UAB
Universitat Autònoma de Barcelona

2023/2024

Protein Chemistry and Engineering

Code: 100762
ECTS Credits: 6

Degree	Type	Year	Semester
2500250 Biology	OT	4	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

Irantzu Pallares Goitiz

Prerequisites

There are no official prerequisites as this is an optional subject in the fourth year, but it is assumed that the student has previously acquired enough solid knowledge on Structure and Function of Biomolecules, Chemistry, Cell Biology, Metabolism and Bioinformatics during the first three courses of the degree.

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

Proteins are effector molecules of many biological processes, and knowledge of their structure and function is fundamental for the consolidation of concepts acquired in a number of subjects of the Biology degree. In Protein Chemistry and Engineering we will study the structural and functional characteristics of amino acids, peptides and proteins both from basic and applied points of view, the methodologies used in their analysis and modification and their applications to biomedicine and biotechnology. The specific objectives of the course 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.

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- 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 knowledgein the interpretation of the results of scientific experiments using the appropriate scientific terminology.

Competences

- Act with ethical responsibility and respect for fundamental rights and duties, diversity and democratic values.
- Analyse and interpret the origin, evolution, diversity and behaviour of living beings.
- Apply statistical and computer resources to the interpretation of data.
- Be able to analyse and synthesise
- Be able to organise and plan.
- Isolate, identify and analyse material of biological origin.
- Make changes to methods and processes in the area of knowledge in order to provide innovative responses to society's needs and demands.
- Students must be capable of applying their knowledge to their work or vocation in a professional way and they should have building arguments and problem resolution skills within their area of study.
- Students must be capable of collecting and interpreting relevant data (usually within their area of study) in order to make statements that reflect social, scientific or ethical relevant issues.
- Students must be capable of communicating information, ideas, problems and solutions to both specialised and non-specialised audiences.
- Students must develop the necessary learning skills to undertake further training with a high degree of autonomy.
- Students must have and understand knowledge of an area of study built on the basis of general secondary education, and while it relies on some advanced textbooks it also includes some aspects coming from the forefront of its field of study.
- Take account of social, economic and environmental impacts when operating within one's own area of knowledge.
- Take sex- or gender-based inequalities into consideration when operating within one's own area of knowledge.
- Understand and interpret the physicochemical bases of the basic processes of living beings
- Understand the processes that determine the functioning of living beings in each of their levels of organisation.

Learning Outcomes

1. Analyse a situation and identify its points for improvement.
2. Apply statistical and computer resources to the interpretation of data.
3. Be able to analyse and synthesise.
4. Be able to organise and plan.
5. Critically analyse the principles, values and procedures that govern the exercise of the profession.
6. Describe correctly the molecular bases of protein folding, transport, modification and replacement.
7. Design a basic protocol for obtaining mutants of a recombinant protein, expressing them and purifying them.

8. Identify evolutionary relationships between proteins through sequential data analysis and use software for manipulating three-dimensional structures extracted from databases.
9. Identify the capacities of the different structural analysis techniques and decide how to apply them to specific experimental situations.
10. Interpret experimental data on protein stability and folding.
11. Interpret findings from structural studies of proteins and nucleic acids.
12. Propose new methods or well-founded alternative solutions.
13. Students must be capable of applying their knowledge to their work or vocation in a professional way and they should have building arguments and problem resolution skills within their area of study.
14. Students must be capable of collecting and interpreting relevant data (usually within their area of study) in order to make statements that reflect social, scientific or ethical relevant issues.
15. Students must be capable of communicating information, ideas, problems and solutions to both specialised and non-specialised audiences.
16. Students must develop the necessary learning skills to undertake further training with a high degree of autonomy.
17. Students must have and understand knowledge of an area of study built on the basis of general secondary education, and while it relies on some advanced textbooks it also includes some aspects coming from the forefront of its field of study.
18. Take account of social, economic and environmental impacts when operating within one's own area of knowledge.
19. Take sex- or gender-based inequalities into consideration when operating within one's own area of knowledge.
20. Use these techniques from protein chemistry and recombinant DNA to identify, clone and express target genes and proteins that can be used to design and obtain enzymes.

Content

T H E O R Y

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 r e l a t i o n s h i p s .

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 sequenceof proteins.Chemical synthesis of peptides; c o m b i n a t o r i a l   l i b r a r i e s .

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.

V.   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. P*ost-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. Biochemical e*volution of proteins*

Protein evolutionary relationships. Detection and analysis of homologies; sequential databases; phylogenetic trees. Convergent and divergent evolution; examples. Sequence structure and function. 3D structure prediction; conformational modeling. Evolution of genomes and protein evolution.

XII. *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.

XIII. *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. Denovo protein design - computer algorithms.

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.

Methodology

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.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Problem/practical cases solving	7	0.28	2, 9, 10, 11, 3, 20
Theory sessions	38	1.52	6, 7, 9, 8, 10, 11
Type: Supervised			
Homework delivery	4	0.16	2, 9, 8, 10, 11, 3, 4
Seminar preparation	4	0.16	18, 1, 2, 12, 3, 4
Tutorials/seminar preparation	3	0.12	19, 5, 11, 4
Type: Autonomous			
Group or individual work to prepare problems/cases or seminars	20	0.8	2, 9, 10, 11, 4
Group or individual work to prepare problems/cases or seminars	65	2.6	6, 7, 9, 8, 10, 11, 3, 4, 20

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 continuous evaluation with three partial tests, with another final test that allows to examine the content of each of the three 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 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.

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
In-class delivery of problems/cases	5%	1	0.04	7, 9, 10, 11, 17, 15, 13, 14, 3, 4
Partial Problem Evaluation	20%	2	0.08	19, 18, 5, 1, 2, 9, 8, 10, 11, 12, 3
Theory partial tests	75%	6	0.24	6, 9, 8, 10, 11, 16, 3, 20

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/