SYLLABUS

Name of the department / clinic providing the course: Department of Functional Genomics

Course title: The use of proteomic repositories in scientific research

Course profile: molecular

Discipline: medical sciences

Level of course unit: international doctoral school
Course unit title: The use of proteomic repositories in scientific research
Course unit code:-
Type of course unit: elective
Course aims: The aim of the course is to familiarize doctoral students with the available resources of proteomic repositories useful in searching for information about the structure of proteins, their biological function, post-translational modifications, and protein interactions. In addition, the PhD student will become familiar with the database mapping all human proteins in cells, tissues and organs using various antibody-based ommics technologies.The seminar will also present useful tools for protein visualization and for classifying the biological functions of protein products of genes whose expression changes in pathological conditions. PhD students will acquire practical skills in applying knowledge from repositories and programs for protein visualization, ontological analysis, and presenting the results of their own research.
Form of study: on-line
Year and semester of study: summer semester (all years)
Types of educational activities and number of hours allocated:

Subject	Language course	Self-study	Lecture	Exercises	Laboratory	Seminar	Practical	e-learning	Profession practice	Other (what?)	ECTS points
						10					

Number of ECTS credits allocated and their structure according to students' form of learning:-

Names of course unit's faculty: Faculty of Biomedical Sciences, Faculty of Medicine

Prerequisites: None

Learning activities and teaching methods:
Seminars - verbal communication; multimedia presentation, individual work

Course unit content:
Protein sequence resources (UniProt, ExPASy), structural databases (RCSB-PDB, PDBsum, PDBe, PDBj), protein domain databases (InterPro, Pfam), protein interactions (STRING, MINT, BioGRID, GeneMania), and protein structure visualization and comparison programs (CN3D, VAST, PyMol, RasMol, SPDBV), ontological analysis (PANTHER Classification System, ShinyGO, Metascape, DAVID), tool for researchers studying protein localization and expression in human tissues and cells (Human Protein Atlas) are presented. Practical use of the acquired resources on selected examples.
Course objectives:

Knowledge:
After graduating, the student knows and understands:

(P8S_WG) scientific research methodology

Skills:
After graduating, the student is able to:

- (P8S_UU) use knowledge from various fields of science to creatively identify, formulate and innovatively solve complex problems or perform research tasks
- (P8S_UW) use knowledge from various fields of science to creatively identify, formulate and innovatively solve complex research problems, and in particular: define the purpose and subject of scientific research, formulate a research hypothesis; develop research methods, techniques and tools and apply them creatively; draw conclusions based on the results of scientific research; critically analyze and evaluate the results of scientific research, expert activity and other creative work and their contribution to the development of knowledge; transfer the results of scientific activities to the economic sphere
- (P8S_UU) prepare and present data and draw conclusions based on research results
- (P8S_UK) communicate on specialist topics to an extent that enables active participation in the international scientific community
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Attitudes and transferrable (generic) competencies:

After graduating, the student is able to:

(P8S_KK) critical assessment of achievements within a given scientific discipline, critical assessment of one's own contribution to the development of the discipline, recognition of the importance of knowledge in solving cognitive and practical problems

Required and recommended learning resources (readings):

Required:

1.Riffle M, Eng JK. Proteomics data repositories. Proteomics 2009 Oct;9(20):4653-63
2.Chen Ch, Huang H, Wu C.H. Protein Bioinformatics Databases and Resources Methods Mol Biol. 2017; 1558: 3–39.
3. Ullah S, Gao T, Rahman W, Ullah F, Jahan R, Ullah A, Ahmad G, Ijaz M, PanY. LDBPR: Latest Database of Protein Research. Journal of Bioinformatics and Systems Biology 5 (2022): 34-44.
4. Lehne B, Schlitt T. Protein-protein interaction databases: keeping up with growing interactomes. Hum Genomics. 2009 Apr;3(3):291-7
5. Perez-Riverol Y, Alpi E, Wang R, Hermjakob H, Vizcaíno JA. Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. Proteomics. 2015 Mar; 15(5-6): 930–950.
6. Szklarczyk D, Kirsch R, Koutrouli M, Nastou K, Mehryary F, Hachilif R, Annika GL, Fang T, Doncheva NT, Pyysalo S, Bork P, Jensen LJ, von Mering C. The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest.
Nucleic Acids Res. 2023 Jan 6;51(D1):D638-646.
7. H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, P.E. Bourne, The Protein Data Bank (2000) Nucleic Acids Research 28: 235-242

Recommended:

https://www.uniprot.org/
https://www.rcsb.org/
https://www.expasy.org/
http://www.ebi.ac.uk/thornton-srv/databases/pdbsum/
https://www.ebi.ac.uk/pdbe/
https://www.ebi.ac.uk/interpro/
https://string-db.org/
https://thebiogrid.org/
https://www.ncbi.nlm.nih.gov/structure

Assessment methods and criteria:

Attendance at the seminar, active participation and completion of planned tasks during classes.

Additional information:

Contact person Elżbieta Płuciennik, associate professor
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Statement and signature of the course leader:

I hereby state that the content of the curriculum included in the syllabus below is the result of my individual work completed as part of a work contract/cooperation resulting from a civil law contract and that author rights to this title are not the property of a third party.

