

Protein Chemistry and Engineering

Code: 100857
ECTS Credits: 6

Degree	Type	Year	Semester
2500252 Biochemistry	OB	2	1

The proposed teaching and assessment methodology that appear in the guide may be subject to changes as a result of the restrictions to face-to-face class attendance imposed by the health authorities.

Contact

Name: Salvador Ventura Zamora
Email: Salvador.Ventura@uab.cat

Use of Languages

Principal working language: catalan (cat)
Some groups entirely in English: No
Some groups entirely in Catalan: Yes
Some groups entirely in Spanish: No

Teachers

Susana Navarro Cantero

Prerequisites

There are no official prerequisites. However, in order to ensure the proper follow-up of the subject by the student and the achievement of the learning outcomes proposed, it is recommended that the student would have acquired solid knowledge of the following subjects of the 1st year: Organic Chemistry Of the Biochemical Processes, Foundations of General Chemistry, Cell Biology, Biochemistry I and Basic Instrumental Techniques.

On the other hand, in a scientific discipline such as Chemical and Protein Engineering, where many of the sources of information, or at least the most up-to-date ones, are in English, it is highly recommended that students have some basic knowledge of this language .

Objectives and Contextualisation

The subject Chemical and Protein Engineering is part of the subject "Molecular Biology", in which the structural and functional characteristics of amino acids and proteins are studied from a basic and applied point of view. Since proteins constitute the effector molecules of many biochemical and biological processes, knowledge of its structure and function is essential for the understanding of a good number of subjects in the Degree in Biochemistry. The theoretical knowledge acquired in the subject of Protein Chemistry and Engineering is complemented by a practical training in the laboratory in the context of Integrated Laboratory 3.

The training objectives are: that the student, at the end of the subject, would be able to:

- Know the chemical and structural properties of amino acids.
- Describe the methods of sequencing and synthesis of peptides.
- Describe the elements of secondary, tertiary and quaternary structure of the proteins, the determinants of

their stability and folding.

- Structurally classify proteins.
- Explain the different methods for the determination of the three-dimensional structure of the proteins.
- Describe the molecular bases of the folding of proteins, their molecular dynamics, their post-translational processing and their traffic to the different cellular compartments.
- Explain the biochemical bases of the evolution of proteins.
- Describe the properties of the human proteome and the methods used for its characterization.
- Know the methods for artificial production, modification and optimization of the properties of the proteins
- Integrate and apply the theoretical knowledge acquired to interpret the results of scientific experiments and to solve experimental problems.
- Use of the appropriate scientific terminology.

Competences

- Collaborate with other work colleagues.
- Define the structure and function of proteins and describe the biochemical and molecular bases of their folding, intracellular traffic, post-translational modification and replacement.
- Interpret experimental results and identify consistent and inconsistent elements.
- Make an oral, written and visual presentation of ones work to a professional or non-professional audience in English and understand the language and proposals of other specialists.
- Manage bibliographies and interpret the information in the main biological databases, and also know how to use basic ICT tools.
- Read specialised texts both in English and ones own language.
- Use ICT for communication, information searching, data processing and calculations.

Learning Outcomes

1. Classify proteins in structural families based on data on sequence and secondary and tertiary structures.
2. Collaborate with other work colleagues.
3. Deduce evolutionary relationships between macromolecules from the analysis of sequential data.
4. Describe correctly the molecular bases of protein folding, transport, modification and replacement.
5. Extract information from genomic and proteomic databases.
6. Extract three-dimensional structures of macromolecules from databases and use the software needed to visualise and understand structure-function relationships.
7. Identify conserved protein motifs and domains.
8. Indicate the capacity of the different structural analysis techniques and decide which to apply in specific experimental situations.
9. Interpret experimental data on protein stability and folding.
10. Interpret experimental results and identify consistent and inconsistent elements.
11. Make an oral, written and visual presentation of ones work to a professional or non-professional audience in English and understand the language and proposals of other specialists.
12. Read specialised texts both in English and ones own language.
13. Use ICT for communication, information searching, data processing and calculations.

Content

I. FUNDAMENTAL PROPERTIES OF AMINO ACIDS AND PROTEINS.

Proteins, peptides and their functions for living organisms. Structure and physico-chemical properties of amino acids. Chemical reactivity. Differential contribution of the amino acids to the properties of the proteins. Evolutionary relationships between amino acids.

II. PEPTIDE BOND AND POLYPEPTIDIC SEQUENCE.

Stereochemistry of the peptide bond. Types of natural peptides. Chemical reactivity of peptides. Structural and functional implications of the polypeptide sequence. Strategies for the determination of the protein sequence. Chemical synthesis of peptides; Combinatorial libraries

III. CONFORMATIONAL DETERMINANTS. SECONDARY STRUCTURES

Levels of three-dimensional structure. Types of stabilizing forces for the protein conformation. Cooperativity of weak interactions. Conditions of protein folding. Main types of secondary structures; Amino acids that participate.

IV. STRUCTURAL CLASSIFICATION OF PROTEINS

Supersecondary structures and motifs. Structural domains. Tertiary structure. Proteins α . Proteins α / β . Proteins β . Classification methods. Conformation and function in fibrous proteins: α -keratin, fibroin, collagen.

V. DETERMINATION OF THE THREE-DIMENSIONAL STRUCTURE OF PROTEINS.

General methodologies for structural characterization of proteins. Analysis in solution or in films: IR, DC, UV-Vis, fluorescence, RPE. Analysis in crystals: X-ray and ME. NMR spectroscopy. Other methods: chemical probes, susceptibility to proteases ...

VI. FOLDING AND CONFORMATIONAL DYNAMICS.

Protein folding and unfolding: native state and unfolded state. Methods of analysis of folding. Thermodynamic and mechanical characteristics of the folding process. Models that describes folding. Folding and aggregation; Conformational diseases. Protein folding in vivo: molecular chaperones. Proteostasis. Molecular protein dynamics.

VII. POST-TRANSLATION PROCESSES AND MODIFICATIONS.

Types of post-translation modifications and functional implications. Glycosylation. Transport associated modifications. Limited proteolysis: pre-proteins, zymogens. Systems regulated by limited proteolysis: blood clotting, digestive proenzymes. Degradation and half protein life.

VIII. ENGINEERING OF PROTEINS: REDESIGN AND SYNTHESIS DE NOVO.

Rational design: targeted mutagenesis as a tool for analyzing and modifying proteins. Examples and applications of protein engineering in the analysis of structure, stability, and functionality. Modification and improvement of the properties of proteins. Targeted evolution: protein engineering by combinatorial methods. Examples of recombinant proteins. Protein design de novo.

PROBLEMS

The content of this section, which will be presented in the form of a dossier at the beginning of the semester, consists of a determined amount of problems related to the topics developed in Theory. The own characteristics of the various parts of the Theory's program make the problems to concentrate on certain specific aspects that are: properties of amino acids, protein sequencing, protein stability and three-dimensional structure of proteins.

Methodology

The training activities are divided into three sections: theory classes, problem classes and seminars each with their specific methodology. These activities will be complemented by a series of tutoring sessions that will be programmed additionally.

Theory classes

The teacher will explain the content of the program with the support of audiovisual material that will be available to the students in the Virtual Campus of the subject in advance at the beginning of each of the subjects of the course.

These lectures will be the most important part of the theory section. It is recommended that students have the material published on the CV in printed form so that they can follow the classes more comfortably.

The tutor would advise the student about the strategies to follow in their learning.

Problem classes

The group will be divided into two subgroups of about 30 students, whose lists will be made public at the beginning of the year. Students will attend the sessions programmed for their group.

At the beginning of the semester a dossier of problems will be presented through the Virtual Campus. They will be resolved throughout the sessions.

Students will work out problems outside class hours. Non-expositive classroom sessions will be devoted to the resolution of previously worked problems during the previous week, which will be discussed and corrected with the participation of all students.

Seminars

At the beginning of the semester a proposal of subjects will be presented through the Virtual Campus on which students aggrouped in 4-6 groups will be able to prepare a seminar. The difficulties that arise on this self-study material and other issues / problems would be discussed in tutoring classes. The tutor will advise students on the strategies to follow in their elaboration.

Tutorials

These will be carried out with students divided into the same subgroups of problem classes. Its programming will be announced at the beginning of the semester. The purpose of these sessions is to resolve doubts, revise concepts with a high conceptual difficulty and carry out debates on the subjects for which autonomous learning is programmed. These sessions will not advance the subject of the official agenda, but instead 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.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Problems solving	12	0.48	13, 2, 3, 6, 5, 7, 8, 9, 10, 12
Theory classes, seminars	33	1.32	1, 2, 3, 4, 6, 5, 7, 8, 9, 10, 12, 11

Type: Supervised			
Group tutorials	4	0.16	3, 5, 7, 8, 9
Seminars preparation	7	0.28	13, 1, 2, 3, 5, 7, 9, 10, 12, 11
Type: Autonomous			
Search for information and information management in the process of self-learning (group)	24	0.96	13, 1, 2, 3, 4, 6, 5, 7, 8, 9, 10, 12, 11
Study autonomous work	60	2.4	1, 3, 4, 6, 5, 7, 8, 9, 10, 12

Assessment

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 a continuous evaluation with two partial tests, with another recuperation exam that allows to examine the content of each one of the two partials not previously surpassed, or both simultaneously, if you do not pass any of the partial ones.

The objective of the continuous evaluation is to encourage the student's ongoing effort throughout the course, allowing him to be aware of the degree of follow-up and understanding of the subject.

The students who have passed the partial exams with a note greater than 3.5 on a total of 10 points, can choose to obtain the average theory note of the two partials. Those who have not surpassed the value of 3.5 of either partial will have to examine for the final examination the subject of the partial or partials in question, in this case the qualification of the last examination partial is the one that will be taken to calculate the final grade of theory.

The specific weight of the set of these two tests, or the recuperation exam, is 75% of the total of the mark of the subject.

Problems

The weight of the evaluation of problems will be 20% of the total.

Mixed group / individual assessment:

- Resolution of the problems worked throughout the course and evaluated by the teacher (5%)
- Written proof of problems on the date assigned for the final exam of the subject (15%). The students who have passed the partial exams with a note greater than 3.5 on a total of 10 points, can choose to obtain the average problem note of the two partials. Those who have not surpassed the value of 3.5 of either partial will have to examine for the final examination the subject of the partial or partials in question, in this case the qualification of the last examination partial is the one that will be taken to calculate the final grade of problems.

Seminars

To the overall assessment of the subject participation in seminars will weigh up to 5% of the total. Thematic seminars may be proposed complementarily to the subject and always about subjects not directly addressed in the classroom or the program. In the exceptional case that this section cannot be carried out for logistical reasons, it will be replaced by research seminars given by prestigious researchers and its content will be evaluated in the theory exam, which in this case will weigh a total of 80% of the note.

Global evaluation:

· The subject will be passed when the sum of the different parts weighted by their specific weight in the subject exceeds 5.0 on 10 points.

To be eligible for the retake process, the student should have been previously evaluated in a set of activities equaling at least two thirds of the final score of the course or module. Thus, the student will be graded as "No Available" if the weight in of all conducted evaluation activities is less than 67% of the final score

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Partial theory tests (individual assessment)	75%	2	0.08	1, 3, 4, 6, 5, 7, 8, 9, 10, 12, 11
Problem Testing (Individual Assessment)	15%	2	0.08	13, 1, 3, 6, 7, 8, 9, 10, 12, 11
Problem solving in class and seminars	5%	4	0.16	13, 2, 3, 4, 6, 5, 7, 10, 11
Seminaris	5%	2	0.08	13, 1, 2, 4, 6, 12, 11

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, *Document electrònic, accessible UAB*)
- Kessel, A. & Ben-Tal, N., Introduction to Proteins: Structure, Function and Motion (2010) CRC Press (2015, *Document electrònic, accessible UAB*)
- Williamson, M., How Proteins Work (2012) Garland Science
- Walsh, G. Proteins: Biochemistry and Biotechnology (2014) Wiley (2019, *Document electrònic, accessible UAB*)
- Lesk, A.M., Introduction to Protein Science 3rd ed. (2016) Oxford University Press
- Bahar I., Jernigan R.L. & Dill, K.A., Protein Actions (2017) Garland Science
- Backman, L. Protein Chemistry (2020) De Gruyter

Complementary

- Buckel, P. (ed), Recombinant Protein Drugs (2001), Birkhäuser Verlag
- 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
- Kyte, J. Structure in 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 links:

You can find them at : https://catalegclassic.uab.cat/search*cat/r?SEARCH=100857

Software

FoldIt

<https://fold.it>