

Subject card

Subject name and code	Proteomics, PG_00156242						
Field of study	Bioinformatics						
Date of commencement of studies	October 2025		Academic year of realisation of subject		2026/2027		
Education level	Bachelor's studies		Subject group		Optional subject group		
Mode of study	full-time studies		Mode of delivery		at the university		
Year of study	2		Language of instruction		Polish		
Semester of study	4		ECTS credits		3.0		
Learning profile	academic		Assessment form		credit		
Conducting unit	Intercollegiate Faculty of Biotechnology UG-MUG -> Rector						
Name and surname of lecturer (lecturers)	Subject supervisor		dr hab. Paulina Czaplewska				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	30.0	0.0	0.0	30
	E-learning hours included: 0.0						
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		0.0		45.0	75
Subject objectives	• learning and acquiring basic concepts and terminology used in mass spectrometry (K_W04) • mastering the knowledge and skills necessary to independently sample preparation and conduct proteomic analysis of peptides and proteins (K_W04, K_U04, K_U05) • familiarization with methods and software for protein identification based on ESI mass spectra (K_W04, K_U0,4 K_U05, K_K01) • familiarization with bioinformatics analysis, including quantitative analysis, functional analysis, graphic preparation of proteomic data (K_W43, K_U04, K_U05)						
Learning outcomes	Course outcome		Subject outcome		Method of verification		
	[BIOINL3_U05] Graduate has the ability to use scientific literature, including English-language sources on bioinformatics; has ability to use appropriate databases		The student skillfully uses scientific information, including English-language information, regarding bioinformatics analyses; and is able to use electronic sources and appropriate databases (KU_05)		[SU3] text preparation/written work		
	[BIOINL3_W04] Has knowledge of basic research techniques and tools used in bioinformatics		The aim is to familiarize the student with the basics of the technique and basic types of mass spectrometers used in proteomic analyzes (KW_04)		[SW1] oral statement/ conversation/discussion		
	[BIOINL3_U04] Graduate effectively plans and organizes work independently or as part of a team		The student effectively plans and organizes work independently or as part of a team (KU_04)		[SU3] text preparation/written work		

Subject contents	Introduction to mass spectrometry, physical basis of MS spectrum measurement, equipment and basics of recording MS spectra. Qualitative and quantitative analysis in proteomic analysis using mass spectrometry. Sample preparation methods for MS analysis, registration and analysis of peptide and protein spectra (ESI, MALDI). Analysis of post-translational modifications in MS. Protein depletion before MS analysis, solution digestion and in-gel digestion. MS data analysis: use of fragmentation spectra, dedicated specialized software and protein databases for protein identification. Bioinformatics analysis: conducting quantitative analysis using statistical analysis (t-student test, determining the p or q value, determining the fold changes, determining statistically significant changes). Functional analysis: linking proteins with statistically significant changes with their associated gene ontology concepts (GO analysis), KEGG and Reactome analysis		
Prerequisites and co-requisites	It is required to obtain knowledge, skills and competences specified for the following courses: Bioorganic chemistry		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Final project	51.0%	100.0%
Recommended reading	Basic literature	A. Literature required to finally pass the course: A.1. used during classes - Johnstone Robert A.W. I Malcolm E. Rose, Spektrometria mas, PWN 2001 - De Hoffmann, Edmond, Charette, Jean Joseph, Stroobant, Vincent, Spektrometria mas, Wydawnictwa Naukowo-Techniczne 1998 - Primers for Proteomics Edited by: Paulina Czaplewska (University of Gdańsk, Poland & Medical University of Gdańsk, Poland), Katarzyna Macur (University of Gdańsk, Poland & Medical University of Gdańsk, Poland), and Paweł Ciborowski (University of Nebraska Medical Center, USA), doi.org/10.1142/13595 May 2024, ISBN" 978-987-12-8336-9 World Scientific A.2. Studied independently by the student - The latest literature on proteomics, review papers provided by the lecturer B. Additional literature K. Macur, J. Grzenkiewicz-Wydra, L. Konieczna, J. Bigda, C. Temporini, S. Tengattini, T. Bączek. A (2018) Proteomic Based Approach to Study the Mechanism of Cytotoxicity Induced by Interleukin1 and Cycloheximide Chromatographia 81:4756 (doi.org/10.1007/s10337-017-3382-3) M. Rafalik, M. Spodzieja, A.S. Kołodziejczyk, S. Rodziewicz-Motowidło, A. Szymańska, A. Grubb, P. Czaplewska (2018) The identification of discontinuous epitope in the human cystatin c monoclonal antibody hCC3 complex. Journal of Proteomics (doi.org/10.1016/j.jprot.2018.04.020) - M Prądzińska, I Behrendt, M Spodzieja, AS. Kołodziejczyk, S Rodziewicz-Motowidło, A Szymańska, SL. Lundström, RA. Zubarev, K Macur, P Czaplewska (2016). Isolation and characterization of autoantibodies against human cystatin C. Amino Acids (DOI 10.1007/s00726-016-2271-7) - AE. Lewandowska, K. Macur, P. Czaplewska, J. Liss, K. Łukaszuk, S. Oldziej. (2017) Qualitative and Quantitative Analysis of Proteome and Peptidome of Human Follicular Fluid Using Multiple Samples from Single Donor with LC-MS and SWATH Methodology. J Proteome Research (DOI: 10.1021/acs.jproteome.7b00366)	
	Supplementary literature	Primers for Proteomics https://doi.org/10.1142/13595 May 2024 Pages: 250 Edited by: Paulina Czaplewska (University of Gdańsk, Poland & Medical University of Gdańsk, Poland), Katarzyna Macur (University of Gdańsk, Poland & Medical University of Gdańsk, Poland), and Paweł Ciborowski (University of Nebraska Medical Center, USA)	
	eResources addresses		

Example issues/ example questions/ tasks being completed	Identification of proteins based on fragmentation spectra (in free programs available online)Statistical analysis for proteomics in Perseus and R softwareCreating a network of interactions (String server) and data visualization (Cytoscape)Functional analysis
Work placement	Not applicable

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