Universitat Autònoma de Barcelona

2023/2024

Biomolecule Structure

Code: 42887
ECTS Credits: 9

Degree	Type	Year	Semester
4313794 Biochemistry, Molecular Biology and Biomedicine	OT	0	1

Contact

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Teaching groups languages

You can check it through this link. To consult the language you will need to enter the CODE of the subject.
Please note that this information is provisional until 30 November 2023.

Teachers

Francesc Xavier Avilés Puigvert

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External teachers

Ana Joaquina Pérez Berna

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Xavier Fernández-Busquets

Prerequisites

University degree in Biochemistry, Biotechnology, Biology, Biomedical Sciences, Genètica, Microbiology, Chemistry, Informatics, Phisics, Veterinary, Pharmacy or Medicine.

Objectives and Contextualisation

The general objective of the course is to provide an introduction to the different techniques and tools for structural analysis of biomolecules used in biomedical research. The student is expected to reach a level of knowledge that will allow him to understand the usefulness of the set of biophysical and bioinformatic techniques for the structural and functional analysis of macromolecules and macromolecular complexes. The student will be introduced to the potential of these techniques in the design de novo of biomolecules, and their applications in Biotechnology and Biomedicine.

Competences

- Analyse research results to obtain new biotechnological or biomedical products to be transferred to society.
- Communicate and justify conclusions clearly and unambiguously to both specialist and non-specialist audiences.
- Continue the learning process, to a large extent autonomously.
- Develop critical reasoning within the subject area and in relation to the scientific or business context.
- Identify and propose scientific solutions to problems in molecular-level biological research and show understanding of the biochemical complexity of living beings.
- Identify and use bioinformatic tools to solve problems in biochemistry, molecular biology and biomedicine.
- Integrate contents in biochemistry, molecular biology, biotechnology and biomedicine from a molecular perspective.
- Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
- Use acquired knowledge as a basis for originality in the application of ideas, often in a research context.
- Use and manage bibliography and IT resources related to biochemistry, molecular biology or biomedicine.
- Use scientific terminology to account for research results and present these orally and in writing.
- Work individually and in teams in a multidisciplinary context.

Learning Outcomes

1. Analyse research results to obtain new biotechnological or biomedical products to be transferred to society.
2. Apply techniques of structural biology to solve scientific problems in molecular biomedicine .
3. Communicate and justify conclusions clearly and unambiguously to both specialist and non-specialist audiences.
4. Continue the learning process, to a large extent autonomously.
5. Develop critical reasoning within the subject area and in relation to the scientific or business context.
6. Distinguish the different biophysical and biochemical methods in order to apply them to problems related to biomedicine.
7. Identify the properties of biomolecules can be characterised using the biophysical techniques being studied.
8. Interpret and analyse biomolecule structures in structural databases (PDB).
9. Interpret and reconstruct protein structures by computer.
10. Know the most advanced methods for structurally characterising the biological systems under study (e.g. protein crystallography, nuclear magnetic resonance, electron microscope, and X-ray diffraction).

11. Process and analyse experimental data from X-ray diffraction.
12. Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
13. Use acquired knowledge as a basis for originality in the application of ideas, often in a research context.
14. Use and manage bibliography and IT resources related to biochemistry, molecular biology or biomedicine.
15. Use scientific terminology to account for research results and present these orally and in writing.
16. Work individually and in teams in a multidisciplinary context.

Content

1- Circular dichroism and fluorescence spectroscopy. Initial techniques for the study of protein folding, stability and interactions. Applications to protein design (3h Theory)

2- Intrinsically disordered proteins. Application to the study of degenerative processes. (3 h Theory)

3- Dynamic scattering of light. Applications to the study of macromolecules and aggregate systems (1h Theory + 5h Laboratory practices)

4- Proteomics and interactomics. (1.5 h Theory)

5- Advanced microscopies

a) Infrared microscopy for the study of neurodegenerative diseases. (3h Theory + 1.5 h Practices)

b) X-ray fluorescence microscopy for the study of neurodegenerative diseases (1.5 h Theory + 1.5 h Practices).

c) X-ray transmission microscopy. X-ray cryotomography. Applications to the study of organelles, microorganisms and intracellular infection processes, (3h Theory + 1h visit to Mistral ALBA station)

d) -Transmission and scanning electron microscopy, electron cryotomography and atomic force microscopy. Application to the study of chromosome structure.

-Nanotechniques for the study of interactions between biomolecules. Optical tweezers; Fluorescence correlation spectroscopy; Total internal reflection fluorescence microscopy (TIRF); Atomic force microscopy; Confocal microscopy (FRET,...); Near Field Scanning Optical Microscopy (NSOM); Super-resolution fluorescence microscopy. Applications in biomedicine.

(7.5 h Theory)

e) Electron cryomicroscopy (3h theory + 1h visit to ALBA installation)

6- Nuclear Magnetic Resonance applied to the 3D study of macromolecules (3h Theory)

7- Crystallography and X-ray diffraction applied to the resolution of 3D structures of macromolecules (2h Theory + 2h Laboratory + 5h practices in the computer room + 1h visit to Xaloc station and Xaira ALBA)

8- Structural Bioinformatics.

a) Prediction and analysis of 3D structures of macromolecules (1h Theory + 5h Computer classroom practices)

b) Prediction and analysis of complexes (1 h Theory + 2 h Computer classroom practices)

c) Molecular dynamics. Theoretical bases. Simulation of biomolecular systems. Applications in biomedical and pharmaceutical research. (1 h Theory + 2 h Practices Computer room)

Methodology

- The work methodology will combine face-to-face classes with autonomous work of the student. There will be classes in the computer room and also sessions in the laboratory. It is mainly intended that the course has a more practical than theoretical nature. The ALBA synchrotron will also be visited with an explanation of its use in different workstations.

Annotation: Within the schedule set by the centre or degree programme, 15 minutes of one class will be reserved for students to evaluate their lecturers and their courses or modules through questionnaires.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Knowledge of biophysical methods and identification of biomolecules properties	70	2.8	2, 10, 6, 7
Type: Supervised			
X-ray data processing and protein model building with computers	35	1.4	8, 9, 11
Type: Autonomous			
New idea development in research and critical arguing	52	2.08	1, 5, 4, 13
Scientific communication	30	1.2	3, 15
use of acquired knowledge	35	1.4	12, 16, 14

Assessment

- The evaluation of the module will be based on attendance (which is mandatory), class participation, continuous evaluation and a brief multiple-choice exam on the main contents of the subject.

Calculation of the final qualification:

Final grade = T* 0,40 + Av* 0,4 + PC* 0,2

T (final theory qualification)

Av (continuous assessment qualification)

PC (class participation assessment)

- It will be considered "not evaluable" when the evaluation activities (final test and attendance) do not allow to obtain a minimum overall grade of 5.0.

Important: If plagiarism is detected in any of the works submitted, it may lead to the student failing the entire module.

There will also be the possibility of performing a recovery test once the module is finished.

To participate in the recovery, students must have been previously evaluated in a set of activities whose weight equals to a minimum of two thirds of the total grade of the subject or module. Therefore, students will obtain the "Non-Valuable" qualification when the evaluation activities carried out have a weighting of less than 67% in the final grade.

- Single assessment regulations:

Students requesting single assessment must complete all sessions of laboratory practices, practical sessions in the computer room and field trip (visit to the synchrotron) in person.

Single assessment consists of a single examination (with multiple-choice questions on the content of the theory sessions and variable-format questions on the contents of the sessions of the other types).

The single assessment examination coincides with the examination date of the module in the calendar. The calculation of the final grade for students who request the single assessment will be:

Final grade = T* 0,90 + PC* 0,1

T (mark of the final exam that includes evaluation of all types of teaching)

PC (note participation in laboratory classes, computer room and field trip)

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Active student involvement	20	0	0	5, 12, 3, 4, 13, 15
Continued evaluation	30	1.12	0.04	1, 2, 10, 6, 7, 8, 9, 11, 16, 14
Writing of test evaluation	50	1.88	0.07	1, 2, 10, 6, 7, 8, 9, 11, 16, 14

Bibliography

- Each lecturer will provide particular bibliography corresponding to their specific topics.

ebook:

Integrative structural biology with hybrid methods / Haruki Nakamura, Gerard Kleywegt, Stephen K. Burley, John L. Markley, editors. Llibre en línia | 2018

Links:

•Protein Crystallography course. Structural Medicine. Cambridge University, MRC-LMB:

http://www-structmed.cimr.cam.ac.uk/course.html

•Dpt. de Biología Estructural. CSIC, Madrid

http://www.xtal.iqfr.csic.es/Cristalografia/index-en.html

- Training and outreach portal of the Protein Data Bank

https://pdb101.rcsb.org

Software

UCSF Chimera; VMD; CCP4 interfase package; Coot; Phenix; Pymol; Modeller; Autodockv4; AlphaFold2