Course Guide
44695 Omics technologies

COURSE DATA

DATA SUBJECT

Code: 44695
Name: Omics technologies
Cycle: Master's Degree
ECTS Credits: 5
Academic year: 2025-26

STUDY (S)

Degree	Center	Acad. year	Period
2224 - Master's Degree in Research and Development in Biotechnology and Biomedicin	Facultat de Ciències Biològiques	1	First quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
2224 - Master's Degree in Research and Development in Biotechnology and Biomedicin	New technology	COMPULSORY

COORDINATION

SANCHEZ DEL PINO MANUEL MATEO

SUMMARY

Omics technologies hold since late last century a leading role in many of the scientific discoveries in the fields of biology covered by this Master. Genomics The term was coined 25 years ago to refer to the sub-discipline of Genetics dedicated to the study of mapping, sequencing and analysis of the functions of whole genomes. Subsequently has extended the \"omics\" suffix to many other disciplines have in common being globalizing and used in all fields of Current Biology. Since much of the content of these omics is methodological and most prospective students must already possess basic concepts about them this subject focuses mainly on the study of methodologies and applications that have at this time research in 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

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Access the necessary information within the specific subject area (databases, scientific articles, etc.) and have sufficient judgement to interpret and apply it.

Adquirir destrezas en el manejo de las metodologías avanzadas empleadas en las biociencias moleculares y en el registro anotado de actividades.

Apply critical reasoning and argumentation based on rational criteria.

Apply research experience acquired both in private companies and public organisations.

Apply the knowledge acquired to identify career opportunities and sources of employment.

Aprendizaje del uso de la instrumentación y equipamientos empleados en los laboratorios de biotecnología y biomedicina.

Aprendizaje en la redacción de artículos científicos en los campos de la Biomedicina y la Biotecnología.

Be able to integrate new technologies in their professional and/or research work.

Consider entrepreneurship as a professional alternative.

Critically analyse one's own work and that of colleagues.

Demonstrate motivation for quality and continuous improvement, acting with rigour, responsibility and professional ethics.

Demonstrate respect for fundamental rights and equality between men and women.

Design multidisciplinary experimental strategies in the field of molecular biosciences to solve complex biological problems, especially those related to human health.

Develop scientific results obtained by oneself or other scientists into practical applications with social and/or economic profitability.

Gain personal skills that facilitate professional integration and development.

Handle scientific information sources appropriately and assess them critically, integrating the information to contribute knowledge to multidisciplinary research teams.

Know and use job search techniques and tools.

Make proper use of IT tools, statistical and data simulation methods, applying IT tools and statistics to biomedical and biotechnological problems.

Make rapid and effective decisions in complex situations within one's professional or research activity by developing new and innovative working methodologies adapted to the scientific/research, technological or professional field in which the activity takes place.

Master the scientific method, the design of experimental protocols and the interpretation of results in the biomedical and biotechnological fields.

Mejorar la capacidad de trabajar con seres vivos o muestras biológicas.

Mejorar la capacidad para trabajar de manera autónoma, responsable y rigurosa en el laboratorio, aplicando los conocimientos sobre los aspectos legales y prácticos en la manipulación y eliminación de agentes de riesgo.

Prepare, write and present reports and projects in public in a clear and coherent manner, defend them with rigour and tolerance and respond satisfactorily to any criticism that may arise from the presentation.

Project the knowledge, skills and competencies acquired to promote a society based on the values of freedom, justice, equality and pluralism.

Select and manage available resources (instrumental and human) to optimise research outcomes.

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 demonstrate self-directed learning skills for continued academic growth.

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

Tener una visión integrada del funcionamiento de los sistemas vivos utilizando el enfoque que proporcionan las ciencias ómicas.

Use inclusive and non-discriminatory language in all the above-mentioned areas of communication.

Work in a team, without discriminating between men and women, carry out professional or research work efficiently and acquire the ability to participate in research projects and scientific or technological collaborations.

DESCRIPTION OF CONTENTS

1. General concepts of omics technologies

The era of omics. functional genomics and other omics. Subject of study, globalizers approaches and analysis of results.

2. Methods for DNA sequencing whole genomes.

Historical description of genome sequencing. Current methodologies of high-trouhgput sequencing (HTS). Third generation HTS methodologies and the future of technology. Assembly of complete genomes. Annotation of genomes. Metagenomics

3. Methods for global gene expression analysis.

Methods of analysis of global gene expression. Comparison of individual analysis methods and global analysis. The serial analysis of gene expression (SAGE) and derived methods. DNA Chips or microarrays: fundamentals and applications. transcriptomic studies with DNA chips. Ultrasequencing for transcriptome studies: RNAseq and other techniques. Analysis of the results. Study of other parameters of gene expression. Metatranscriptomics.

4. Interactomics, Epigenomics and Phenomics.

Interactions between DNA and proteins: ChIP-chip and ChIP-seq. Three-dimensional organization of the genome. Epigenomics. RNA-protein interactions and RNA structure. Global phenotypic studies: phenomics. Collections of deletion mutants of genes. Essential genes. Collections of gene fusions. Analysis techniques phenotypic studies.

5. Sample preparation and separation in Proteomics

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

6. Mass spectrometry: instrumentation and procedures.

Ionization techniques biological samples. Types of mass analyzers and its application in proteomics. Fragmentation and de novo sequencing of peptides. Experiments LC-MS / MS. dependent and independent data acquisition.

7. Protein identification.

Protein identification methods. Using search engines. Analysis of macromolecular complexes.

8. Protein quantitation

Protein quantitation methods using fluorescent and isotopic labeling. Quantification techniques without marking. Directed proteomics (SRM / MRM). Analysis of interaction networks and metabolic pathways.

9. Metabolomics

Analysis techniques in metabolomics. Identification and quantification of metabolites.

WORKLOAD

PRESENCIAL ACTIVITIES

Activity	Hours
Theory	50,00
Total hours	**50,00**

NON PRESENCIAL ACTIVITIES

Activity	Hours
Attendance at other activities	0,00
Individual or group project	35,00
Independent study and work	40,00

Preparation of lessons	0,00
Preparation for assessment activities	0,00
Resolution of case studies	0,00
Total hours	**75,00**

TEACHING METHODOLOGY

The following teaching methodologies will be used for the activities of this module: 1) Theoretical classes. Based on the lecture / lecture method and case studies 2) Seminars prepared by the students tutored by the teacher 3) Seminars given by experts on current issues. 4) Personal tutorials. Help and guide students in relation to problems that arise during the development of face-to-face and non-face-to-face activities.

EVALUATION

The evaluation will be based on an examination of the two parts of the subject: proteomics / metabolomics (value 40%) and genomics (value 60%). To pass, it will be necessary to exceed 30% of the grade for each part in order to average the two grades. The exam will constitute 80% of the final grade. The other 20% will be based on seminars given by the students that will be evaluated by the corresponding professor based on the content of the seminar, quality of the presentation and the answers to the questions that are asked about its content.

REFERENCES

Proteomics:

- Sociedad Española de Proteómica (2014) Manual de proteómica – Volumen I
- Sociedad Española de Proteómica (2019) Manual de proteómica – Volumen II

Genomics portals:

- EMBL (European Molecular BIology Laboratory), Bioinformatics: https://www.ebi.ac.uk/
- ExPASy (Expert Protein Analysis System). http://us.expasy.org/
- GenomeNet (Kyoto University Bioinformatics Center). http://www.genome.jp/

Open access databases:

- (Genomes Online Database). http://www.genomesonline.org/
- KEGG (Kyoto Encyclopedia of Genes and Genomes). http://www.genome.jp/kegg/kegg2.html

- MINT: Molecular Interaction Database. http://mint.bio.uniroma2.it/
- NCBI (National Center for Biotechnology Information). http://www.ncbi.nlm.nih.gov/
- Saccharomyces Genome Database. http://www.yeastgenome.org/

Cell Atlas:
- https://www.humancellatlas.org
- https://www.singlecellatlas.org
- https://tabula-muris-senis.sf.czbiohub.org
- https://www.czbiohub.org/sf/tabula-muris/

Sequencing Platforms:
- https://www.illumina.com/
- https://www.pacb.com/
- https://nanoporetech.com/es

Single-Cell Genomics Platforms:
- https://www.10xgenomics.com/
- https://www.parsebiosciences.com/
- https://atrandi.com/
- https://www.m20genomics.com/

Prokaryote-Related Databases:
- https://img.jgi.doe.gov/
- https://gtdb.ecogenomic.org/
- https://registry.seqco.de/

Reference books:

- McElreath, R. (2016). Statistical Rethinking: A Bayesian Course with Examples in R and Stan (1st ed.). Chapman and Hall/CRC.https://doi.org/10.1201/9781315372495
- Teetor, P. (2011). R cookbook. O'Reilly Media.
- Kappelmann-Fenzl, M. (Ed.). (2021). Next generation sequencing and data analysis. Springer. MLA Style.

In addition, specific complementary bibliography will be provided for each topic.