UAB
Universitat Autònoma de Barcelona

Protein Chemistry and Engineering

Code: 100935
ECTS Credits: 6

2025/2026

Degree	Type	Year
Biotechnology	OB	3

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Teachers

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Teaching groups languages

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

Prerequisites

There are no official prerequisites, but it is assumed that students have previously acquired enough solid knowledge on subjects like Fundamentals of Chemistry, Organic Chemistry, Biochemistry and Recombinant DNA Technology.

As in most subjects, much of the literature is in the English language, which is also used in the figures projected in theory classes and also for oral communication, when needed.

Objectives and Contextualisation

The course on Protein Chemistry and Engineering belongs to the main subject "Proteins and nucleic acids: structure, function and engineering" of which a part has been taught in the second year of the Biotechnology degree. This course examines the structural and functional characteristics of amino acids, peptides and proteins both from a basic and applied point of view, the methodologies used in their analysis and modification, and their biomedical and biotechnological applications.

Proteins are effector molecules of many biochemical and biological processes, most of which have been studied in the first two years. However, knowledge of their structure and function is crucial to a deep understanding of a number of subjects in the Biotechnology degree. The knowledge acquired in the course of Protein Chemistry and Engineering is complemented by a practical training in the Integrated Laboratory Course 5. The specific objectives are:

- To reach a deeper understanding of the physicochemical characteristics of amino acids and peptides
- To describe and apply methods for the analysis of protein sequences and peptide synthesis.

- To recognize the structural elements, the different complexity levels, the types of protein folding and their capacity to build higher order structures.
- To reach a knowledge on the use of information resources to establish structural classifications of proteins.
- To understand and explain the most common methods for the analysis of the conformation and stability of proteins, including three-dimensional analysis.
- To describe the molecular basis of protein folding, molecular dynamics, post-translational processing and intra- and extracellular protein traffic.
- To establish evolutionary relationships and learn the methods of structural analysis and structure prediction.
- To understand and apply the most common methods for the production and purification of recombinant proteins.
- To design strategies for modifying and optimizing the properties of proteins and to understand the basis for protein design and the methodologies used in these processes.
- To achieve an global vision about the structure-function relationships in proteins and about the application of these biomolecules in medicine, industry and research.
- To integrate the theoretical knowledge in the interpretation of the results of scientific experiments using the appropriate scientific terminology.

Learning Outcomes

1. CM15 (Competence) Work collaboratively in teams to solve problems in the field of biochemistry.
2. KM13 (Knowledge) Describe the principles of bioenergetics and enzymatic catalysis.
3. KM14 (Knowledge) Accurately describe the molecular bases of protein folding, trafficking, modification, and turnover.
4. SM13 (Skill) Apply the different methods for obtaining mutants of a recombinant protein and their purification.
5. SM13 (Skill) Apply the different methods for obtaining mutants of a recombinant protein and their purification.
6. SM14 (Skill) Correctly interpret data and observations in the field of biochemistry.
7. SM14 (Skill) Correctly interpret data and observations in the field of biochemistry.
8. SM15 (Skill) Analyse three-dimensional structures of macromolecules.

Content

THEORY

I. Fundamental properties of amino acids and proteins

Proteins, peptides and their functions in living beings. Structure and physicochemical properties of amino acids. Chemical reactivity. Differential contribution of amino acids to protein properties. Evolutionary relationships.

II. The peptide bond and the sequence polypeptide

Stereochemistry of the peptide bond. Types of natural peptides. Chemical reactivity of peptides. The polypeptide sequence. Strategies for determining the sequence of proteins. Chemical synthesis of peptides; combinatorial libraries.

III. Conformational determinants. Secondary structures

Structural hierarchy. Types of conformation-stabilizing forces. Cooperativity of weak interactions. Determinants of protein folding. Main types of secondary structures.

IV. Structural Classification of Proteins

Supersecondary structures and motifs. Structural domains. Tertiary structure. Domain classification. Conformation and function of fibrous proteins. IDPs- intrinsically disordered proteins.

Structure-function correlation . Examples

General functions of proteins. Enzymatic proteins: examples. Proteins that bind to nucleic acids: examples. Molecular motors: examples. Membrane proteins.

VI. Quaternary structure of proteins

Advantages of quaternary structures. Protomers and subunits. General principles: interfaces, geometries, symmetries. Examples of oligomeric proteins: structure-function and regulation of the activity

VII. Determining the three-dimensional structure of proteins

General methodologies for the structural characterization of proteins. Dissolution analysis: IR, DC, UV-Vis, fluorescence. Analysis in solid phase: X-ray crystallography and cryo-electron microscopy. NMR spectroscopy: 3D structure in solution.

VIII. Folding and conformational dynamics

Protein folding and unfolding: native state and unfolded state. Methods for the analysis of folding. Thermodynamics and mechanistics of the folding process; models that describe it. Folding and aggregation; conformational diseases. Protein folding *in vivo*: the molecular chaperones. Molecular dynamics of proteins.

IX. Post-translational modifications

Types of post-translational modifications and their functional implications. Transport and associated changes. Limited proteolysis: pre-proteins, zymogens. Examples of regulation by limited proteolysis: coagulation, digestive enzymes. Degradation and protein turnover *in vivo*.

X. Protein-ligand interaction

Forces involved in protein-ligand association. Methods of study of the interaction. Determination of kinetic and thermodynamic parameters. Designing drugs based on the structure.

XI. Protein engineering: rational design

Rational design: directed mutagenesis as a tool for the analysis and modification of proteins. Examples and applications of protein engineering in the analysis, modification and improvement of the structure, stability,and functionality.

XII. Protein engineering: directed evolution and de novo synthesis

Directed evolution: random mutagenesis and combinatorial protein engineering methods. Methods for the generation and selection of variants. Examples of redesigned proteins. *De novo*protein design - computeralgorithms.

PROBLEMS

The content of this section will be given in the form of a dossier at the beginning of the semester via the Virtual Campus. It involves a certain amount of problems related to the topics developed in the theory class. The dossier will be updated periodically. The characteristics of the various parts of the theory syllabus make the subjects of the problems class to be concentrated in a limited number of aspects. Thus, the evaluation of problems may vary between partial examinations.

Activities and Methodology

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Problem/practical cases solving	7	0.28	CM15, SM13, SM14, CM15
Theory sessions	38	1.52	KM13, KM14, SM13, SM15, KM13
Type: Supervised			
Homework delivery	4	0.16	CM15, KM14, SM14, CM15
Seminar preparation	4	0.16	CM15, KM13, SM13, SM14, CM15
Seminar presentations	3	0.12	CM15, SM13, SM14, CM15
Type: Autonomous			
Group or individual work to prepare problems/cases or seminars	20	0.8	CM15, SM13, SM14, SM15, CM15
Study - autonomous work	65	2.6	CM15, KM14, SM13, SM14, SM15, CM15

The
training activities are divided into two sections: theory classes
and problem classes, each with its own specific methodology. These
activities can be complemented by tutorial sessions that will be
programmed additionally.

Theory Classes
The teacher will explain the content of the syllabus with the support of audiovisual material that will be made available to students in the Moddle classroom of the subject. These expository sessions will constitute the most important part of the theory section.

Problem Classes
At the beginning of the course the class will be divided into 2 subclasses of problems. A set of statements of problems of the subject (related to the topics developed in Theory) will be made available to students and will be accumulated in the form of a dossier in the Moddle classroom, which will be solved throughout the sessions. Students will work on the problems outside class hours individually and there will be some deliveries in a group way. The non-expository face-to-face sessions will be dedicated to problem solving. The solved problems will be delivered that will be discussed and corrected with the participation of all students.

Seminars
In addition or alternatively, seminars may be organized to provide students with this type of teacher training more alive and additional to theory.

Tutorials
They will be made at the request of the students. The objective of these sessions is to resolve doubts, review concepts with a high conceptual difficulty and carry out debates on the topics of the program. These sessions will not be expository nor will they advance the official agenda, but will be sessions of debate and discussion.

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
In-class delivery of problems/cases	5%	1	0.04	CM15, SM13, SM15
Parcial Problems Evaluation	20%	3	0.12	KM13, KM14, SM13, SM15
Partial exams	75%	5	0.2	KM13, KM14, SM13, SM14, SM15

Theory. The total weight of the evaluation of the theoretical part will be 75% of the total grade of the subject. The main evaluation of this part of the subject will have the format of continuous evaluation with two partial tests, with another final test that allows to examine the content of each of the two partial tests not previously passed. The objective of the continuous evaluation is to encourage the continuous effort of the student throughout the entire syllabus, also allowing him to become aware of his degree of follow-up and understanding of the subject.
Students who have passed the partial theory and problems with a grade higher than 4.0 out of 10 points, can choose to obtain the average grade of the two partials. Those who have not exceeded the value of 4.0 of any of the two partial theory and problems must be examined on the date set by the final exam of the subject, in this case the qualification of the last partial exam made is the one that will be taken to calculate the final grade of theory.

In order to take the final exam (recovery), students must have previously submitted to a continuous number of activities that at least equal to 2/3 of the final grade.

Problems. The weight of the evaluation of this section will be 25% of the total: 20% of it will be for the 2 particular exams of these activities, which will take place in parallel to the second and third partial of Theory (10% each). The other 5% will be allocated to group deliveries of the problems-exercises.

Seminars (optional). People who choose to prepare a seminar may be added up to 0.5 points to the final grade achieved in the previous calculation.

Overall assessment. To pass the subject it is necessary to obtain an average of 3.5 in the theory partial tests and obtain ≥ 5 as an overall grade.

Single Evaluation:

The single assessment consists of a single synthesis test with multiple-choice questions (may include short questions) on the contents of the entire theory program 75%); as well as 2 problems to be solved (25%).

The single assessment test shall be carried out coinciding with the same date fixed in the calendar for the last continuous assessment test and the same recovery system shall be applied as for the continuous assessment.

Bibliography

Basic

(from oldest to newest)

- Brandën C. & Tooze J., Introduction to Protein Structure (1999) Garland Science
- Gómez-Moreno C i Sancho J. (eds.) Estructura de Proteínas (2003) Ariel Ciencia
- Petsko, R. & Ringe, D., Protein Structure and Function (2003) Blackwell Publishing
- Whitford, D., Proteins: Structure and Function (2005) Wiley
- Buxbaum, E., Fundamentals of Protein Structure and Function (2015), Springer (2015, *Electronic document, UAB accessible*)
- Kessel, A. & Ben-Tal, N., Introduction to Proteins: Structure, Function and Motion (2010) CRC Press (2015, *Electronic document, UAB accessible*)
- Williamson, M., How Proteins Work (2012) Garland Science
- Kuriyan, J., Konforti, B. & Wemmer, D. The Molecules of Life (2013) Garland Science
- Walsh, G. Proteins: Biochemistry and Biotechnology (2014) Wiley (2019, *Electronic document, UAB accessible*)
- Lesk, A.M., Introduction to Protein Science 3rd ed. (2016) Oxford University Press
- Almeida, P., Proteins. Concepts in Biochemistry (2016) Garland Science
- Bahar I.,Jernigan R.L. & Dill, K.A., Protein Actions (2017) Garland Science
- Backman, L. Protein Chemistry (2020) De Gruyter

Any of these books contains many interesting notions for the course. However, no one of them may be used as a lone-standing textbook. Some are more didactically-oriented (Petsko & Ringe, Williamson, Brandën & Tooze) but every reading will be enjoyable

Complementary

- Buckel, P. (ed), Recombinant Protein Drugs (2001), Birkhäuser Verlag

- Bujnicki, J.M. (ed.) Prediction of protein structure, functions and interactions (2008) Wiley

- Creighton T.E., Proteins. Structures and Molecular Properties. (1993) (2nd ed.) Freeman W.H. & Co.

- Fersht A. Structure and Mechanism in Protein Science (1999) W.H. Freeman & Co.

- Glick, B.R. & Pasternak, J.J. Molecular Biotechnology (1998) ASM Press

-Kamp, R.M., Calvete, J. J., Choli-Papadopoulou, T. Methods in Proteome and Protein Analysis (2004) Springer-Verlag

- Kraj, A. & Silberring, J. (eds) Introduction to Proteomics (2008) Wiley

- Kyte, J. Structurein Protein Chemistry 2nd ed. (2007) Garland Science

- Lutz, S., Bornscheuer,U.T. (eds.) Protein Engineering Handbook (2008) Wiley

- Nussinov, R. & Schreiber, G. Computational Protein-Protein Interactions (2017) CRC Press

- Oxender D.L. & Fox C.F., Protein Engineering (1987) Alan Liss Inc.

- Patthy, L. Protein Evolution (2007) (2nd ed.) Wiley

- Perutz M., Protein Structure. New Approaches to Disease and Therapy. (1992). Freeman W.H. & Co.

- Schultz, G.E. & Schirmer, R.H. Principles of Protein Structure (1979) Springer Verlag

- Park, S.J., Cochran, J.R. Protein Engineering and design (2009)CRC Press

- Sternberg M.J.E. Protein Structure Prediction. (1996) IRL- Oxford University Press

- Tompa, P. & Fersht, A. Structure and function of intrinsically disordered proteins (2009) CRC Press

- Twyman, R., Principles of Proteomics (2004) Taylor & Francis

- Veenstra, T.D. & Yates, J.R. Proteomics for Biological Discovery (2006) Wiley

Internet sites

Links to selected sites may be found at:https://catalegclassic.uab.cat/search*cat/r?SEARCH=100935

Software

PyMol: https://pymol.org/2/

JMol: http://jmol.sourceforge.net/

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
(PAUL) Classroom practices	431	Spanish	first semester	morning-mixed
(PAUL) Classroom practices	432	Spanish	first semester	morning-mixed
(SEM) Seminars	431	Catalan	first semester	morning-mixed
(TE) Theory	43	Catalan	first semester	morning-mixed