	Aebersold R., Mann M., Mass-spectrometric exploration of proteome structure and function, Nature, 2016, 537, 347–355. Gillet L.C. i wsp., Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis, Molecular & Cellular Proteomics, 2012, 11. Current manuals, tutorials, and documentation for MS-DIAL, DIA-NN, MetaboAnalyst, and UniProt.
	Supplementary literature	https://systemsomicslab.github.io/compms/msdial/main.html https://www.metaboanalyst.ca/ https://www.uniprot.org/ https://aptila.bio/
	eResources addresses	
Example issues/ example questions/ tasks being completed	1. Discussing the differences between targeted and untargeted analysis and between DDA and DIA acquisition strategies. 2. Designing a metabolomics or proteomics experiment, including randomization, control samples, and quality control. 3. Processing untargeted metabolomics data using MS-DIAL. 4. Assessing data quality, filtering signals, normalization, and metabolite annotation. 5. Analyzing DIA shotgun proteomics data using DIA-NN. 6. Interpreting FDR values and the criteria for reliable peptide and protein identification. 7. Downloading an appropriate FASTA sequence database from UniProt and using information on protein function, localization, and biological pathways. 8. Performing statistical analysis and visualization using MetaboAnalyst, including PCA, cluster analysis, heat maps, and analysis of differences between groups. 9. Biologically interpreting the results and identifying the limitations of the analysis. 10. Preparing an individual report and orally presenting the results.	
Practical activities within the subject	Not applicable	

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