COURSE/MODULE DESCRIPTION (SYLLABUS)

1.	Course: **Systems biology**
2.	Language of instruction: **English**
3.	Faculty: **Faculty of Biotechnology**
4.	Course/module code: **29-BT-S2-E2-EngSB**
5.	Course/module type (*mandatory* or *elective*): **mandatory**
6.	Programme: **Medical Biotechnology**
7.	Study cycle: **2nd cycle**
8.	Year: **1st year**
9.	Semester *(autumn* or *spring):* **spring**
10.	Form of tuition and number of hours: **Lecture: 15 hours**
11.	Name, Surname, academic title: **Małgorzata HEIDORN-CZARNA, PhD**
12.	Initial requirements (knowledge, skills, social competences) regarding the course/module and its completion: **The student should have knowledge about the molecular basis of biological phenomena and processes. The student should have knowledge about the structure and function of proteins, nucleic acids, carbohydrates and lipid compounds and their metabolism. The student should also possess knowledge about the processes of replication, transcription and translation, as well as understand the concept of gene expression. The student should be familiar with basic techniques of molecular biology and biochemistry.**
13.	Objectives: **Understanding the concept of systems biology as scientific approach based on "omics" types of research in order to understand the global picture of biological processes. Becoming familiar with various methods and databases based on the "omics" approaches used in systems biology, and especially in plant systems biology, such as genomics, transcriptomics, proteomics, metabolomics, lipidomics, interactomics, etc. Getting acquainted with the examples of scientific data described in the latest scientific**

	literature using different types of “omics” approaches.	
14.	Content: **The concept of „systems biology”, especially systems biology of plants as a scientific approach combining information from "omics" types of studies. “Omics” methods, with particular reference to the latest trends: phenomics (large-scale phenotyping of plants); genomics (deep sequencing); transcriptomics (microarrays, quantitative PCR); ribosomal profiling; proteomics (2D-DIGE, SILAC, iTRAQ, COFRADIC; protein identification by mass spectrometry: PMF, MS/MS, LC-MS/MS; targeted proteomics based on mass spectrometry: MRM); metabolomics (HPLC, gas and liquid chromatography combined with mass spectrometry: GC-MS, LC-MS); interactomics (cross-linking); lipidomics. Biological database servers based on the “omics” types of research for the model plant organism *Arabidopsis thaliana* (Genevestigator Expression Data, e-FB Browser, AtgeneExpression Visualization Tool, AtProteome, The Plant Proteome, ATTED-II, BioGRID, etc.). Functional genomics. The use of reverse genetics in the study of gene functions by means of "omics" methods. Correlation between the level of transcripts and the level of proteins in model organisms. Methods of post-transcriptional and post-translational regulation of gene expression.**	
15.	Learning outcomes: Students: • provide qualitative and quantitative descriptions of complex biological phenomena and processes; • consistently apply and disseminate the principle of strict interpretation of biological phenomena and biochemical processes in research and practical activities which are based on empirical data; • possess advanced knowledge of biological sciences, namely biochemistry, bioinformatics and molecular biology; • possess in-depth knowledge of genetics and structural biology in understanding relationships and interrelations in biological systems; • apply advanced technology and research tools in biological sciences, namely biochemistry, bioinformatics and molecular biology; • efficiently make use of scientific literature in the field of biomedicine and biotechnology; read professional literature in English; • show ability in critically analysing and selecting information, especially from electronic resources, including literature and sequential databases; • use statistical methods, computer tools and technology to describe biological phenomena and perform analysis of specialist data; • collect and interpret experimental data, synthesise it and make appropriate conclusions; • understand the need for a systematic review of professional literature in order to broaden and	Outcome symbols: K_W01, K_W02, K_W03, K_W04, K_U01, K_U02, K_U03, K_U05, K_U06, K_K05

	deepen his or her knowledge.	
16.	Recommended literature • **Systems Biology, Robert A. Meyers, John Wiley & Sons, 2012** • **Mandatory: publications and other materials provided by a tutor.**	
17.	Methods of verification of the assumed learning outcomes: **Written exam**	
18.	Conditions of earning credits: **Written exam**	
19.	Student’s workload:	
	Activity	Number of hours for the activity
	Hours of instruction (as stipulated in study programme): • lecture: 15 hours • consultations: 3 hours	18 hours
	Student’s own work: • reading of literature: 5 hours • preparation for exam: 10 hours	15 hours
	Total number of hours:	**33 hours**
	Number of ECTS:	**2 ECTS**