University of Gdańsk

Subject card

Subject name and code	Proteomics, PG_00156242		
Field of study	Bioinformatics		
Date of commencement of studies	October 2026	Academic year of realisation of subject	2027/2028
Education level	Bachelor’s studies	Subject group	Optional subject group 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	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_U04] Graduate effectively plans and organizes work independently and 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
	[BIOINL3_W04] Has advanced knowledge of 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_U05] Graduate has the ability to use scientific literature, including English-language sources on bioinformatics; has the 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

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 spectrometrySample preparation methods for MS analysis, registration and analysis of peptide and protein spectra (ESI, MALDI)Analysis of post-translational modifications in MSProtein depletion before MS analysis, solution digestion and in-gel digestionMS data analysis: use of fragmentation spectra, dedicated specialized software and protein databases for protein identificationBioinformatics analysis: conducting quantitative analysis using statistical analysis (t-studnet 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.

Studyed independently by the student

- The latest literature on proteomics, review papers provided by the lecturer

B. Additional literature

- K. Macur,·J. Grzenkowicz-Wydra, L. Konieczna, J. Bigda, C. Temporini, S. Tengattini, T. Bączek. A (2018) ProteomicBased 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. Ołdziej. (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