Università
degli Studi
di Padova

PhD in Biomedical Sciences

Course unit English denomination	Protein Structure Analysis: Databases, Visualization, and Functional Insights
SS	BIO10, BIOS-07/A - Biochimica
Teacher in charge (if defined)	Emanuela Leonardi
Teaching Hours	10
Number of ECTS credits allocated	2
Course period	To be defined
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes (80% minimum of presence) ☐ No
Course unit contents	Throughout the course, students will explore the intricate relationships between protein structure, function, and interactions. Participants will learn to navigate and retrieve protein structures from primary databases like the Protein Data Bank (PDB) and AlphaFoldDB and visualize them using tools such as PyMOL. The course covers essential structural elements—such as binding sites, secondary structure motifs, and active sites—and examines their roles in protein function and interactions. Additionally, advanced methods based on residue interaction networks (RINs) will be introduced for analyzing structure-function relationships and predicting residue interactions relevant to drug design and biotechnology. The course consists of five two-hour lessons structured as follows: Lesson 1: Introduction to protein structure and databases Lesson 2: Visualization tools and structural analysis Lesson 3: Structural prediction and homology modeling Lesson 4: Function, interactions, and biotechnological implications Lesson 5: Residue Interaction Networks (RIN) and their applications
Learning goals	At the end of the course, students will have acquired knowledge on: • The fundamental principles of protein structure and their functional implications. • Structural prediction methodologies, including homology modeling and AI-based approaches (AlphaFold). • Residue Interaction Networks (RIN), their role in structural analysis, and the tools for their construction and interpretation. Students will be able to:

	• Consult and use structural databases to extract and analyze protein-related information. • Use molecular visualization software to explore protein structures and identify key structural elements. • Generate structural models through homology modeling and assess their reliability. • Build and analyze Residue Interaction Networks (RIN) to identify functional residues and evaluate the effects of mutations. By the end of the course, students will have developed the ability to: • Apply a critical approach to protein structure analysis, integrating data from various bioinformatics sources. • Effectively communicate the results of structural analysis using graphical representations and accurate descriptions.
Teaching methods	Lectures, practical exercises, group work
Course on transversal, interdisciplinary, transdisciplinary skills	☐ Yes ☒ No
Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	
Examination methods (if applicable)	Multiple-choice test
Suggested readings	
Additional information	