

**Subject card**

<b>Subject name and code</b>	Functional analysis of sequences in Eukaryot, PG_00147776						
<b>Field of study</b>	Genetics and Experimental Biology						
<b>Date of commencement of studies</b>	October 2024	<b>Academic year of realisation of subject</b>			2026/2027		
<b>Education level</b>	undergraduate studies	<b>Subject group</b>			Obligatory subject group in the field of study Optional subject group		
<b>Mode of study</b>	full-time studies	<b>Mode of delivery</b>			at the university		
<b>Year of study</b>	3	<b>Language of instruction</b>			Polish		
<b>Semester of study</b>	5	<b>ECTS credits</b>			2.0		
<b>Learning profile</b>	academic	<b>Assessment form</b>					
<b>Conducting unit</b>	Pracownia Molekularnych i Komórkowych Podstaw Strategii Nutr -> Katedra Biologii i Genetyki Medycznej -> Faculty of Biology						
<b>Name and surname of lecturer (lecturers)</b>	<b>Subject supervisor</b>		dr Marta Moskot				
	<b>Teachers</b>						
<b>Lesson types</b>	<b>Lesson type</b>	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	<b>Number of study hours</b>	0.0	0.0	15.0	0.0	0.0	15
	E-learning hours included: 0.0						
<b>Learning activity and number of study hours</b>	<b>Learning activity</b>	Participation in didactic classes included in study plan		Participation in consultation hours		Self-study	SUM
	<b>Number of study hours</b>	15		2.0		8.0	25
<b>Subject objectives</b>	1. Familiarization with genetic sequence databases.2. Acquiring the ability to use methods and techniques for gene ontology in Eukaryota (GORilla, AmiGO, ShinyGO programs)3. Identification of the role of a protein product based on molecular pathway analysis (KEGG database)4. Functional analysis of DNA sequences using results obtained from databases (GEO).						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[GBEL3_U04] Capable of reading scientific texts in English and Polish with comprehension, synthesizing the knowledge contained within them, preparing well-documented studies on biological issues, as well as those related to research commercialization.	Student expands acquired knowledge by reading additional materials	[SU1] oral statement/conversation/discussion [SU5] implementation of a problem task
	[GBEL3_K07] Lifelong learning and updating knowledge in the field of molecular genetics and other disciplines.	Student acquires knowledge about new databases and methods analysis, and the possibility of their applications.	[SK1] oral statement/conversation/discussion [SK5] implementation of a problem task
	[GBEL3_W06] the development and current state of knowledge, as well as the latest trends in molecular genetics and related fields; indicating their relationship with other disciplines in the natural or medical sciences and the possibilities of their practical application.	Student is able to find and verify the tools and describe the results of the analyses carried out with their use.	[SW1] oral statement/conversation/discussion [SW5] implementation of a problem task
	[GBEL3_W05] the principles of research planning based on achievements in biological sciences and related fields, the potential application of their results in practice, the principles of operation of equipment and apparatus used in molecular genetics research, and the principle of interpreting biological phenomena and processes based on empirical data in research and practical activities, with consideration for sustainable use of biological diversity.	Student makes a synthesis of knowledge available in the versatile sources by preparing well-documented studies of biological problems.	[SW1] oral statement/conversation/discussion [SW5] implementation of a problem task
	[GBEL3_W03] The molecular mechanisms of genetic information transmission and gene expression, as well as the molecular and genetic basis of human physiology and diseases, including infectious diseases.	Student knows the mechanisms of genetic information analysis and gene expression, and can use gene ontology analysis (GO) to find and assign genes' their role and places in biological processes.	[SW1] oral statement/conversation/discussion [SW5] implementation of a problem task
	[GBEL3_W01] Understanding the structure and properties of basic types of biological macromolecules, molecular mechanisms of metabolic pathways and genetic information flow, as well as sources of genetic variability in organisms and mechanisms of evolution; explaining the rules of inheritance, elucidating differences in the structure and functioning of prokaryotic and eukaryotic cells, and understanding the structure and functional relationships at the cellular and tissue levels.	The student understands the meaning of biological processes in functioning of the cell and whole eukaryotic organisms.	[SW1] oral statement/conversation/discussion [SW5] implementation of a problem task
Subject contents	Basic methods and research approaches of genetics. Gene ontology, annotation of the eucariotic DNA sequence. Bioinformatics methods for the study of gene expression, function and regulation. Bioinformatics databases data and their application in the functional comparative analysis of organisms.		
Prerequisites and co-requisites	Basic knowledge of cell biology, molecular biology and genetics.		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Analyses made with the knowledge learned on the classes (about programs and databases)	51.0%	100.0%
Recommended reading	Basic literature	The Gene Ontology Handbook, Christophe Dessimoz, Nives Škunca, 2017	
	Supplementary literature	Scientific publications in the field of gene ontology analysis, with particular emphasis on taking into account the work describing the methodology used during the classes (programs and databases).	
	eResources addresses	Uzupełniające Adresy na platformie eNauczanie:	

Example issues/ example questions/ tasks being completed	1.Which database traces the pathways of drug development? 2.List genes belonging to: hsa00590 Arachidonic acid metabolism. 3.Which software would you use to search for the genes belonging to the biological process for Glycine Max? 4.What program and type of analysis would you choose to perform an ontological analysis of a group of genes belonging to Vibrio cholerae? 5. Which of the learned programs for ontological analysis would you use in your own research and why?
Work placement	Not applicable

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