

Degree programme	Type	Course
Nanoscience and Nanotechnology	OP	4

Contact lecturer

Name : David Reverter Cendros

Email : david.reverter@uab.cat

Teaching staff

David Reverter Cendros

Group languages

You can consult this information at the [end](#) of the document.

Prerequisites

There are no previous formal requirements, but it is assumed that the student acquired beforehand solid knowledge on the subjects of the three first courses, particularly on the subjects of the 1st course on the basis of Biochemistry, Chemical reactivity and Cell biology, of the 2nd course on Molecular biology and Organic Chemistry, and on the 3rd course on Molecular spectroscopy and Analytical chemistry.

As in other subjects, most of the bibliography is in english, language that is also used in an important way in the presentations displayed at the classes and other activities. The use of this language by the students in the supervised activities (Problems and Practical classes, Seminarsetc), will be positively evaluated.

Objectives

General goals. This subject will deal with the structural and functional characteristics as well as with the reactivity/interaction of amino acids, peptides and proteins. Also, on how they have evolved biologically and how they can be transformed by rational redesign, directed evolution or chemo-biological modifications at the laboratory in order they adopt structures, superstructures and properties of fundamental and applied interest. Proteins are structural molecules, regulatory and effectors in most biochemical and biological processes, natural/ pathological/ of industrial interest, as well as frequent protagonists, and among the most diverse among them. The knowledge on their properties and strategies to transform them is fundamental for the deep understanding of a significant number of subjects within the degree of Nanoscience and Nanotechnology.

Specific goals.

- Get a deep knowledge of the physico-chemical characteristics of amino acids, peptides and proteins, as well as of their reactivity and modifications.
- Describe and apply the methodologies for the analysis of the sequence of proteins and the synthesis of

peptides.

- Recognize the structural elements, the different levels of complexity, the types of folding for proteins and their capability in the formation of higher order structures..
- To know how to consult and get access to the information sources to analyze and classify proteins structurally.
- To know and be able to describe and apply the most used methods for the analysis of the conformation and stability of proteins, including the three-dimensional analysis.
- Describe the molecular basis of the folding of proteins, of its molecular dynamics, post-translational modification, intra- and extra- cellular transit.
- To know how to establish the evolutionary relationships among proteins, and know the methods for the structural analysis and prediction.
- Understand and know how to apply the most usual methodologies for the production and purification of recombinant proteins.
- To know how to select the best strategies for the modification and optimization of the properties of peptides and proteins. Understand the basis for its design, for the construction of mini-, super-structures and mimetics, and the methodologies used in such processes. Also, to know about approaches that have been valid to form nanostructures and nanoprobe with them.
- Get an overall view of the structure-function relationships in proteins, and about the applications of such biomolecules in medicine, industry and research.
- Integrate the acquired theoretical knowledge to interpret the results of scientific experiments and to solve experimental problems, using the proper scientific terminology.

Learning outcomes

- KM43 (Identify the dynamic and functional properties that allow for the different stages of protein folding.) Identify the dynamic and functional properties that allow for the different stages of protein folding.
- SM34 (Perform basic genetic engineering and protein engineering procedures.) Perform basic genetic engineering and protein engineering procedures.

Contents

List of topics of theory proposed for the subject PROTEIN CHEMISTRY AND ENGINEERING

I. Fundamental properties of amino acids and proteins

II. The peptide bond and the polypeptidic sequence

III. Structural determinants. Secondary structures

IV. Structural classification of proteins

V. Structure-function correlations in proteins. Examples

VI. Protein quaternary structure

VII. Determination of the three-dimensional structure of proteins

VIII. Protein folding and conformational dynamics

IX. Post-translational processes and modifications

X. Interaction protein-ligand

XI. Protein engineering: rational design

XII. Protein engineering: directed evolution and *de novo* synthesis

Learning activities and methodology

Title	Hours	ECTS	Learning outcomes
Problems	22.5	0.9	KM43, SM34
Tutorials	8	0.32	KM43, SM34
Study in general	61.5	2.46	KM43, SM34
Theory classes	34	1.36	KM43, SM34
Problems	18	0.72	KM43, SM34

The training activities are divided into two sections: theory classes and problem classes and / or seminars, each one with its 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 syllabus with the support of audiovisual material that will be made available to students in the Moddle classroom of the subject. These lectures will be the most important part of the theory section.

Problem Classes and / or Seminars A set of statements of subject problems (related to the topics developed in Theory) will be made available to students and will be accumulated in the form of a dossier on the Virtual Campus, which will be resolved throughout the sessions. Students will work out problems outside class hours individually. Non-expositive classroom sessions will be devoted to the resolution of previously worked problems during the previous week. Complementary or alternatively, seminars may be organized to provide students with this type of teaching that is more lively and additional to that of theory.

Tutorials Students will be made available. The purpose of these sessions is to resolve doubts, revise concepts with a high conceptual difficulty and carry out debates on the topics of the program. These sessions will not be exhibited nor in them will be advanced matter of 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

Continuous assessment activities

Title	Weight	Hours	ECTS	Learning outcomes
Problem evaluation	30%	3	0.12	KM43, SM34
Theory evaluation	70%	3	0.12	KM43, SM34

Theory.

The main evaluation of this part of the subject will have the format of continuous evaluation with two partial tests (35% each), with another final test that allows to examine the content of each one of the two partial not previously surpassed, or both simultaneously, in case you do not pass any of the partial ones. The objective of the continuous assessment is to encourage the continuous effort of the student along the entire subject, allowing also to become aware of its degree of follow-up and understanding of the subject. Students who have passed the theory and problems partitions with a score greater than 4.0 on 10 points, may choose to obtain the average mark of both partial. Those who have not passed the value of 4.0 of either partial shall be examined on the date signed for the final exam of the subject of the partial or partial question, in this case the qualification of the student, The last partial exam is the one that will be taken to calculate the final grade.

Problems and / or Seminars. The weight of the evaluation of this section will be 30% of the total: 15% of this total will be allocated to individual deliveries, problems-exercises, seminars and / or active participation in class, and the other 15% will be for exams Individuals of these activities, which will take place in parallel to the Theory exams.

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. Students who do not, with just cause, participate in the continuous evaluation, can be evaluated through the final test. To opt for the recovery (final exam) it is necessary to present 2/3 of the activities of the subject.

If the student has only been evaluated for a maximum of 25% of the tests and drops, the final grade will be NOT EVALUATED.

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 (70%); as well as 2 problems to be solved (30%).

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.

In this course, the use of Artificial Intelligence (AI) technologies is not permitted at any stage of the learning process. Any work containing AI-generated content or excerpts will be considered a breach of academic integrity and may result in a partial or total reduction of the grade for the assessed activity, or more severe sanctions in cases of serious misconduct.

Any irregularity committed in an assessment activity (including academic fraud, plagiarism, or improper use of Artificial Intelligence (AI), unless such use is expressly authorized in the course guide) that may lead to a significant alteration of the assessment result will result in a grade of 0 (zero) for that assessment activity.

If the course guide establishes that obtaining a minimum grade in that assessment activity is an essential requirement to pass the course, or if multiple irregularities occur in the assessment activities of the same course, the final grade for the course will be 0 (zero). In addition, disciplinary proceedings may be initiated against any student who commits any of these irregularities.

Bibliography

Basic

- Brandén C. & Tooze J., Introduction to Protein Structure (1999) Garland Pub.
- Buxbaum E. Fundamentals of Protein Structure and Function (2007) Springer.
- Gómez-Moreno C y Sancho J. (eds.), Estructura de Proteínas (2003) Ariel Ciencia.
- Kessel A. & Ben-Tal N., Introduction to Proteins. Structure, Function and Motion (2011) CRC Press
- Petsko, R. & Ringe, D., Protein Structure and Function (Primers in Biology) (2008) Blackwell Publishing.
- Whitford, D., Proteins: Structure and Function (2005, 1ª edic / 2016, 2ª edic) Wiley.

Complementary

- Buckel, P. (ed), Recombinant Protein Drugs (2001), Birkhäuser Verlag
- Bujnicki, J.M. (ed.) Prediction of protein structure, functions and interactions (2008) Wiley
- Buxbaum, E., Fundamentals of Protein Structure and Function (2007), Springer
- 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
- Lesk, A.M. Introduction to Protein Science (2010) Oxford University Press
- Lutz, S., Bornscheuer, U.T. (eds.) Protein Engineering Handbook (2008) Wiley
- Oxender D.L. i 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.
- Remigopalakrishnan V., Carey P.R. & Smith I.C.P. Proteins : Structure, Dynamics & Design (2013).
- Sternberg M.J.E. Protein Structure Prediction. (1996) IRL- Oxford University Press.
- Twyman, R., Principles of Proteomics (2004) Taylor & Francis
- Veenstra, T.D. & Yates, J.R. Proteomics for Biological Discovery (2006) Wiley
- Walsh, G. Proteins: Biochemistry and Biotechnology (2001) Wiley

Software

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

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

Course groups and languages

The information provided is provisional until November 30. After this date, you will be able to consult the language of each group through this [link](#). To access the information, you will need to enter the course CODE

Type of teaching	Group	Language	Semester	Shift
(TE) Theory	1	Catalan	second semester	morning-mixed
(PAUL) Classroom practices	1	Catalan	second semester	morning-mixed