

**COURSE DATA****DATA SUBJECT****Code:** 43458**Name:** Omic technologies**Cycle:** Master's Degree / Doctorate**ECTS Credits:** 3**Academic year:** 2026-27**STUDY (S)**

Degree	Center	Acad. year	Period
2210 - Master's Degree in Research in Molecular, Cellular and Genetics Biology	Facultat de Ciències Biològiques	1	First quarter
3173 - PhD in Biomedicine and Biotechnology	Escola de Doctorat		First quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
2210 - Master's Degree in Research in Molecular, Cellular and Genetics Biology	Omic technologies	COMPULSORY
3173 - PhD in Biomedicine and Biotechnology		

COORDINATION

GIL GARCIA ROSARIO

SUMMARY

The subject "Omics Technologies" is scheduled in the first semester of the Master of Research in Molecular and Cellular Biology and Genetics at the University of Valencia. It is a mandatory subject, so it must be taken by all students.

Omics technologies have occupied since late last century a leading role in many of the scientific discoveries in the biological fields covered by this Master. The term Genomics was coined in 1986 to refer to the subdiscipline of genetics devoted to the study, mapping, sequencing and analysis of complete genomes. Subsequently the suffix "omics" has been extended to many other current disciplines in all fields of Biology that share this globalizing approach. The omics sciences have an important methodological component, and most prospective students must possess basic knowledge on this subject. Therefore, this module focuses mainly on the study of methodologies and applications in current research on Molecular and Cellular Biology, Genetics and Microbiology.

PREVIOUS KNOWLEDGE



RELATIONSHIP TO OTHER SUBJECTS OF THE SAME DEGREE

There are no specified enrollment restrictions with other subjects of the curriculum.

OTHER REQUIREMENTS

COMPETENCES / LEARNING OUTCOMES

2210 - Master's Degree in Research in Molecular, Cellular and Genetics Biology

Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.

Be able to access to information tools in other areas of knowledge and use them properly.

Be able to make quick and effective decisions in professional or research practice.

Diseñar experimentos para abordar análisis de poblaciones celulares, expresión génica, cuantificación de mRNAs o proteínas.

Ser capaz de interpretar los resultados derivados de la aplicación de las nuevas técnicas ómicas en biología molecular y celular.

Students should apply acquired knowledge to solve problems in unfamiliar contexts within their field of study, including multidisciplinary scenarios.

Students should be able to integrate knowledge and address the complexity of making informed judgments based on incomplete or limited information, including reflections on the social and ethical responsibilities associated with the application of their knowledge and judgments.

Students should communicate conclusions and underlying knowledge clearly and unambiguously to both specialized and non-specialized audiences.

Students should possess and understand foundational knowledge that enables original thinking and research in the field.

To be able to assess the need to complete the scientific, historical, language, informatics, literature, ethics, social and human background in general, attending conferences, courses or doing complementary activities, self-assessing the contribution of these activities towards a comprehensive development.

DESCRIPTION OF CONTENTS

1. The era of the omics sciences

Functional genomics and other omics. Study subject, global approaches and analysis of results.
Professor Rosario Gil



2. DNA sequencing methods for complete genomes

Current high throughput sequencing (HTS) methodologies. Third generation sequencing technologies. Complete genomes assembly. Annotation and functional analysis of genomes. Metagenomics and Metatranscriptomics.

Professor Rosario Gil

3. Methods of analysis of global gene expression

Comparison of methods for individual and global analysis. Serial analysis of gene expression (SAGE) and derivative methods. The chips or DNA microarrays: principles and applications. Analysis of results. Transcriptomic studies with DNA chips. The functional organization of eukaryotic genomes. HTS for transcriptomics. ChIP-chip and ChIP-seq.

Professor José García Martínez

4. Global phenotypic studies

Phenomics. Deletion mutant collections or with iRNA. Gene fusions collections. Analysis techniques for phenotypic studies.

Professor José García Martínez

5. Separation of proteins for proteomics

Preparation of samples for analysis by proteomic techniques. Separation techniques for peptides and proteins. Bottom-up and Top-down Proteomics.

Professor Manuel Sanchez del Pino

6. Mass spectrometry: instrumentation and procedures

Ionization of biological samples and mass analyzers used in proteomics. Fragmentation and de novo sequencing of peptides. Experiments of LC-MS/MS and data acquisition methods.

Professor Manuel Sanchez del Pino

7. Protein identification and quantitation

Protein identification methods. Using search engines. Analysis of macromolecular complexes. Protein quantitation: labeling and label-free methods. Targeted proteomics (SRM / MRM). Analysis of interaction networks and metabolic pathways.

Professor Manuel Sanchez del Pino

WORKLOAD

**PRESENCIAL ACTIVITIES**

Activity	Hours
Theory	17,00
Other activities	3,00
Computer classroom practice	3,00
Classroom practices	7,00
Total hours	30,00

NON PRESENCIAL ACTIVITIES

Activity	Hours
Attendance at other activities	0,00
Individual or group project	0,00
Independent study and work	0,00
Preparation of lessons	0,00
Preparation for assessment activities	45,00
Resolution of case studies	0,00
Total hours	45,00

TEACHING METHODOLOGY

The following teaching methods will be used for the activities in this module:

1. Theoretical lectures and case-study sessions.
2. Practical activities in small groups. Visit to the Genomics and Proteomics facilities (SCSIE) to have a first-hand knowledge of the functioning of the sequencing, mass spectrometry and two-dimensional electrophoresis equipment.
3. Presentation of case studies and interpretation of results.
4. Tutorial sessions, in order to assist and guide students regarding problems arising during the development of the course.

EVALUATION

1. Written test with three parts, each one of 45 minutes. One of the questions will correspond to the resolution of a practical case. The final grade of the written test will be the average of all three parts. It will be necessary to achieve at least a score of 3 out of 10 in each part in order to pass the subject. This test will represent 95% of the final course grade.

On the second call, it will be not necessary to repeat the part of the subject in which the student reached a score at or above 5 on the first call, if the student considers it appropriate.

2. Participation in visits to Sequencing and Proteomics Services at SCSIE: 2.5% for each visit.

REFERENCES



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STRING. <https://string-db.org> The ENCODE Project: ENCyclopedia Of DNA Elements. <http://www.genome.gov/10005107> The Human Protein atlas. <https://www.proteinatlas.org>