UAB
Universitat Autònoma de Barcelona

Structure of Biomolecules

Code: 42887
ECTS Credits: 9

2025/2026

Degree	Type	Year
Bioquímica, Biología Molecular y Biomedicina	OP	1

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Teachers

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Teaching groups languages

You can view this information at the end of this document.

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.

Learning Outcomes

1. CA24 (Competence) Draw on techniques and technologies for the structural and functional analysis of macromolecules to solve problems in new or little-known contexts in the fields of Biochemistry, Molecular Biology and Biomedicine.
2. CA25 (Competence) Conduct projects that address the emerging challenges of biomolecule structuring in industry and biomedicine, and do so ethically and with respect for fundamental rights and duties, diversity and democratic values.
3. KA34 (Knowledge) Identify the utility of the set of techniques and technologies for the structural and functional analysis of macromolecules, in accordance with current developments in the field.
4. KA35 (Knowledge) Use biophysical techniques to characterise the properties of biomolecules.
5. KA36 (Knowledge) Cite current advances in techniques and technologies in the field of structural and functional analysis of biomolecules.
6. SA33 (Skill) Use the most advanced methods to structurally characterise biological systems.
7. SA34 (Skill) Analyse biomolecular structures deposited in structural databases (PDBs), as well as experimental data obtained by X-ray crystallography.
8. SA35 (Skill) Apply bioinformatics tools to solve and build biomolecular structures of academic or professional interest.

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. Proteomics. Methodologies to measure protein-protein interactions (ITC and SPR) (3 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)

Activities and Methodology

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Knowledge of biophysical methods and identification of biomolecules properties	70	2.8	
Type: Supervised			
X-ray data processing and protein model building with computers	35	1.4	
Type: Autonomous			
New idea development in research and critical arguing	52	2.08	
Scientific communication	30	1.2	
use of acquired knowledge	35	1.4	

- 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.

Restricted use of AI: the use of Artificial Intelligence (AI) technologies is allowed exclusively in support tasks, such as bibliographic or information search and translations. The student will have to clearly identify which parts have been generated with this technology, specify the tools used and include a critical reflection on how they have influenced the process and the final result of the activity. Failure to be transparent about the use of AI in this assessable activity will be considered a lack of academic honesty and may result in a partial or total penalty in the grade of the activity, or greater penalties in cases of seriousness."

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.

Assessment

Continous Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Active student involvement	20	0	0	SA34, SA35
Continued evaluation	30	1.12	0.04	CA24, CA25, KA34, KA35, KA36, SA33
Writing of test evaluation	50	1.88	0.07	

- 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)

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; Autodock; AlphaFold

Groups and Languages

Please note that this information is provisional until 30 November 2025. You can check it through this link. To consult the language you will need to enter the CODE of the subject.

Name	Group	Language	Semester	Turn
(PAULm) Classroom practices (master)	1	English	first semester	morning-mixed
(PCAMm) Field practices (master)	1	English	first semester	afternoon

(PLABm) Practical laboratories (master)	1	English	first semester	morning-mixed
(SEMm) Seminars (master)	1	English	first semester	morning-mixed
(TEm) Theory (master)	1	English	first semester	morning-mixed