



**COURSE GUIDE**

2024/25

**Faculty** 310 - Faculty of Science and Technology

**Cycle** .

**Degree** BMYBM204 - Master in Molecular Biology and Biomedicine

**Year** .

**COURSE**

505643 - Proteomics in Biomedicine

**Credits, ECTS:** 5

**COURSE DESCRIPTION**

Proteomics describes the study of the complete set of proteins (proteome) that is expressed at a given time in a cell, tissue, organ or organism. Modern proteomics involves the integration of a wide range of analytical tools and bioinformatics to identify qualitative and quantitative changes in proteins and specifically proteoforms; for example, in the detection of altered protein abundance associated with a disease. Additionally, mass spectrometry-based proteomic approaches have greatly contributed to the present knowledge of post translational modifications (PTMs) that are often causally influenced or changes in human diseases.

"Proteomics in Biomedicine" covers leading and emerging technologies for sample preparation, protein fractionation, separation, PTM enrichment, mass spectrometry and data analysis for protein/PTM detection and quantification. The subject describes numerous investigations in the area of biomedicine in which, among others, distinct proteomic approaches have been successfully applied to better understand the molecular mechanisms underlying a disease, to uncover the pathways targeted by a drug or to discover biomarkers.

This subject combines theoretical classes and lab practical sessions in which students, through practice-related learning, understand the logic and methodology underpinning protein fractionation, sample preparation and mass spectrometry. Moreover, distinct informatics sessions allow students explore critical thinking by examining facets of experimental design and data analysis through self-directed learning tasks and facilitated activities.

The main objective of "Proteomics in Biomedicine" is to provide students with knowledge about the principles and practical uses of proteomics and the current available technology platforms to perform quantitative and qualitative analysis of proteins and PTMs. In this way, the student will be qualified to apply a critical and independent thinking to the planning of experiments using a wide range of methods in order to generate relevant data answering a specific scientific question related to his/her investigation.

**COMPETENCIES/LEARNING RESULTS FOR THE SUBJECT**

**COMPETENCIAS DE LA ASIGNATURA**

**RESULTADOS DE APRENDIZAJE DE LA ASIGNATURA**

Describe the distinct methodologies for sample preparation prior to MS analysis: protein enrichment, protein digestion and protein/peptide fractionation

Differentiate between shotgun and targeted proteomics, as well as describe different bottom-up proteomics approaches: data dependent acquisition (DDA) & data independent acquisition (DIA).

Perform the steps involved in a workflow to identify the proteins present in a complex mixture.

Analyze proteomics data. Filter MS-based data following specific criteria and perform bioinformatic analyses to extract the biological meaning.

Plan an experiment using appropriate methods taking into account the constraints of the available technology, sample number, and the underlying hypothesis.

**Theoretical and Practical Contents**

- 1.- Introduction: From single protein studies to proteome investigation
- 2.- Sample preparation prior to mass spectrometry analysis
- 3.- Mass spectrometry for proteomics
- 4.- Shotgun proteomics & data independent acquisition
- 5.- Targeted proteomics
- 6.- Quantitative proteomics
- 7.- Protein post-translation modification (PTM) analysis by mass spectrometry
- 8.- Bioinformatics tools for processing proteomics data
- 9.- A visit to the Proteomics Facilities in CICbioGUNE and UPV/EHU: Equipment and techniques

**METODOLOGIA (ACTIVIDADES FORMATIVAS)**

Actividad Formativa	Hours	Porcentaje presencialidad
Utilization of Computer Programs	15	67 %
Laboratory practicals	25	20 %



Working with it equipment	25	40 %
Drawing up reports and presentations	25	0 %
Computer practicals	25	20 %
Seminars	25	20 %
Expositive classes	50	40 %

## TYPES OF TEACHING

Types of teaching	M	S	GA	GL	GO	GCL	TA	TI	GCA
Hours of face-to-face teaching	20	10		10	10				
Horas de Actividad No Presencial del Alumno/a	30	15		15	15				

**Legend:** M: Lecture-based S: Seminar GA: Applied classroom-based groups  
 GL: Applied laboratory-based groups GO: Applied computer-based groups GCL: Applied clinical-based groups  
 TA: Workshop TI: Industrial workshop GCA: Applied fieldwork groups

## Evaluation tools and percentages of final mark

Denominación	Ponderación mínima	Ponderación máxima
Attendance at classes	0 %	2 %
Attendance and participation	50 %	50 %
Attitude Scales	5 %	5 %
Drawing up reports and presentations	30 %	30 %
Evaluation of assignments by topic (educational and summative evaluation).	0 %	3 %
Computer practicals	15 %	15 %

## ORDINARY EXAMINATION PERIOD: GUIDELINES AND OPTING OUT

Attendance is compulsory. Excused absences may be made up with the activity indicated by the person in charge of the session.

The intervention of the student in the classes will be valued, the questions and comments made in each session will be valued. A high participation and attendance to 100% of the sessions allows to pass the course.

An unexcused attendance of less than 80% of the sessions will result in the failure of the course. In the case of absence with a justified cause (more than 30%), an exam/test of the subject adjusted to the specific situation will be carried out.

## EXTRAORDINARY EXAMINATION PERIOD: GUIDELINES AND OPTING OUT

The extraordinary call will involve the realization of an exam/test of the subject that will consist of the development of a topic of the subject to choose between two chosen at random.

## MANDATORY MATERIALS

e-Gela platform from the UPV/EHU <https://egela.ehu.eus/login/index.php>

## BIBLIOGRAPHY

### Basic bibliography

Manual de proteómica, Volumen I. Sociedad Española de Proteómica, 2014  
 Manual de proteómica, Volumen II. Sociedad Española de Proteómica, 2019  
 Mass spectrometry data analysis in proteomics. R. Matthiesen. Humana Press, Springer, Heidelberg, 2013  
 Proteomics for biological discovery. T.D. Veenstra & J.R. Yates III. Wiley, Hoboken, New Jersey, 2006

### Detailed bibliography

Aebersold R, Mann M. (2016) Mass-spectrometric exploration of proteome structure and function. Nature 537:347-355  
 Cox J, Mann M. (2011) Quantitative, high-resolution proteomics for data-driven systems biology. Annu. Rev. Biochem. 80:273-299  
 Ebhardt HA, Root A, Sander C, Aebersold R. (2015) Applications of targeted proteomics in systems biology and translational medicine. Proteomics 15:3193-3208  
 Geyer PE, Holdt LM, Teupser D, Mann M. (2017) Revisiting biomarker discovery by plasma proteomics. Mol. Syst. Biol. 13:942



- Lundberg E, Borner GHH. (2019) Spatial proteomics: a powerful discovery tool for cell biology. *Nature Reviews*. 25(5):285-302
- Meissner F, Geddes-McAlister J, Mann M, Bantscheff M. (2022). The emerging role of mass spectrometry-based proteomics in drug discovery. *Nature Reviews DrugDiscovery*. 21, 637-654.
- Olsen JV, Mann M. (2012) Status of large-scale analysis of post-translational modifications by mass spectrometry. *Mol.Cell. Proteomics* 12:3444-3452
- Picotti P, Aebersold R. (2012) Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. *Nat. Methods* 9:555-566
- Sabidó E, Selevsek N, Aebersold R. (2012) Mass spectrometry-based proteomics for systems biology. *Curr. Opin.Biotechnol.* 23:591-597
- Uzozie AC, Aebersold R. (2018) Advancing translational research and precision medicine with targeted proteomics. *J.Proteomics* 189:1-10
- Walther TC, Mann M. (2010) Mass spectrometry-based proteomics in cell biology. *J. Cell Biol.* 190:491-500

## **Journals**

## **Web sites of interest**