Master in Biomedical Research

2026-2027

List of potential laboratories

Other laboratories would also be accepted

(by alphabetical order using the last name of each principal investigator)

Note: **admissions to the Master in Biomedical Research (BIOMED) are prioritized for students that have been accepted to do his/her research *practicum* in a research laboratory.**

A main orientation of the BIOMED master is to continue towards a PhD thesis, and the majority of students enrolling in this master have, at the time of pre-registration, been accepted in research groups to do a PhD after they finish the master. However, there are students who have a motivation to do this master, and eventually a PhD, but who may not know how to contact a suitable laboratory.

This document contains a few guidelines to help candidate students in finding a research group, and also a list of potential laboratories to which they can submit applications.

This list is orientative, and students can do their research in another laboratory that they can find on their own. Also, this list is not just to choose a laboratory: you will contact the group you are interested in, arrange an online interview, and get the written acceptance of the investigator in charge of that group.

Master in Biomedical Research

2025-2026

List of potential laboratories

(the list is in alphabetical order using the last name of each principal investigator)

Note: the list of groups is orientative. Students can also find by themselves research groups (in Spain or abroad) that are not in this list, and submit the acceptance letter of the researcher responsible (principal investigator) of the group together with the rest of the documentation when they send their application to this master.

Howerer, groups in this list had ***already expressed their interest in hosting a student of the UPF Master in Biomedical Research****, and therefore have the resources (space, money and time) to properly train a potential candidate.* Training a master student is a substantial effort for the group, so we advice that each group only selects one student.

See also important information about projects and groups in the next page

Admissions to the Master in Biomedical Research (BIOMED) are prioritized for students that have been accepted in a research group for their *practicum*.

If more than two students are opting to the same group, the master coordinator may recommend that some of the applicants be redirected to other groups based on their motivation profile and academic criteria.

a) If you have already been accepted to a research group for doing the master research *practicum*, please submit the acceptance letter by the group's supervisor/director. The group can be in Spain or in a foreign country.

b) If you do not have a host research group at the time of registering, you must indicate your first 5 choices, in order of preference, **from the list of groups** offered by the BIOMED master. Knowing these choices gives us additional information to assess your application.

Important:

b1) When listing your 5 choices, please write the name of the PI for each group. Don't just say "group in tumor modelling" or something like that.

Besides telling us your 5 choices from the list, you can search for a research group (in Spain or abroad) that is not in this list. You do not need to indicate that in addition to your 5 choices above.

b2) Keep in mind that indicating your choices does not mean that you will be assigned to a group automatically. You are encouraged to actively seek acceptance in a group because having a group will increase your chances of being accepted to the master.

You must contact the group you are interested in (from the list provided here or from your own searches), arrange an interview, and get the written acceptance of the investigator in charge of that group.

The next page outlines some guidelines to help candidate students to find a research group.

It also has a list of potential laboratories to which you can submit applications. This list can be updated with some new groups in the next months.

“How to: getting accepted in a research laboratory”

1- You have to know what you would like to work on.

2- Be specific: you should be able to say what are the questions that are important to you and why.

Not very good: I want to work in neurosciences, I have always liked it.

Much better: I want to understand the processes and mechanisms that make neurons more sensitive to oxidative stress and oxygen deprivation in patients with neurodegenerative diseases such as...

Not very good: I want to work in regenerative medicine, I think that stem cells have a lot of potential to cure diseases.

Much better: I want to contribute to the identification of proteins that when expressed in a differentiated cell such as a fibroblast, can cause it to dedifferentiate and acquire functional characteristics of a pluripotent cell.

3- Find out who is working on what.

Websites of universities and research centers, PubMed searches, Google...

It takes time! (don’t wait till last minute to begin looking for your favorite lab)

4- Write to the group that interests you.

5- Contacting a group.

a) Motivation letter: tell them why you want to work with them (for this, you need to know something about what they do and about current questions in the field).

It takes time! (don’t wait till last minute to begin looking for your favorite lab)

Also tell them why you are good. Labs appreciate commitment, responsibility, ability to work in a team, ability to persevere and a strong motivation.

Ask them for an interview to show them how good you are.

Do not write a generic letter to copy-paste and send to ten different laboratories changing only the name of the group leader.

Choose your labs and send a personal, specific letter to each one.

b) Keep in mind that a person working full time in a cellular-molecular biology lab can spend more than 1000 euros/month in materials, besides a lot of time required to train you and supervise you until you begin to get solid results.

Expect that during the first 6 months it is more likely that you will produce more trouble and expenses than productive results. Laboratories are very careful with how they

spend their money because they get their funding from competitive grants that are given or denied based on productivity (that means getting results) and publications in internationally respected journals.

Do not get discouraged with rejections, learn from them to improve your application.

c) Do not forget important details in your CV:

1- Give names of senior persons that can be a reference.

Be careful with “clone” reference letters from teachers that don’t really know you and will just say general things.

2- Include your university scores. If they are not too good, you should be ready to explain why, either in your application letter or in an interview. Be honest and realistic about it. If the teaching/exam system of your university hasn’t worked for you, you will know the reasons better than anyone else, so be prepared to speak frankly about it.

University scores are not an exact indicator of who will become a successful scientist, but they say that a person has gone through 4-5 years of serious effort with a better than average performance.

Most people will interpret this as a sign of self-discipline, organization, capacity to work even if you have a bad day, and to get things done regardless of whether they are more fun or plainly boring.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: METABOLIC CONTROL OF IMMUNE RESPONSES

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: METABOLIC CONTROL OF IMMUNE RESPONSES

Project supervisor (principal investigator of the laboratory)
Name: Jose Aramburu
Mail: jose.aramburu@upf.edu
Group name: GENIMMUNE
Institution: Universitat Pompeu Fabra
Webpage of the group: https://www.upf.edu/web/genimmune
https://www.upf.edu/web/jose-aramburu
Main grant associated with this project:
Principal investigator: Jose Aramburu and Cristina López-Rodríguez
Agency: Plan Estatal I+D+i, Ministerio de Ciencia e Innovación, Agencia Estatal de Investigación
Reference/ years: PID2024-159862OB -I00 (2025-2028)

Brief summary of the project or current research lines of the group
Metabolism regulates immune responses, both ensuring energy and metabolites necessary for immune functions as well as influencing gene expression and functional specialization of immune cells. Metabolism and immune response co-regulate each other, and immune cells are capable of adapting their metabolism to be able to function in different niches and even hostile conditions, while on the other hand altered metabolic conditions can lock immune cells in a detrimental functional state.
We are currently studying how metabolic pathways altered in obesity influence the immunohematopietic system and immune responses in pathological settings, such as cancer. We have combined high-throughput RNA-sequencing analyses and metabolomics to identify metabolic pathways and metabolism-regulated gene signatures and functions in different populations of immune cells in these scenarios. We offer a master position in a project that will aim at modifying specific metabolic pathways in T lymphocytes and macrophages to redirect immune responses. The selected candidate will acquire conceptual fluency in current trends in immunometabolism research, in parallel with hands-on experience in diverse cellular, molecular and immune function techniques (for instance flow cytometry, gene expression and chromatin analyses, cell differentiation assays, metabolic activity, antitumor function) of primary immune cells isolated from gene-edited mice under different pathological settings.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Cell Cycle Control: Regulation of the G1/S Transition

Project supervisor (principal investigator of the laboratory/group)
Name: José Ayté
eMail: jose.ayte@upf.edu
Group name: Oxidative Stress and Cell Cycle
Institution: UPF
Webpage of the group: https://www.upf.edu/web/osccg/

Main grant associated with this project:
Principal investigator: José Ayté
Agency: Ministerio de Ciencia, Innovación y Universidades
Reference/ years: PID2025 (2026-2029)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

In our laboratory, we are ultimately interested in deciphering the mechanisms that control cell cycle progression using fission yeast as model organism. Recently, we have started a new project to obtain a more profound understanding of how CDKs (the central core of the cell cycle machinery) are regulated. Cdc2 (CDK1) is the single CDK kinase described to regulate cell cycle progression in fission yeast, like in all other yeasts. However, despite several global phosphoproteomic and genome-wide studies to determine which are the target(s) of the CDK activity in the G1/S transition, up-to-now it is unknown which are the primary targets of Cdc2 in this cell cycle phase. We have been recently investigating the role of an alternative CDK, Pef1, which was originally described to be involved in controlling TORC1 pathway and autophagy. Interestingly, we have observed an impact on cell cycle regulation, since cells lacking Pef1 are smaller than wild type cells. Using different biochemical and cell biology approaches, we can demonstrate that Pef1 is required for completion of mitotic S phase. We have analysed the proteome and phosphoproteome of a wild type, *Δpef1*, and a conditional Pef1 strains from asynchronous cultures and we have found several candidate proteins that can be phosphorylated by Pef1. The candidate will determine direct targets of Pef1 involved in cell cycle progression using some wide-range technologies, including protein purification, microscopic fluorescence quantification, cytometry and CRISPR-directed mutagenesis.

Some related publications from the group are:

Gálvez-Merchán et al. **iScience** 29:114576
Murciano-Julià et at. **EMBO Rep.** 26:5048-5069
Murciano-Julià et at. **PLoS Biol.** 23:e3002969
Salat-Canela et al. **Trends Cell Biol.** 33:124-137
Hummer et al. **Cell Rep.** 37:109893
Salat-Canela et al. **Cell Rep.** 37: 109951
González-Medina et al. **Nucleic Acids Res.** 47:8439-8451
Alves-Rodrigues et al **Cell Rep.** 14:885-895
Gomez-Escoda et al. **EMBO Rep.** 12:84-89
Moldon et al. **Nature** 455:997-1000

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Protease-Targeting Probes for Cancer and Immunity

Project supervisor (principal investigator of the laboratory/group)
Name: Marta Barniol-Xicota
eMail: marta.barniol@upf.edu
Group name: Chemical Biology and Peptide Theranostics
Institution: Pompeu Fabra University
Webpage of the group: https://barniolxicotalab.com/

Main grant associated with this project:
Principal investigator: Marta Barniol-Xicota
Agency: Agencia Estatal de Investigación
Reference/ years: *Grant Nº PID2023-148652NA-I00 funded by MICIUN/AEI/10.13039/501100011033 and by "ERDF A way of making Europe" (2024-2027)*

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The MSc student can join **one of two projects** within the following research lines:

1.Precision diagnostics through high-throughput probe discovery
We develop high-throughput strategies to discover selective chemical probes for medically relevant enzymes. By combining cyclic peptide design, reactive linkers, and phage display, we map enzyme activity and generate probe candidates for translational diagnostics. We are expanding this platform to new protein classes and probe modalities.
Project (what you'll do)**:** Contribute to ongoing efforts to optimize cyclic peptides targeting a cancer-associated protease (CRC context), aiming to develop probe candidates for precision diagnostics and therapeutic concepts.
Skills you'll gain: peptide synthesis, medicinal chemistry, activity assay development, cell culture.

2. Immune-focused tool development
We build chemical and peptide tools to interrogate immune-cell-restricted proteases that regulate cytotoxic function and antigen-related pathways. In parallel, we design targeting strategies (e.g., peptides) for selective cargo delivery to immune receptors. Our goal is to enable functional measurements in complex immune environments relevant to immunotherapy.
Project (what you'll do)**:** Develop and benchmark experimental systems to study immune proteases in native-like contexts, then design/test substrates or probe candidates to quantify activity and regulation.
Skills you'll gain: protein expression/purification in native-like systems, activity assays, peptide substrate/probe development.

Candidate profile: Background in chemistry, chemical biology, biochemistry, or related fields; motivated to work at the chemistry–biology interface; interest in proteases, diagnostics, or immunology.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Dissecting the function of large-scale genetic changes in cancer

Project supervisor (principal investigator of the laboratory/group)
Name: Francisco M. Barriga
eMail: fbarriga@vhio.net
Group name: Cancer Genome Engineering Laboratory
Institution: Vall D´Hebron Institute of Oncology (VHIO)
Webpage of the group: https://barrigalab.net; https://vhio.net/pf/cancer-genome-engineering-group/
Main grant associated with this project:

Principal investigator: Francisco M. Barriga
Agency: ERC Starting Grant
Reference/ years: 101041659 (Acronym: MACHETE). 01/2023 – 12/2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page) :

The Cancer Genome Engineering Lab was established in January 2023 at VHIO and studies cancer heterogeneity at the genetic and cell state level. From a genetics perspective, we focus on understanding large-scale chromosomal changes known as copy number alterations (CNAs). We combine genome engineering strategies with in vivo models of cancer to uncover the mechanisms by which CNAs enable cancer cells to propagate and resist therapies. We are particularly interested in the role of these alterations in immune surveillance, epigenetics, and cancer genome evolution. We also leverage our genome engineering expertise to devise novel strategies to image, trace, and dissect the function of complex cell states in cancer. We aim to understand how genetic and phenotypic heterogeneity drives cancer progression and therapy resistance, with specific focus on pancreas and ovarian cancers. Our goal is to identify the underlying principles that govern tumor heterogeneity and use this knowledge to design new therapeutic strategies that control cancer and improve patient care.

Ongoing projects:
-Dissecting the role of CNAs on tumor immune evasion.
-Identifying the role of tumor ploidy in cancer progression.
-Understanding the role of oncogene amplification topology in driving genetic heterogeneity.
-Studying CNA cooperation/competition in promoting tumor evolution.
-Determining the cellular response to immunotherapy through combinatorial genetics.

Important: Interested candidates must submit a motivation letter to fbarriga@vhio.net . This letter should state the reasons behind their application, identifying the specific area they would like to study. Before being accepted to work in the lab, selected potential candidates will be invited for an interview with the group, so early application is encouraged to accommodate this.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Light-Powered Tools in Biomedical and Chemical Research

Project supervisor (principal investigator of the laboratory/group)
Name: Ben Bradshaw / Xavier Just-Baringo
eMail: benbradshaw@ub.edu / xavier.just@ub.edu
Group name: Bonding via Radicals (BRAD group)
Institution: Universitat de Barcelona
Webpage of the group: www.bradgroup.org

Main grant associated with this project:
Principal investigator: Ben Bradshaw
Agency: Ministerio de Ciencia e Innovación
Reference/ years: PID2022-139257NB-I00 (2023-2026)

Brief summary of the project:

Light offers a powerful and precise way to control how molecules behave in biological systems. One exciting example is photopharmacology, an emerging field where medicines can be switched "on" and "off" using light. This approach could allow treatments to act only where and when they are needed, reducing side effects and helping to limit the development of drug resistance. By deactivating drugs after their therapeutic action, their accumulation in the body can be minimized, lowering unwanted biological pressure and off-target activity.
Many current light-activated drugs rely on molecular systems that require ultraviolet (UV) light, which can damage tissues and has limited penetration into the body. New strategies are now being developed to enable activation with visible light, which is safer and can reach deeper biological targets. These advances open the door to more precise and clinically relevant light-controlled therapies.[1,2]
In this project, the student will join a multidisciplinary research team working at the interface of chemistry, biology, and medicine. The work will focus on the design and development of new molecules and technologies with potential biomedical applications, contributing to ongoing efforts to create smarter, more selective therapeutic tools.[3,4]

[1] Just-Baringo, X.; Yeste-Vázquez, A.; Moreno-Morales, J.; Ballesté-Delpierre, C.; Vila, J.; Giralt, E. *Chem. Eur. J.* **2021**, *27*, 12987.

[2] Ruiz-Soriano, A.; Lamelza, L.; Pizzamiglio, E.; Just-Baringo, X. *J. Org. Chem.* **2024**, *89*, 17141.

[3] Rodríguez, L. G.; Bonjoch, J.; Bradshaw, B. *Org. Lett.* **2024**, *26*, 10553.

[4] Rodríguez, L. G.; Serra, A.; Bonjoch, J.; Bradshaw, B. *Chem. Sci.* **2025**, *16*, 15478.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Emotion Recognition, Aging and Sex: Exploring the brain circuits involved (

Project supervisor (principal investigator of the laboratory/group)
Name: Arnau Busquets Garcia
eMail: abusquets@researchmar.net
Group name: Cell-type mechanisms in normal and pathological behavior
Institution: Hospital del Mar Research Institute
Webpage of the group:
https://www.imim.cat/programesrecerca/neurociencies/en_mecanismes_cellulars.html

Main grant associated with this project:
Principal investigator: Arnau Busquets Garcia
Agency: Agencia Estatal de Investigación
Reference/ years: PID2024-155295OB-I00 (2025-2028)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The ability to recognize and understand emotions from our conspecifics is critical for social interaction and communication across species. In humans, deficits in emotional recognition are often observed in different neurodevelopmental and/or neurodegenerative diseases such as Alzheimer's disease (AD), Down Syndrome (DS) or some autistic-like disorders. Investigating the underlying brain mechanisms that governs this social ability can provide insights into both normal emotional processing and the alterations seen in age-related diseases such as AD. This project from the lab aims to (i) investigate the brain mechanisms underlying emotional recognition in adult mice identifying potential sex differences; (ii) compare emotional recognition capabilities and its associated brain mechanisms in adult, aged, and a mouse model of AD and (ii) use pharmacological and chemogenetic approaches to overcome deficits on emotional recognition in aged and AD mice. The master student recruited for this project will be involved (i) in the histopathological characterization of the brain circuits underlying social preference and/or recognition through techniques ranging from brain slicing to microscopy quantification and; (ii) in the behavioral quantification of social behavioral tasks linked to emotion recognition.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Studying molecular mechanisms underlying drug synergies in Acute Myeloid Leukaemia

Project supervisor (principal investigator of the laboratory/group)
Name: Marcus Buschbeck
eMail: mbuschbeck@carrerasresearch.org
Group name: Chromatin, metabolism and cell fate
Institution: Josep Carreras Leukaemia Research Institute (IJC)
Webpage of the group: https://buschbecklab.org/
Local supervision by Paula Roquero

Main grant associated with this project:
Principal investigator: Marcus Buschbeck
Agency: European Commission + AGAUR
Reference/ years: EPPERMED2025-134 / 2026-2029

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):
Acute myeloid leukemia (AML) is among the most devastating cancers worldwide with overall 5-year survival rates of less than 30% (Sperling et al., Nat. Rev. Cancer 2017). Non-transplantable AML patients are treated with the chemotherapeutic agent cytarabine (Ara-C). Although use of Ara-C is an effective treatment regime for some patients; unfortunately, many develop resistances, attributing to poor prognoses (Pollyea et al., Haematol. 2011). The most promising solution to avoid and overcome resistances is the combination of multiple drugs attacking the disease from different angles. Our laboratory works on the identification of urgently needed novel combinatorial drug targets for improving Ara-C-based therapies.
We have experience in applying genetic loss-of-function screens to identify targets for add-on drugs. For instance, senior post-doc Dr. Diesch previously identified CBP as a major sensitizer of Azacitidine (Diesch et al. Nature Communications, 2021). In the current project, led by PhD student Paula Roquero and co-supervised by Dr. Diesch and Dr. Marcus Buschbeck, we have performed a CRISPR-knockout screening on AML cell lines to identify genes whose inhibition increases sensitivity to Ara-C. In our unpublished results, we have identified and validated two hits derived from the screen. More specifically, commercially available drugs inhibiting these hits show synergistic interactions with Ara-C. We were able to validate these results through different in vitro experiments and in a broad panel of AML cell lines.
Currently, we are working on further validating these promising results in primary samples from AML patients, as well as in patient-derived xenograft (PDX) in vivo mouse models. In parallel, we are studying the underlying molecular mechanisms and signalling pathways involved in these synergistic interactions.
This project potentially includes a variety of techniques and analysis, the specific interests of the student will also be taken into consideration.
Molecular and cell biology
• Cell culture: In vitro drug assays (Viability & apoptosis assays, competitive growth assays, colony-forming unit assays, etc.)
• Generation of complex cell lines (Knockdown of genes of interest)
• Flow cytometry
• qRT-PCR
• Western blotting
Genomics analysis
• RNA sequencing
In vivo experiments
• Drug testing in PDX-derived mice

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title:

Project supervisor (principal investigator of the laboratory/group)
Name: Felix Campelo (PI) & Eugènia Almacellas (Postdoctoral researcher)
eMail: felix.campelo@upf.edu
Group name: MAPCell (Molecular and Physical Principles of Cell Organization)
Institution: MELIS-UPF
Webpage of the group: under construction (temporary: https://felixcampelo.wixsite.com/home)

Main grant associated with this project:
Principal investigator: Felix Campelo
Agency: PGC 2022 - AEI
Reference/ years: PID2022-138282NB-I00 (2022-2026)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The secretory pathway constitutes the main biosynthetic route for transmembrane proteins and soluble secreted factors, thereby governing the processing and export of more than 30% of the human proteome. Although the molecular determinants of protein secretion are well characterized, key questions remain unresolved. For instance, why does the trans-Golgi network (TGN) employ multiple export routes to deliver cargo from the Golgi to the plasma membrane? One possibility is that this diversity enables context-dependent regulation tailored to specific cellular needs. Essential cellular processes—from inflammation to tissue regeneration—rely heavily on the secretory pathway. Yet, most mechanistic insights have been derived from 2D cell culture systems, despite the fact that cells in living tissues reside within 3D microenvironments, where they polarize and are subjected to mechanical forces. Recent work from our group has shown that the Golgi apparatus can sense and adapt to mechanical cues. By exposing adherent cells to substrates of varying stiffness, studying cell spreading on distinct extracellular coatings, or applying equibiaxial strain, we demonstrated that the Golgi mechanoresponses involve tubulin acetylation and an increase in Golgi membrane tension, correlating with enhanced formation of secretory carriers. Building on this framework, we now investigate how extracellular matrix (ECM) stiffness and viscoelasticity influence secretion in physiologically relevant 3D contexts, using polarized cells cultured in complex ECM environments and patient-derived colorectal cancer organoids. We hypothesize that TGN export routes are differentially regulated in response to extracellular mechanical forces, thereby fine-tuning the cellular secretome. Understanding the crosstalk between Golgi mechanoadaptation and cellular behaviour may open new lines of research with important implications for human biology.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: From Nanoscopy to Tissue Regeneration – Investigating Cell Fate Across Scales

Project supervisor (principal investigator of the laboratory/group)
Name: Maria Pia Cosma
eMail: pia.cosma@crg.es
Group name: Reprogramming & Regeneration
Institution: CRG
Webpage of the group: https://piacosmalab.com

Main grant associated with this project:
Principal investigator: La Caixa Health
Agency: La Caixa
Reference/ years: 2025-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The main interests of the group are to dissect the mechanisms and factors that control somatic cell reprogramming and tissue regeneration in mammals. Computational approaches are employed to identify the key regulators and mechanisms underlying retinal regeneration in mammals and to translate these fundamental discoveries into applications such as cell therapies for retinal degeneration. An additional focus of the group is the study of chromatin organization and 3D genome folding in somatic, stem, and cancer cells, using an integrated and innovative methodology that combines state-of-the-art super-resolution microscopy with genomic approaches. AI-driven and computational methods are applied to analyze super-resolution imaging data in order to elucidate, identify, and reconstruct the biological functions observed in cells, tissues, and organs.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Characterizing the role of the immune system in neurodegenerative diseases

Project supervisor

Name: Oriol Dols-Icardo
eMail: odols@santpau.cat
Group name: Neurobiology of dementia
Institution: Institut de Recerca Sant Pau
Webpage of the group: NA

Main grant associated with this project:

Principal investigator: Oriol Dols-Icardo
Agency: Alzheimer's Association and Instituto de Salud Carlos III
Reference/ years: AARF-22-924456 (2023-2026) and PI24/01087 (2025-2027)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Neuroinflammation is a pathological hallmark of neurodegenerative diseases and is characterized by the expansion of microglia and astrocytes within the central nervous system (CNS) parenchyma, leading to a reactive state. Importantly, accumulating evidence suggests that systemic inflammation and the infiltration of peripheral immune cells into the CNS contribute to neuroinflammation and the pathophysiology of neurodegenerative diseases; however, their role has been underappreciated (1). In this project, we are characterizing blood and cerebrospinal fluid (CSF) immune cells from patients with neurodegenerative diseases (including amyotrophic lateral sclerosis (2), frontotemporal dementia, and Alzheimer's disease) using single-cell RNA sequencing. Our aim is to identify alterations in gene expression, cell-type proportions, and cell-cell communication patterns. The most relevant findings will be further investigated by the student in human post-mortem brain tissue and cell culture models to assess their impact on neurodegeneration and neuroinflammation. Ultimately, our data will provide novel insights into immune-based biomarkers and therapeutic strategies for the treatment of neurodegenerative diseases.

1. Berriat F, Lobsiger CS, Boillée S. The contribution of the peripheral immune system to neurodegeneration. *Nat Neurosci*. 2023;26(6):942-954.

2. Álvarez-Sánchez E, Carbayo Á, Valle-Tamayo N, Muñoz L, Aumatell J, Torres S, Rubio-Guerra S, García-Castro J, Selma-González J, Alcolea D, Turon-Sans J, Lleó A, Illán-Gala I, Fortea J, Rojas-García R, Dols-Icardo O. Single-cell RNA sequencing highlights the role of distinct natural killer subsets in sporadic amyotrophic lateral sclerosis. *J Neuroinflammation*. 2025;22(1):15.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title:
Structural Biochemistry and Flagellar Engineering for Biomedical Innovation.

Project supervisor (principal investigator of the laboratory/group)
Name: Ulrich Eckhard.
eMail: ulrich.eckhard@ibmb.csic.es
Group name: ynthetic Structural Biology Group.
Institution: Molecular Biology Institute of Barcelona (IBMB-CSIC).
Webpage of the group: https://www.ibmb.csic.es/en/department-of-structural-and-molecular-biology/synthetic-structural-biology/

Main grant associated with this project:
Principal investigator: Ulrich Eckhard.
Agency: Ministerio de Ciencia e Innovación.
Reference/ years: RYC2020-029773-I (09/2022-02/2028), CNS2024-154537 (07/2025-06/2027), PID2021-128682OA (09/2022-08/2025), PID2024-159901OB-I00 (09/2025-08/2028)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

We are an international research team at IBMB-CSIC seeking motivated Master's students for projects at the intersection of structural biochemistry, synthetic microbiology, and computational protein design. Our work focuses on two main research lines:

- **Structural Biochemistry.** Explore proteolytic enzymes, inhibitors, and de novo protein binders. We use biochemistry, biophysics, and structural biology (Crystallography and Cryo-EM) to uncover molecular mechanisms and design novel applications.
- **Functionalized Flagella.** Develop the biotechnological and biomedical potential of bacterial flagella. You will engineer systems for pathogen targeting and bioremediation using Cryo-EM, protein engineering, and structure-driven synthetic microbiology.

Techniques & Mentorship. Both lines integrate molecular cloning, protein expression/purification, motility assays, imaging, and structural modeling. We provide comprehensive training and mentorship in a collaborative environment, dedicated to advancing your scientific career.

About the Lab. Located at the Barcelona Science Park (PCB) within the IBMB-CSIC, our lab offers state-of-the-art facilities and a collaborative environment. Our international, English-speaking team has a strong track record of mentoring students for successful careers in academia and industry.

Requirements. We seek candidates with a strong background in molecular biology, biochemistry, or structural biology, fluent English, and excellent communication and problem-solving skills.

To Apply. Please send your CV, academic records, and a brief motivation statement to Ulrich Eckhard (ulrich.eckhard@ibmb.csic.es).

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: N-glycosylation modulation and selective inhibition of $Ca_V2.1$ in pathological *CACNA1A* mutations using patient iPSC-derived neurons: toward targeted and personalized therapies

Project supervisor (principal investigator of the laboratory/group)
Name: José Manuel Fernández Fernández
eMail: jmanuel.fernandez@upf.edu
Group name: Laboratory of Molecular Physiology
Institution: Department of Medicine and Life Sciences, University Pompeu Fabra
Webpage of the group: http://www.upf.edu/fisio/

Main grant associated with this project:
Principal investigator: José Manuel Fernández Fernández
Agency: National Research Agency, Ministerio de Ciencia e Investigación
Reference/ years:

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Gain-of-function (GOF) mutations in *CACNA1A*, encoding the alpha1A subunit of the $Ca_V2.1$ calcium channel, cause disorders such as familial hemiplegic migraine (FHM1), congenital ataxia, and developmental and epileptic encephalopathy (DEE42), yet targeted therapies remain scarce. Preliminary work identified selective $Ca_V2.1$ inhibitors: some preferentially suppress Ca^{2+} currents in HM-mutant channels versus wild type, and also normalized hyperactive neuronal networks in a murine HM model. In addition, boosting glycosylation by MPI inhibition plus mannose supplementation can partially reverse GOF for some mutations but not others, indicating mutation- and domain-dependent efficacy.

The project will combine whole-cell patch clamp, calcium imaging, and glycosylation analysis across three complementary systems: HEK293 cells, primary cortical neurons from FHM1 knock-in mice (R192Q), and patient iPSC-derived neurons. In HEK293 cells, three pore-domain epilepsy-linked variants of unknown function will be characterized for the first time (F363S, F1506S, L1803R), along with two voltage-sensor mutations (R192Q, R583Q). Patient iPSC neurons will carry five pathogenic variants affecting distinct channel domains (S218L, A713T, V1393M, R1349Q, R1667P) and will be differentiated into excitatory glutamatergic neurons, consistent with GOF being prominent in excitatory neurons in animal models.

The $Ca_V2.1$ inhibitors will be benchmarked against reference blockers (ω-agatoxin IVA and BHQ). Specific aims are: (1) the functional profiling of F363S/F1506S/L1803R; (2) to determine pharmacological potency (IC_{50}) of the $Ca_V2.1$ inhibitors against 10 pathogenic variants in heterologous and neuronal systems; (3) to test how N-glycosylation modulation alters GOF across mutations; and (4) to build an integrated database linking channel structure, mutation, drug efficacy, and response to glycosylation modulation. Overall, the work addresses an unmet medical need by delivering translational pharmacological tools and a foundation for personalized, genotype-guided therapies in *CACNA1A*-related channelopathies.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title:
From molecular structures to therapy: linking Mycoplasmas infections to lipids metabolism and uptake. Interactions of *Mycoplasma pneumoniae* with atherosclerotic plaques and fatty liver.

Project supervisor (principal investigator of the laboratory/group)
Name: Prof. Ignacio Fita Rodríguez ***eMail:*** ifrcri@ibmb.csic.es
Group name: Mycoplasma Structural Pathobiology ***Institution:*** IBMB (CSIC)
Webpage of the group: https://ibmb.csic.es/en/department-of-structural-and-molecular-biology/mycoplasma-structural-pathobiology/

Main grant associated with this project:
Principal investigator: Prof. Ignacio Fita Rodríguez
Agency: Agencia estatal de investigación (Ministerio de Ciencia, Innovación y Universidades)
Reference/ years: PID2024-159663OB-C22/ Jan2026-Dec2028

Brief summary of the project:
Our group studies host–pathogen interactions with a focus on lipid acquisition by Mycoplasmas. These microorganisms, which include a large diversity of important human and animal pathogens, lack the capacity of synthesizing lipids, in particular cholesterol, that are essential for their viability. In the last few years, using an integrated functional and structural (mainly Electron cryo-Microscopy and X-rays macromolecular crystallography) approach, our group has characterized, in the human pathogen *Mycoplasma pneumoniae,* the first Mycoplasma protein (P116) capable of scavenging lipids from the infected hosts. P116, essential for *M. pneumoniae* cells survival and colonization[1,2], is a promising target for therapeutic and immunological intervention. The project is now exploring the interaction of *M. pneumoniae* with lipid-rich pathological tissues, including atherosclerotic plaques, the fatty liver, and the lung, the primary infection site. By combining structural biology with disease-relevant cellular models, this line of research aims to define how P116 interactions influence tissue targeting, host inflammatory and metabolic responses, together with the implications for therapeutic interventions. Importantly, research is now been extended to identify and functionally characterize P116-related systems in (all) other Mycoplasma species.

References:
1. Sprankel, L., Vizarraga, D., Martín, J. *et al.* Essential protein P116 extracts cholesterol and other indispensable lipids for *Mycoplasmas*. ***Nature Struct. Mol. Biol.*** **30**, 321–329 (2023). https://doi.org/10.1038/s41594-023-00922-y

2. Vizarraga, D., Marcos, M., Rotllan, N. *et al.* Sources of essential lipids for *Mycoplasma pneumoniae* via P116 to target liver and atherosclerotic lesions. ***Nature Commun.*** **16**, 11159 (2025). https://doi.org/10.1038/s41467-025-66129-5

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Rejuvenating aged somatic stem cells and their niche

Project supervisor (principal investigator of the laboratory/group)
Name: M. Carolina Florian
eMail: mflorian@idibell.cat
Group name: Stem Cell Aging
Institution: IDIBELL, ICREA
Webpage of the group: IDIBELL and P-CMRC and ICREA and Linkedin

Main grant associated with this project:
Principal investigator: M. Carolina Florian
Agency: Spanish Ministry of Science, ERC Consolidator Grant (101002453) European Commission
Reference/ years: 2021-2027

Brief summary of the project or current research lines of the group:
Our research aims at further grow our understanding of epigenetics and microenvironment changes that drive stem cell aging. To pursue our research goals, we combine single-cell profiling (single cell RNAseq and ATACseq; single cell RNA/DNA FISH, single cell 3D immunofluorescence, single cell transplants) with molecular biology, flow cytometry and FACS sorting, advanced optical/confocal microscopy and analysis, whole-mount histology, *in vivo* mouse models, *in silico* computational modelling and deep learning strategies. Using these approaches and bridging knowledge from different fields (stem cell biology, aging, haematology and epigenetics, mechanobiology, deep learning and computational science), we have provided several key contributions to the field (most recent):

- Mejía-Ramírez, E., Picazo, P. I., Walter, B., Montserrat-Vazquez, S., Affuso, F., Wieser, S., Pezzano, F., Reymond, L., Castillo-Robles, J., Matteini, F., Mularoni, L., Maciá, D., Raya, Á., Ruprecht, V., Zheng, Y., Petrone, P., and **Florian, M. C.** (2025) Targeting RhoA nuclear mechanoactivity rejuvenates aged hematopoietic stem cells. ***Nat. Aging*** 1–20
  - News&Views by Wang C. and Mohrin M. in *Nature Aging*. "Squishing, squeezing and stretching age hematopoietic stem cells"
- Matteini, F., Thambyrajah, R., Montserrat-Vazquez, S., Jung, S., Ferrer-Perez, A., Herrero Molinero, P., El Jaramany, D., Lozano-Bartolomé, J., Mejia-Ramirez, E., Gonzalez Miranda, J., Del Sol, A., Bigas, A., and **Florian, M. C.** (2025) A Notch trans-activation to cis-inhibition switch underlies hematopoietic stem cell aging. ***Blood*** **147**, 164–179
  - Commented in *Blood* by Nadia Carlesso "Jagged2-Notch axis: keeping stem cells in asymmetric balance" (Volume 147, Number 2, January 2026)
- Montserrat-Vazquez, S., Ali, N. J., Matteini, F., Lozano, J., Zhaowei, T., Mejia-Ramirez, E., Marka, G., Vollmer, A., Soller, K., Sacma, M., Sakk, V., Mularoni, L., Mallm, J. P., Plass, M., Zheng, Y., Geiger, H., and **Florian, M. C.** (2022) Transplanting rejuvenated blood stem cells extends lifespan of aged immunocompromised mice. ***Npj Regen. Med.*** **7**, 1–17
  - News Feature by Abbott A. in *Nature*. "How the immune system holds the key to ageing" (Volume 629, May 2024)

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Enzyme filamentation as a molecular driver of drug persistence

Project supervisor (principal investigator of the laboratory/group)
Name: Hector Garcia Seisdedos
eMail: hector.garcia-seisdedos@ibmb.csic.es
Group name: Structural Systems Biology
Institution: IBMB-CSIC
Webpage of the group: https://www.garciaseisdedoslab.org/

Main grant associated with this project:
Principal investigator: Hector Garcia Seisdedos
Agency: **Ministerio de Innovacion, Ciencia y Universidades**
Reference/ years: **PID2024-163069NB-I00 / 2025-2028**

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Antimicrobial resistances have been identified by the EU as one of three major health threats. One route to such resistance is drug persistence. Drug persisters are subpopulations of microorganisms/cancer cells that enter dormancy despite nutrient availability, enhancing their survival during drug treatments. Persistence can precede resistance, whereby persisters acquire mutations that enable all progeny to survive the treatment. Hence, studying persistence is important for basic science, to understand cellular adaptation to sudden challenges, and applied research, to combat drug persisters, and it is in line with the EU's objectives. Persistence shares similarities with starvation, as both are associated with a transient metabolic slowdown. In starvation, global cytoplasmic rearrangements take place, including the formation of enzyme filaments. Some enzyme's filamentation mediates dormancy in yeast, and few cells in growing populations exhibit enzyme filaments. Can enzyme filamentation serve as a mechanism of persister formation in yeast, and is this mechanism conserved?

This project aims to: 1) profile the transcriptome of *S. cerevisiae* drug persisters, establishing this organism as a model for studying persistence and identifying persistence markers; 2) elucidate the relationship between enzyme filamentation and persistence; and 3) assess the conservation of this relationship from yeast to human cancer cells.

In summary, this project will investigate an uncharted, potentially conserved mechanism underlying cellular drug persistence. It will advance our understanding of cellular adaptation to sudden environmental changes and potentially contribute to the development of strategies to combat persisters and, thereby, the emergence of drug resistance.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Rebuilding beta cells: From insights into beta cell mass development to direct reprogramming strategies for type 1 diabetes therapy

Project supervisor (principal investigator of the laboratory/group)
Name: ROSA GASA
eMail: RGASA@recerca.clinic.cat

Group name: Translational Research in Diabetes, Lipids and Obesity
Institution: IDIBAPS
Webpage of the group: www.clinicbarcelona.org/ca/idibaps/arees-i-programes/fetge-sistema-digestiu-i-metabolisme/recerca-translacional-en-diabetis-lipids-i-obesitat

Main grant associated with this project:
Principal investigator: ROSA GASA
Agency: Ministerio de Ciencia, Innovación y Universidades
Reference/ years: PID2022-139450OB-I00, 2023-2026

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

A deficit in functional pancreatic beta cells is a defining feature of diabetes. Our group in interested in regenerative medicine strategies aimed at replacing or restoring lost beta cells.

1- One major line of research centers on the direct reprogramming of human skin fibroblasts into insulin-producing cells using beta cell developmental transcription factors. This approach aims to generate transplantable, patient-specific beta-like cells without passing through a pluripotent state.

2-In parallel, we are developing strategies to improve the success of cell transplantation therapies, with a key focus on enhancing graft vascularization to support cell survival and function.

3- We have long focused on uncovering the molecular mechanisms that regulate beta cell mass, and over the years this has remained a central objective of our research. While earlier work focused on embryonic beta cell development, our current efforts emphasize postnatal regulation, with the aim of uncovering intrinsic and extrinsic factors that can inform strategies for beta cell regeneration and the development of novel beta cell replacement therapies for diabetes.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Bioactive lipids in endocytosis

Project supervisor
Name: Maria Isabel Geli
eMail: mgfbmc@ibmb.csic.es
Group name: Bioactive lipids in the endocytic pathway
Institution: Institute for Molecular Biology of Barcelona (IBMB)
Webpage of the group: https://ibmb.csic.es/en/department-of-cells-and-tissues/the-endocytic-pathway-and-the-actin-cytoskeleton/

Main grant associated with this project:
Principal investigator: Maria Isabel Geli
Agency: AEI
Reference/ years: PID2023-150264NB-I00 (December 1st 2024 to November 30th 2027)

Brief summary of the project or current research lines of the group
A high membrane-lipid diversity is universal in eukaryotes, with more than 1000 species described in humans. Lipid diversity is seen from the scale of a membrane leaflet to that of a whole organism, suggesting that lipids fulfil many, yet-to-be-discovered, essential functions. Consistently, alterations of membrane lipid homeostasis are linked to various pathologies and their lipidome can serve as marker for disease progression. Further, mutations in enzymes involved in lipid synthesis, consumption or transport, are linked to many genetic disease, which mostly develop as neuro-pathologies (Haramaya & Riezman 2018 Nat Rev Mol Cell Biol). Interdisciplinary approaches have begun to reveal novel lipid functions and the intersection of the lipid metabolic networks with other cellular machineries. In this context, our group has unveiled that particular species of sterols and sphingolipids play an important role in endocytic uptake and that sterol and sphingolipid biosynthetic and transport systems accumulate in specialized endoplasmic reticulum subdomains called ERSES, which physically and functionally interact with the endocytic invaginations (Encinar et al 2017 Dev Cell; Encinar et al 2021 J Cell Biol).
Using a multidisciplinary approach that combines lipid-click chemistry, biophysics, live-cell fluorescence microscopy and Time Resolved Electron Microscopy (TREM), we study the functional architecture of the sterol and ceramide metabolic networks, the mechanisms whereby these lipids are directly transferred from the endoplasmic reticulum (ER) to endocytic sites in a non-vesicular manner, and the physicochemical properties that promote membrane deformation. The project will give the opportunity to the student of digging into the cell biology of lipids, an emerging field with great biomedical implications.

Harayama, T. and H. Riezman, Understanding the diversity of membrane lipid composition. Nat Rev Mol Cell Biol, 2018. ***19****(5): p. 281-296.*
Encinar del Dedo J, Fernández-Golbano I-M, Pastor, L., Meler P, Ferrer C, Rebollo E, Geli MI. Coupling of the sterol synthesis and transport machineries at ER-Endocytic Contact Sites. (2021) ***J. Cell Biol.*** *220(10):e202010016.*
Encinar del Dedo J, Idrissi F-Z, Fernandez-Golbano I M, Garcia P, Rebollo E, Krzyzanowski M K, Grötsch H, Zimmermann T, Geli MI. ORP-mediated ER contact with endocytic sites initiates actin polymerization. (2017) ***Dev. Cell.*** *43:588-602.*

Call for project proposals,

master in Biomedical Research practicum, 2027, UPF

Project Title: ***Biochemistry and molecular Biology of proteins of biomedical interest***.

Project supervisor (besides the name, title and position, please include the relevant contact information: e-mail, phone postal address, and webpage).

F. Xavier Gomis-Rüth
Proteolysis Laboratory
Department of Structural Biology
Barcelona Science Parc, Helix Building
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08028 Barcelona
Tel. 934020186 / Fax. 934034979 / e-mail. xgrcri@ibmb.csic.es /
https://www.ibmb.csic.es/proteolysis

Main grant associated with this project: PID22-137827OB-00I
Principal investigator: F. Xavier Gomis-Rüth
Agency: State Research Agency (AEI), Ministry of Science and Innovation
Reference/ years: 2023-2026

Summary of project summary or current research lines (less than 300 words).

The research group is centered on the study of proteolytic enzymes of biotechnological or biomedical interest, their protein inhibitors and regulation. Target molecules include proteins of mammals, protozoans and prokaryotes, as well as their interacting partners. The student would participate in the cloning, overexpression and purification of such protein targets under the supervision of experienced members of the lab. In addition–or alternatively–, she/he could participate in the biochemical, biophysical, functional, and structural characterization. The candidate should have strong marks and a very hard-working capacity, dedication and lab skills. In principle, this work could be continued within the frame of a Ph.D. thesis.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Role of Mitochondrial metabolism and H_2O_2 fluxes in aging

Project supervisor:

Elena Hidalgo
elena.hidalgo@upf.edu
Oxidative Stress and Cell Cycle Group
Universitat Pompeu Fabra
www.upf.edu/osccg

Main grant associated with this project:

Principal investigator: Elena Hidalgo
Agency: MICINN (Spain)
Reference/ years: 2025-2028

Brief summary of the project or current research lines of the group:

Our group is interested in studying the components and molecular mechanisms controlling cellular fitness, in particular during aging. Thus, the master project proposal will be chosen among, but not exclusively, the following:

(i) Study cellular processes linked to healthy aging; specifically, how mitochondrial homeostasis and morphology control respiratory efficiency
(ii) Use of genetically encoded H_2O_2 biosensors to measure peroxides emanating from the mitochondria and controlling longevity
(iii) activation of general and selective autophagy in response to nutrient deprivation

We use the fission yeast ***Schizosaccharomyces pombe*** as a model system. To obtain more information about the laboratory and about our research interests, please consult our group's web page (www.upf.edu/osccg). Some recent publications include:

Barrios et al. 2025. Genome Biol. 26:419.
Vega et al. 2023. Nucleic Acids Res. 51:12161-12173
Salat-Canela et al. 2023. TiCB 33:124.
Salat-Canela et al. 2021. Cell Rep. 37:109951.
Corral-Ramos et al. 2021. Autophagy 23:1-16.
Boronat et al. 2020. iScience 23:101725
Cabrera et al. 2020. Cell Rep. 30:2430-2443
Carmona et al. 2019. Nat. Commun. 10:4526.
García-Santamarina et al. 2014. Nature Protocols 9:1131.
Calvo, I.A. et al. 2013. Cell Reports 5:1413.
Zuin, A. et al. 2010. EMBO J. 29:98

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Imaging Cell dynamics in live embryos

Project supervisor (principal investigator of the laboratory/group)
Name: Esteban Hoijman
eMail: ehkbmc@ibmb.csic.es
Group name: Embryonic cell bioimaging
Institution: Molecular Biology Institute of Barcelona-CSIC
Webpage of the group: https://www.embryobioimaging.com/

Main grant associated with this project:
Principal investigator: Esteban Hoijman
Agency: MICINN
Reference/ years: PID2023-151237NB-I00/2024-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The dynamic nature of cells is key for establishing tissue function. Because many cellular activities are shaped by interactions with their mechanical, chemical, or biological environment, fully understanding cell behavior and its biomedical implications requires studying cells within their natural context. We study dynamic processes across biological scales, from molecules to tissues, using quantitative live imaging and transcriptomics in zebrafish, mouse, and human embryos. Early embryos are among the most plastic biological systems, capable of adapting to major perturbations while still developing successfully. Our lab is dedicated to uncovering the mechanisms that drive this remarkable robustness, with a particular focus on protective processes that preserve the environment in which embryonic cells develop. One such mechanism is phagocytosis, which we have recently shown is carried out by epithelial cells in early embryos. This process contributes to the correction of internal developmental errors (Hoijman et al., Nature 2021;
Santavanond et al, Science Advances 2025) and the elimination of pathogens (Roncero-Carol et al., Cell Host & Microbe 2025), marking the onset of innate immune functions.
We pursue two central research goals: 1) to investigate the interplay between developmental and immune programs during early embryogenesis, and 2) to elucidate how epithelial tissues carry out phagocytic functions, which are also active in adult organs. We hope our work contributes to uncovering the fundamental cellular behaviors that drive development, maintain homeostasis, and contribute to disease.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: **Function and specificity of human histone H1 variants in the organization and control of the genome.**

Project supervisor (principal investigator of the laboratory)
Name: Albert Jordan
Mail: ajvbmc@ibmb.csic.es
Group name: Chromatin regulation of human and viral gene expression
Institution: Institut de Biologia Molecular Barcelona IBMB-CSIC, Dept. Structural and Molecular Biology

Webpage of the group: https://www.ibmb.csic.es/albert-jordan-lab

Main grant associated with this project:
Principal investigator: Albert Jordan
Agency: Ministerio de Ciencia e Innovación – Plan Nacional BFU
Reference/ years: PID2023-146239OB-I00 (2024-27)

Brief summary of the project or current research lines of the group

Histone H1 participates in the stabilization of DNA around the core histone octamer that constitutes the nucleosome, in the spacing between adjacent nucleosomes, in nucleosome mobility, and in further levels of chromatin compaction. As a consequence, H1 is seen as a chromatin structural protein that might be involved in DNA compaction, heterochromatin formation and stabilization, and in the regulation of nuclear processes such as transcription, replication, DNA repair, etc. Nonetheless, in mammalians, histone H1 is not a single protein but an evolutionary diverse gene family that comprises up to seven members in somatic cells. Although considered for long time H1 variants to be redundant, we and others have described structural and functional differences between variants that include their distribution within the genome and nuclei, and diverse consequences upon depletion of particular H1 variants.

We have recently described that H1 variants show distinct abundances among different repetitive and transposable elements (TE), with an enrichment of H1 variants that are located within high GC regions (H1X and H1.4) at TE that have incorporated recently into the human genome along its evolution. These variants may be involved in the repression of these TE. In parallel, we have found that depletion of these variants causes transcription from cryptic promoters. On the other hand, variants enriched within low GC DNA (H1.2, H1.3, H1.5 and H1.0) are enriched at TE incorporated early in evolution, are preferentially located at peripheral heterochromatin and may have a role in maintaining heterochromatin identity and tethering to nuclear lamina. Our hypothesis is that histone H1 participates in the repression of such elements by participating in heterochromatin maintenance, and does this in a variant-specific manner. Besides, depletion of multiple H1 variants induces and interferon response in some cell types that could be used to induce immunoresponse against tumors.

We propose to study the involvement of histone H1 variants:

1. In the repression of cryptic transcription.

2. In the control of transposable elements.

3. In maintaining heterochromatin identity and the organization of nuclear compartments.

4. In preventing the viral mimicry phenomenon that may induce an interferon response in tumor cells, and its consequences in cancer progression and sensitivity to immunotherapy.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title:

Project supervisor (principal investigator of the laboratory/group)
Name: Marta Llimargas Casanova
eMail: mlcbmc@ibmb.csic.es
Group name: Mechanisms of morphogenesis and organogenesis
Institution: Institut de Biologia Molecular de Barcelona, IBMB-CSIC
Webpage of the group: https://www.ibmb.csic.es/en/department-of-cells-and-tissues/mechanisms-of-morphogenesis-and-organogenesis/

Main grant associated with this project:
Principal investigator: Marta Llimargas Casanova
Agency: Ministerio de Ciencia e Innovación
Reference/ years: PID2024-157683NB-I00 -- 2025-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Intrinsic and extrinsic mechanisms regulating the morphogenesis and function of tubular epithelia

A fundamental question in biology is to understand how organs form during development, i.e., how individual cells organise and coordinate to generate a functional structure. Intrinsic genetic programs as well as interactions with the surrounding environment are known to instruct organogenesis.
We investigate organ formation using mainly the tracheal (respiratory) system of the fruitfly Drosophila melanogaster, as well as other organs, as amenable and tractable models.
Our projects focus around three main questions:
1) Interactions and requirements of the extracellular matrices (apical and basal ECMs) with the underlying epithelia during morphogenesis. This approach should provide new insights into how organs form in the context of a whole organism and may inform about tissue engineering oriented studies.
2) Remodelling and contribution of cell adhesion and cell polarity to tracheal formation and epithelial morphogenesis in general. Cell adhesion and polarity are key features of epithelial tissues and this approach may help to understand tissue remodelling and homeostasis.
3) Unbiased analysis of tracheal morphogenesis. We identified in previous screens in the lab different factors with putative roles in tracheal morphogenesis. The comprehensive analysis of these factors is helping us to understand how to generate mature and functional organs.

Our work lies at the interface of developmental biology, morphogenesis and cell biology, and requires advanced imaging techniques, as well as genetic, cell biology, molecular biology and biochemical techniques.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title:
PROTECTING HEMATOPOIETIC STEM CELLS (HSC) FROM INFLAMMATORY STRESS

Project supervisor (principal investigator of the laboratory)
Name: Cristina Lopez-Rodriguez
Mail: cristina.lopez-rodriguez@upf.edu; jose.aramburu@upf.edu
Group name: GENIMMUNE
Institution: Universitat Pompeu Fabra, Department of Medicine and Life Sciences
Webpage of the group: https://www.upf.edu/web/genimmune
https://www.upf.edu/web/cristina-lopez-rodriguez

Main grant associated with this project:
Principal investigator: Cristina Lopez-Rodriguez
Agency: ICREA Acadèmia 2023- 2027 (https://www.upf.edu/recercaupf/-/asset_publisher/RVNxhLpxnc9g/content/four-upf-lecturers-scale-up-their-research-thanks-to-icrea-s-2022-academia-grants/10193)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page) :

We will address a major challenge related to stem cell fitness and aging, supported by the interdisciplinary expertise of our group, cutting-edge methodologies, experimental models of disease in mice, access to state-of-the-art core facilities, expert collaborators, and funding from national and international grants.

Hematopoietic reconstitution after stress, trauma or infection requires hematopoietic stem cells (HSCs) mobilization from quiescence, a process that makes them highly vulnerable to inflammatory signals that can exhaust the HSC pool. We have identified a mechanism that limits systemic production of type I interferon (IFN-I) by inflammatory cells in vivo, thus protecting HSCs from excess exogenous IFN-I while allowing for IFN-I protection against infection (2,3).

In this project, we will study what inflammatory signals target directly stem cells under chronic inflammatory stress signals that increase during aging, and also analyse how stem cells deploy protective mechanisms that safeguard their viability and progenitor potential in response to chronic inflammation. Knowledge in these mechanisms will guide our blocking of HSC aging in mouse models by using immunotherapy, pharmacological antagonists and CRISPR-directed modulation. This project has interest in clinical haematology and could also advance knowledge on stem cell function in other systems.

Selected recent publications of the group:

1) Zadra, Abad, Krasko, Cerdán Porqueras et el., A novel mismatch repair deficient lung adenocarcinoma model for immunotherapy research. 2025 Cancer Letters. DOI: 10.1016/j.canlet.2025.217882

2) Traveset, Cerdán Porqueras et al., NFAT5 counters long-term IFN-1 responses in hematopoietic stem cells to preserve reconstitution potential. 2024 Blood Advances. DOI: 10.1182/bloodadvances.2023011306

3) Huerga Encabo et al., The transcription factor NFAT5 limits infection-induced type I interferon responses. 2020 Journal of Experimental Medicine. DOI: 10.1084/jem.20190449

4) Aramburu and López-Rodríguez, Regulation of inflammatory functions of macrophages and T lymphocytes by NFAT5. 2019 Frontiers in Immunology. DOI: 10.3389/fimmu.2019.00535

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Role of B cells in Mucosal Inflammation and Cancer Immune Surveillance: From Systems Immunology to Antibody Discovery and Engineering

Project supervisor (principal investigator of the laboratory/group)

Name: Giuliana Magri; eMail: gmagri@ub.edu
Group name: Mucosal Immunology Lab; Institution: University of Barcelona

Main grant associated with this project:

Principal investigator: Giuliana Magri
Agency: Ministero de Ciencia, Innovacion y Universidades: PID2023-148826OB-I00 2024-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Systems Immunology represents an emerging field of systems biology that aims at understanding the operating principles of an immune response by integrating a large number of variables, using high-throughput molecular profiling technologies. In the last decade, systems immunology approaches have been successfully employed to evaluate immune responses to infection and vaccination. The field of immuno-oncology and chronic inflammation offers also great potential for systems studies because of the complex and poorly understood mechanisms underlying these diseases. A central aspect of the immune response developed during chronic inflammation and tumor immunity is the involvement of the adaptive responses orchestrated by T and B lymphocytes. The importance of T cells has been well established, providing the fundamental basis for effective immunotherapies. In contrast, the contribution of B cells and antibodies in mucosal inflammation (i.e. inflammatory bowel disease) and cancer immune surveillance has been far less well investigated

The current research lines of our group aim at dissect the role of B cells and mucosal antibodies in chronic inflammation using **systems immunology** approaches. Our work provides a unique opportunity to characterize host-microbiota interaction during inflammation and to lay the groundwork for the development of **monoclonal antibodies targeting specific microbial strains.** Such strategies hold promising potential for developing new therapeutic or diagnostic tools.

PUBLICATIONS OF THE PROJECT SUPERVISOR RELATED TO THE TOPIC OF THE RESEARCH:

1. Gutzeit C et Al. Gut IgA functionally interacts with systemic IgG to enhance antipneumococcal vaccine responses. **Science Advances**. **2025** Feb 14;11(7)

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Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Building Human Spinal Cord Organoids to study human-specific developmental features and Neuro_Developmental Disorders

Project supervisor (principal investigator of the laboratory/group)
Name: Elisa Marti
eMail: emgbmc@ibmb.csic.es
Group name: Development of the Nervous System in health and disease
Institution: IBMB_CSIC
Webpage of the group: https://ibmb.csic.es/en/department-of-cells-and-tissues/development-of-spinal-cord-in-health-and-disease/

Main grant associated with this project: PID2022-139609NB-I00
Principal investigator: Elisa Marti
Agency: AEI
Reference/ years: 2023-2026 (under renewal)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The spinal cord arises from neuro-mesodermal progenitor cells that generate the neural tube, a transient embryonic structure essential for central nervous system formation. Failures in this morphogenetic process cause neural tube defects (NTDs), among the most common congenital malformations. Despite strong genetic associations, the cellular and human-specific mechanisms underlying NTDs remain poorly understood.

We aim to decode the cellular logic of posterior spinal cord development by investigating how the planar cell polarity (PCP) signaling pathway shapes secondary neurulation, and how motor neuron (MN) generation is affected under these genetic conditions. We will exploit our human spine organoids ("hSpine-organoids") the first in vitro human model that recapitulates posterior spinal cord morphogenesis, together with rare embryonic material and single-cell technologies, to map the 4D dynamics of human secondary neurulation in health and in spina bifida. We will systematically analyze the consequences of pathogenic PCP variants using a multimodal strategy: high-resolution imaging, morphometric analysis, time-lapse microscopy, and single-cell transcriptomics. These in vitro datasets will be validated against our 3D reconstructions of human embryos and public omics resources. In parallel, we will test the hypothesis that disrupted MN generation is a primary driver of neuromotor dysfunction in spina bifida.

By integrating developmental biology, organoid modelling, and quantitative imaging, we aim to establish the first mechanistic framework for human-specific secondary neurulation and MN development. Beyond key conceptual advances, the project will generate open-access image libraries, disease-relevant stem cell lines, and molecular signatures with diagnostic potential, laying the foundation for future strategies in NTD diagnosis and prevention.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Neurobiological mechanisms involved in the development of cannabis addiction

Project supervisor (principal investigator of the laboratory/group)
Name: Rafael Maldonado and Elena Martín
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Group name: NeuroPharm
Institution: UPF
Webpage of the group: Web: http://www.upf.edu/neurophar/

Main grant associated with this project:
Principal investigator: Elena Martín García
Agency: PNSD
Reference/ years: 3. PNSD-2023I040/2023-2026

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Cannabis is the most widely used illicit drug worldwide, with major health and socio-economic consequences. Ongoing changes in its legal status may further increase consumption and cannabis-related mental disorders. Cannabis use disorder (CUD) remains highly prevalent, yet reliable biomarkers are lacking and current treatments show limited efficacy and high relapse rates. This project aims to advance understanding of the neurobiological mechanisms underlying CUD, identify biomarkers of vulnerability and resilience, and develop novel therapeutic strategies.
Building on our previous work, we focus on mechanisms shared across addictive disorders. We have demonstrated that food and cocaine addiction share transcriptomic signatures in the medial prefrontal cortex (mPFC), a key region regulating inhibitory control over limbic circuits. Increased mPFC activity promotes resilience to addictive behaviors, highlighting this region as a therapeutic target. We have also shown that addictive-like behaviors are associated with specific microRNA (miRNA) alterations and gut microbiota changes that influence brain function. These findings, published in high-impact journals, position the gut–brain axis as a central mechanism in addiction.
Our working hypothesis is that cannabis exposure induces specific gut microbiota and epigenetic alterations that disrupt prefrontal circuits controlling reward and decision-making. We propose that microbiota–brain crosstalk, coupled with miRNA remodeling, contributes to the development and maintenance of CUD. Using advanced behavioral models, multi-omics, epigenetics, and in vivo calcium imaging in mice, combined with human proof-of-concept studies, we will dissect microbiome–host communication across the spectrum of CUD severity.
We will identify signatures of vulnerability and resilience and evaluate therapeutic strategies targeting both the gut microbiota (e.g., prebiotics and probiotics) and prefrontal activity. In patients, we will assess the efficacy of dorsolateral prefrontal cortex stimulation using repetitive transcranial magnetic stimulation (rTMS), based on its functional equivalence to rodent mPFC. Overall, the project aims to deliver mechanistic insight and pave the way for biomarker-guided, microbiota- and circuit-based interventions for CUD and related psychiatric disorders.

References

Cajiao-Manrique MDM, Casadó-Anguera V, García-Blanco A, Maldonado R, Martín-García E. THC exposure during adolescence increases impulsivity-like behavior in adulthood in a WIN 55,212-2 self-administration mouse model. Front Psychiatry. 2023 May 25;14:1148993. doi:10.3389/fpsyt.2023.1148993. PMID: 37304451.

Cajiao-Manrique MDM, Maldonado R, Martín-García E. A male mouse model of WIN 55,212-2 self-administration to study cannabinoid addiction. Front Pharmacol. 2023 Mar 27;14:1143365. doi:10.3389/fphar.2023.1143365. PMID: 37050910.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Investigating the involvement of the Mitochondrial Integrated Stress Response in pro-longevity interventions in vivo

Project supervisor (principal investigator of the laboratory/group)
Name: Guillermo Martínez Corrales
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Group name: Mitochondria, Redox and Metabolix Diseases
Institution: IBMB
Webpage of the group: https://ibmb.csic.es/en/department-of-cells-and-tissues/mitochondria-redox-and-metabolic-diseases/#lab-people

Main grant associated with this project:
Principal investigator: Guillermo Martínez Corrales
Agency: AEI
Reference/ years: PID2023-146293NA-I00, 01/2023 – 12/2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):
My research group investigates how transient, early-life interventions program long-lasting healthspan and longevity, with a particular focus on the mitochondrial integrated stress response (ISR_{mt}) and transcriptional memory mechanisms. Using *Drosophila* genetics with temporal control systems and complementary cell culture models, we have discovered that brief activation of stress-responsive transcription factors during early adulthood establishes persistent transcriptional programs that extend both lifespan and healthspan long after the initial signal disappears. Our current research addresses three interrelated questions: how tissue-specific ISR_{mt} activation specific organs establishes transcriptional memory through chromatin remodelling, whether upstream mitochondrial proteases can trigger this longevity program and be pharmacologically targeted, and whether canonical longevity interventions like dietary restriction and mild mitochondrial dysfunction converge on this same ISR_{mt} pathway. By integrating *in vivo* experiments with multi-omics approaches and pharmacological tools, we aim to identify evolutionarily conserved mechanisms of healthy aging that could ultimately be translated to improve human health span.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Advanced cell therapies for cancer treatment

Project supervisor (principal investigator of the laboratory/group)
Name: Aura Muntasell
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Group name: NK cell immunotherapy/Cellular Immunology
Institution: Hospital del Mar research Institut Barcelona/Universitat Autònoma de Barcelona
Webpage of the group:
https://www.uab.cat/ca/ibb/immunologia-celular
https://www.imim.cat/programesrecerca/cancer/lab_aura_muntasell/index.html

Main grant associated with this project: Advanced cell therapies for cancer treatment
Principal investigator: Aura Muntasell
Agency: Instituto de Salut Carlos III
Reference/ years: PI25/00609 2026-28

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The efficacy of allogeneic NK cell and CAR T cell therapies for solid tumors is limited by inadequate tumor homing and their sensitivity to suppressive factors such as TGF-. We developed TGF- and Activin A resistant NK cells by knocking out SMAD4 using CRISPR/Cas9. SMAD4-KO NK cells show a strong anti-tumor activity in preclinical models of colorectal and breast cancer. This proposal includes 3 aims focused on the advanced characterization and further developing of this technology: 1) Safety: characterization of off-target editing and potential chromosomal aberrations induced by SMAD4-KO technology; 2) Persistence: evaluating multiplex editing on HLA-I, ICAM1/LFA-3 or CIITA to enhance allogeneic SMAD4-KO NK cell persistence by reducing their immunogenicity; 3) SMAD4-KO CAR-T: assessing the impact of knocking out SMAD4 on anti-CD19 and anti-BCMA CAR T cell function in the presence of TGF-beta. Methodology: scRNA- seq, iGUIDESeq and FISH analysis will identify off-targets and chromosomal aberrations (Aim1); multiplex CRISPR/Cas9 RNP nucleofection will be used for gene editing in primary NK cells (Aim 2); Ari001 and Ari002 CAR constructs will be used for studying CAR T cells (Aim 3). The anti-tumoral efficacy and persistence of engineered NK/T cells will be analysed in tumor spheroids; ex vivo tumor explants, as well as humanized mouse models of CRC and HER+ breast cancer already established in the lab (Aim 2) and novel models for ALL and MM (Aim3).

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Study of the role of mechanoreceptors in neurodegenerative diseases

Project supervisor (principal investigator of the laboratory/group)
Name: Francisco J. Muñoz López
eMail: paco.munoz@upf.edu
Group name: Aging Brain and Neurodegeneration
Institution: MELIS-Universitat Pompeu Fabra
Webpage of the group: https://www.upf.edu/web/lmp/aging-and-neurodegeneration

Main grant associated with this project:
Principal investigator: Francisco J. Muñoz
Agency: Spanish Science and Innovation Ministry
Reference/ years: PID2023-149767OB-I00

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):
Alzheimer's disease (AD) is due to the extracellular aggregation of the amyloid ß-peptide (Aß) into oligomers and fibrils, which are synaptotoxic leading finally to cell death. There is not specific treatments that can cure, prevent of retard the disease.
The hypothesis proposes that oligomeric Aß (oAß) directly or indirectly (by oxidative stress) affect to the physiological function of mechanoreceptors that will have deleterious effects in the growth and maintenance of the synaptic spines, and a rise in intracellular calcium.
The objectives is the characterization of the effect of the oAß binding and/or the oxidative stress induced by oAß on TRPM7 and Piezo1 functions in the synaptic spines. The mechanical forces that drives dendrite growth are related to mechanoreception. In particular, spine growth and the maintenance of the functional shape of the spines are under the control of mechanoreceptors that regulates actin cytoskeleton. Therefore, we will study the effect of oAß on these receptors and how it will affect to synaptic plasticity and the existing spines, and we will also address the study of their role in the dysregulation of intracellular calcium.

The biological materials will be cell lines, neuronal primary cultures from mice and hiPSCs. Results will be validated in brain samples from APPswe/PSEN1dE9 transgenic mice and AD patients and no demented individuals.

The methodology includes molecular biology of proteins and mRNA, gene overexpression and silencing, siRNAs, confocal microscopy, spectrofluorometry, calcium image, path-clamp, flow cytometry and in silico studies.

The expected results of our project are the identification of new molecules involved in Aß pathophysiology that would be considered as therapeutic targets for the treatment of AD.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Metabolic stress and cancer: the Integrated Stress Response as therapeutic target for Non-Small Cell Lung Carcinoma

Project supervisor (principal investigator of the laboratory/group)
Name: Cristina Muñoz Pinedo
Email: cmunoz@idibell.cat
Group name: Preclinical and experimental research in thoracic tumours (PRETT)
Institution: IDIBELL
Webpage:https://idibell.cat/recerca/area-de-cancer/programa-de-mecanismes-moleculars-i-terapia-experimental-en-oncologia-oncobell/prett/

Main grant associated with this project:
Principal investigator: Cristina Muñoz Pinedo
Agency: Ministerio de Ciencia e Innovación
Reference / years: PID2022-140457OB-I00 / 2023-2026

Brief summary of the project or current research lines of the group:
Non-Small Cell Lung Carcinoma (NSCLC) is the tumor that causes more deaths in Spain. With the aim to search for novel tools for diagnosis and treatment, we have investigated metabolic stress and the Integrated Stress Response (ISR) as a possible cause for tumor development and progression. This is due in part to maintainance of an inflammatory phenotype. In this project we aim to generate tools to analyze metabolic stress in datasets that can predict response to therapies, including drugs targeting the effectors of the ISR (PERK, GCN2, phospho-eIF2alpha). We will analyze transcription and translation driven by glucose stress and general metabolic stress driven by nutrient exhaustion, and how the stress and the ISR modulate cell death in specific subsets of NSCLC. We will also analyze how specific proteins secreted by starved cells in an ISR dependent manner affect the immune system and cancer development in preclinical models and donated samples. **The final goal is to identify a novel vulnerability of NSCLC that can potentially be targeted with existing drugs**.

We have applied for a new project as a follow up of this one titled “Interplay between metabolic stress, cell death and inflammation in NSCLC treatment and cachexia”. If granted this would start in 2027 until 2029. In this new project we aim to identify and inhibit the molecules that allow lung cancer cells to survive glucose deprivation. On one hand, we will identify the metabolites that cells consume when they do not have glucose, in regular culture medium and in a defined medium that mimics serum composition. On the other hand, we will study survival and transcriptional signatures in other conditions (for instance, hypoxia and acidity) that may occur simultaneously in vivo and that may affect survival of cells in the hypoglycemic environment.
We will also address whether blocking the unfolded protein response (UPR) and especially, the kinase PERK, may work in vivo in lung cancer cells with specific mutations (RAS/KEAP1/ LKB1). In vivo, we would address why PERK protects from necrosis and from apoptosis induced by glucose deprivation and whether PERK regulates the cell death machinery at the level of transcription or translation.
Lastly, we will test the hypothesis that metabolic stress in the tumor causes cancer cachexia. This hypothesis stems from our observations that cytokines secreted in hypoglycemia cachexia drivers. We will understand how the secretion of these cytokines is regulated and whether inhibition of proteins driving their expression reduces or prevents cachexia.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Integration of the transcriptome, metabolome, and microbiome for the identification of novel biomarkers in Myotonic Dystrophy Type 1 (INTEGRA-DM1)

Project supervisor (Principal Investigator GRENBA/Genetics lead)

Name: Gisela Nogales Gadea/ Marc Corral Juan

eMail: gnogales@igtp.cat, mcorral@igtp.cat

Group name: Grup de Recerca Neuromuscular de Badalona (GRENBA)

Institution: IGTP

Webpage of the group: https://www.germanstrias.org/es/research/neurociencias/5/grupo-de-investigacion-en-enfermedades-neuromusculares-de-badalona-grenba

Main grant associated with this project:

Principal investigator: Gisela Nogales Gadea/Marc Corral Juan

Agency: Fundación Ramón Areces

Reference/ years: 2026-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The main objective of the INTEGRA-DM1 project is to identify novel dynamic biomarkers to improve the clinical management of Myotonic Dystrophy Type 1 (DM1). This will be achieved integrating multi-omics data, including transcriptomics, metabolomics, and microbiome profiling.

The master's student will participate in **16S long-read sequencing**, data analysis and **multi-omics integration**, contributing to biomarker discovery and gaining training in sequencing, bioinformatics, and translational research in **neuromuscular disorders**.

INTEGRA-DM1 characterize microbiome changes through 16S rRNA-based metataxonomic analysis, together with fecal metabolomic profiling, enabling a comprehensive assessment of host–microbiome interactions. Clinical context and lifestyle factors influencing disease progression will be incorporated, alongside genomic and proteomic data previously generated within the **DM1-Hub** project.

This integrative, multi-omics framework aims to uncover dynamic biomarkers and mechanistic insights into disease variability and progression.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Characterization of interruption patterns within the *DMPK* repeat expansion and their impact on clinical phenotype (INTERRUPT)

Project supervisor (Principal Investigator of GRENBA/group)
Name: Gisela Nogales Gadea
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Group name: Grup de Recerca Neuromuscular de Badalona (GRENBA)
Institution: IGTP
Webpage of the group: https://www.germanstrias.org/es/research/neurociencias/5/grupo-de-investigacion-en-enfermedades-neuromusculares-de-badalona-grenba

Main grant associated with this project:
Principal investigator: Gisela Nogales Gadea
Agency: ISCIII
Reference/ years: 2026-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The project INTERRUPT seeks to understand the impact of genetic interruptions of the causative gene in Myotonic Dystrophy type 1 (DM1), a rare disease that affects muscles and other tissues. These interruptions may be present in 50% of patients with DM1. The main objectives of the project are:

1) To **characterize the DMPK interruptions** by longread sequencing.
2) To **stratify DM1 patients with interruptions**, focusing on symptomatology, disease progression, and age-related genetic instability.
3) To study the genetic stability of the interruptions in dividing cells.

Long-read sequencing technologies, combined with advanced patient-derived cellular models, will be used to accurately replicate disease conditions. This innovative approach will allow us to determine how sequence interruptions influence cellular phenotypes, molecular and functional mechanisms, and responses to therapeutic interventions.
The master's student will actively participate in long-read sequencing analysis, genotype–phenotype correlation studies, and cellular modeling experiments, gaining hands-on experience in advanced genomic technologies and translational research in neuromuscular disorders.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Single-Nucleus Long-Read RNA Sequencing in Myotonic Dystrophy Type 1.

Project supervisor (Principal Investigator GRENBA/Senior Bioinformatician)

Name: Gisela Nogales Gadea/Daniel Borras Morales

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Group name: Grup de Recerca Neuromuscular de Badalona (GRENBA)

Institution: IGTP

Webpage of the group: https://www.germanstrias.org/es/research/neurociencias/5/grupo-de-investigacion-en-enfermedades-neuromusculares-de-badalona-grenba

Main grant associated with this project:

Principal investigator: Daniel Borras Morales

Agency: JMC Legacy Research Fund of Germans Trias i Pujol University Hospital

Reference/ years: LLegat/ LE2410, 2024-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

This project aims to apply single-nucleus **long-read RNA sequencing (SNLR-seq)** using Oxford Nanopore Technologies to characterize full-length transcripts, alternative splicing events, and coding variants in skeletal muscle biopsies from DM1 patients and healthy controls. By integrating **transcriptomic data** with **genomic** and **clinical information**, we aim to identify cell-type–specific molecular signatures associated with disease progression and variability.

The student will primarily participate in wet-lab activities, including muscle biopsy processing, nuclei isolation, RNA extraction, and preparation of long-read sequencing libraries. The student will also gain introductory experience in data processing and transcriptomic analysis.

This project offers hands-on training in advanced molecular biology, long-read sequencing technologies, and translational research in neuromuscular disorders within a multidisciplinary precision medicine framework.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Studying the early signs of brain aging

Project supervisor (principal investigator of the laboratory/group)
Name: Andrés Ozaita
eMail: andres.ozaita@upf.edu
Group name: Biology of Cognition
Institution: Universitat Pompeu Fabra
Webpage of the group: https://www.upf.edu/web/biocog

Main grant associated with this project:
Principal investigator: Andrés Ozaita
Agency: Ministry of Science and Technology
Reference/ years:

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Preventing cognitive decline and neurodegeneration is a relevant problem in biomedical research. Aging is associated to the development of cognitive impairment, which can be reduced by treatments that target the endogenous cannabinoid system. Such treatments have been found to improve synaptic plasticity and cognitive performance. Studying mouse models for natural ageing we have found an approach to improve cognitive performance even in adult mice. This approach, that has to do with the inhibition of the main cannabinoid receptor in the organism, may also interact with neuroinflammatory and senescence mechanisms.

We will use *in vivo* (mouse models and behavioural analysis) and *in vitro* techniques (immunoblot, qPCR, immunofluorescence, confocal microscopy analysis, among others) to further explore cellular and molecular effects of cannabinoid receptor inhibition in the context of Down syndrome animal models to reveal the mechanisms of cognitive alleviation.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Decoding cellular adaptation: From yeast to humans.

Project supervisor (principal investigator of the laboratory/group)
Name: Francesc Posas
eMail: francesc.posas@irbbarcelona.org; francesc.posas@upf.edu
Group name: Cell Signaling Group
Institution: IRB Barcelona
Webpage of the group: https://www.irbbarcelona.org/en/research/cell-signaling

Main grant associated with this project:
Principal investigator: Francesc Posas
Agency: Ministerio de Ciencia, Innovación y Universidades.
Reference/ years: Mapping novel conserved activities required for cell adaptation to stress (DECOADAPT). PID2024-156607NB-C21.

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Cells are constantly challenged by environmental fluctuations and must rapidly rewire their internal circuitry to meet new demands while maintaining their identity and maximizing fitness. Failure to adapt can lead to decreased cellular function, impaired survival, and ultimately cell death.
Our lab seeks to unravel the molecular mechanisms behind these adaptive processes, focusing on signaling pathways and adaptive responses that shape cell fate decisions. Our multidisciplinary approach combines cutting-edge techniques in proteomics, genomics, transcriptomics, and single-cell analyses to decode the language of cellular adaptation.

Master's students will have the opportunity to engage in innovative research projects:
Discover novel gene functions essential for stress adaptation through genetic screens (CRISPR screens in yeast or mammalian systems)
Biochemically identify novel targets controlled by stress-activated protein kinases and define their impact on cell physiology
Leverage cutting-edge single-cell RNA sequencing (scRNA-seq) to uncover heterogeneity in adaptive responses
Link molecular profiles to phenotypic outcomes to gain insights into diverse cellular strategies for adaptation

Together, we aim to define novel mechanisms controlling cellular adaptation and bridge the gap between molecular signatures and cellular behavior.
Join our stimulating and collaborative scientific environment, where you will work alongside a multidisciplinary team and engage with international collaborators. By understanding how cells mount adaptive responses, we aim to unlock new insights into health and disease.

Master in Biomedical Research UPF, 2027 projects call:

Lab supervisor: Lidia Perea, Post-Doc, under the Sara Borrell ISC-III grant scheme.
Host group supervisors: Oriol Sibila, Rosa Faner
Offer: We are looking for a highly motivated master student to join our group for the following project with potential to develop a PhD after the master. We will work both in cellular and molecular techniques and be trained in translational research at IDIBAPS-UB.

Project title: The TRAIL Study: Trained immunity, immunomodulatory mechanisms and lung infections in bronchiectasis
Project summary: Bronchiectasis is a chronic and progressive lung disease characterised by permanent bronchial dilatation, chronic airway inflammation and lung infections that significantly worsen clinical outcomes. Patients suffer from chronic cough, expectoration, dyspnoea and recurrent lung infections that significantly increase morbidity and mortality. Unfortunately, they are not yet preventable because its pathophysiology is still poorly understood. Research from our group and others shows a markedly immune dysregulation both at the systemic and pulmonary level, including altered **innate immune responses**, impaired **pathogen clearance**, and an imbalanced inflammatory environment that may perpetuate **tissue damage**. We propose here the study of the novel and revolutionary concept of the **trained immunity**: a form of innate immune memory involving epigenetic, metabolic and proteomic changes in immune cells to offer **long-term protection** against external agents. This will help to decipher novel immunomodulatory pathways related to lung damage and disease progression in bronchiectasis. We aim to characterise the presence or absence of trained immunity in patients with bronchiectasis both at the **pulmonary** and **systemic** level, and its association with lung infections and disease severity.
Tasks of the fellow: the student will be involved in the collection of a variety of systemic and pulmonary samples, learning how to pre-process and analyse them (including blood, sputum, saliva, oropharyngeal swabs, bronchial brushings and bronchoalveolar lavage). The fellow will learn how to perform air-liquid interface cultures to develop a fully pseudostratified epithelium, and use different inflammatory stimuli (i.e. cytokines, pathogen- and damage-associated molecular patterns (PAMPs and DAMPs). Isolation and stimulation of PBMCs will also be performed. Other methods that the fellow will use are: ELISA, flow cytometry, immunofluorescence, qPCR, DNA and RNA extraction, epigenetic profiling, and cilia beating analysis.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Genetics of histone methyltransferase expression in C. elegans

Project supervisor (principal investigator of the laboratory/group)
Name: Marcos Francisco Perez Browne
eMail: mpbbmc@ibmb.csic.es
Group name: Epigenetics and Metabolism
Institution: CSIC Barcelona Molecular Biology Institute (CSIC-IBMB)
Webpage of the group: https://www.ibmb.csic.es/en/department-of-cells-and-tissues/epigenetics-and-metabolism
Main grant associated with this project:
Principal investigator: Marcos Francisco Perez Browne
Agency: Mineco
Reference/ years: Plan Estatal PID2023-151711OA-I00 (3 years)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Covalent modifications of chromatin such as DNA or histone methylation, often referred to as epigenetics, are understood to have a critical role in encoding information to direct gene expression programs in eukaryotic cells.

A different and revolutionary perspective recognises that chromatin is so abundant in the cell that these epigenetic processes can also be understood as metabolic processes, which are regulated by metabolism and affect metabolism in turn by consuming large quantities of intermediate metabolites.

The roundworm *Caenorhabditis elegans* is a popular model organism which has been at the forefront of major discoveries in genetics, epigenetics and development for decades. In *C. elegans,* many histone methyltransferases (HMTs) with strongly differing roles in controlling transcription are nonetheless tightly co-regulated.

We will conduct genetic screens by RNA interference (RNAi) in *C. elegans* to understand how this regulation occurs, and in response to which metabolic or signalling pathways. The student will learn molecular biology techniques, such as DNA extraction and quantitative PCR, fluorescence microscopy and quantitative imaging analysis, in addition to *C. elegans* maintenance and genetics techniques.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Novel strategies for quantifying transcription factor activity *in vivo* in animals

Project supervisor (principal investigator of the laboratory/group)
Name: Marcos Francisco Perez Browne
eMail: mpbbmc@ibmb.csic.es
Group name: Epigenetics and Metabolism
Institution: CSIC Barcelona Molecular Biology Institute (CSIC-IBMB)
Webpage of the group: https://www.ibmb.csic.es/en/department-of-cells-and-tissues/epigenetics-and-metabolism

Main grant associated with this project:
Principal investigator: Marcos Francisco Perez Browne
Agency: Mineco
Reference/ years: Plan Estatal PID2023-151711OA-I00 (3 years)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The correct regulation of gene expression in space and time is orchestrated by transcription factors (TFs), proteins which bind to specific DNA sequences to activate or repress target genes. Nonetheless, TF gene regulatory activity is hard to study – there are hundreds of TFs, and each can regulate thousands of target genes, such that each gene can be regulated by tens of distinct TFs.

Recently I pioneered a computational method to quantify TF activity from transcriptomic data in the popular model animal *C. elegans*. I integrated existing genome-scale resources on TF targets to assemble the largest gene regulatory network in this animal to date - *Cel*EsT - allowing quantitative estimation of the activity of >450 TFs in parallel in a way that disentangles TFs with overlapping target sets (Perez 2024, Genetics, doi: 10.1093/genetics/iyae189)

Making TF activity visible as a quantitative trait via analysis of transcriptomic data with *Cel*EsT opens the door to studying the genome-wide and organism-wide dynamics of TF activity in orchestrating animal development. The current project involves creating novel reporters for experimental quantification of TF activity, to validate and expand on bioinformatic results. These involve tracking TF subcellular localisation using split fluorescent proteins, and building a toolkit using a sensitive luminescence assay to quantify TF activity in any cell type.

The student will learn CRISPR-Cas9 genome editing via microinjection, *C. elegans* maintenance, microscopy and quantitative image analysis, and basic molecular biology techniques such as PCR.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Bio-litography of microneedles on biopolymers to address efficient dermal administration of therapeutic agents

Project supervisor (principal investigator of the laboratory/group)
Name: ANNA ROIG
eMail: roig@icmab.cat
Group name: NANOPARTICLES & NANOCOMPOSITES
Institution: Institute of Materials Science of Barcelona (ICMAB-CSIC)
Webpage of the group: nn.icmab.es

Main grant associated with this project:
Principal investigator: Anna Roig
Agency: Ministerio de Ciencia, Innovación y Universidades
Reference/ years: PID2024-157637OB-I00/ Set 2025-August 2028

Brief summary of the project or current research lines of the group

The proposal, "Engineering BioActivity in Bacterial Cellulose (BACtive)," aims to develop innovative bioactive materials using bacterial cellulose (BC), a highly versatile and sustainable natural polymer with exceptional biomedical potential. BC's high purity, biocompatibility, mechanical strength, and structural similarity to extracellular matrices make it an ideal candidate for advanced healthcare applications. This project aligns with pressing societal challenges, including promoting sustainable bioeconomy practices and addressing critical health issues such as 3D cell culture, antimicrobial resistance, and the need for advanced tissue engineering solutions.

A specific objective of the project is to develop Engineering living materials (ELM) to protect and treat skin infections using novel administration routes that can ensure a controlled and prolonged-release system. The Master's thesis will contribute to this objective by learning lab techniques and protocols through the continuous supervision of a PhD student and the project leader.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Regulation of the centrosome cycle in G2 and M

Project supervisor (principal investigator of the laboratory/group)
Name: Joan Roig Amorós
eMail: joan.roig@ibmb.csic.es
Group name: Cell Cycle and Signaling
Institution: Institut de Biologia Molecular de Barcelona IBMB-CSIC
Webpage of the group: https://www.ibmb.csic.es/en/department-of-cells-and-tissues/cell-cycle-and-signaling/

Main grant associated with this project:
Principal investigator:
Agency: Ministerio de Ciencia, Innovación y Universidades
Reference/ years: PID2024-159596NB-I00, 2025-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Our group is interested in understanding how the G2 and M phases of the cell division cycle are regulated and executed. We focus our research on the roles of the signaling axis formed by the cyclin-dependent kinase CDK1, the polo-like kinase PLK1 and its downstream partners NEK9, NEK6 and NEK7, three related NIMA-family kinases that are activated at the centrosomes. Our previous work has shown how these kinases are central for the control of centrosome separation and maturation during mitotic entry (Bertran *et al.* (2011) *EMBO J.* **30**: 2634-2647; Sdelci *et al.* (2012) *Curr. Biol.* **22**: 1516-1523; Eibes *et al.* (2018) *Curr. Biol.* **28**: 121-129.e4; Gallisà-Suñé *et al.* (2023) *Nat. Commun.* **14**:1–20).

Using genetically modified cell lines produced through CRISPR-Cas9 technology as well as RNAi, the project will involve characterizing novel functions of PLK1 and NEK9/NEK/7 in G2 and early M, and seek to understand how malfunction of these kinases and their substrates may affect the centriole/centrosome duplication cycle and result in abnormal chromosome segregation and the onset of aneuploidy. This will involve the use of a variety of techniques, including different types of microscopy (conventional, super-resolution and expansion microscopy). We will relate our observations with clinical data with the aim of assessing the possible involvement of the studied kinases and their substrates in the process of cell transformation and the apparition of cancer as well as the onset of developmental abnormalities.

We are additionally interested in understanding the roles of the NEKs and their substrates in the organization and functioning of the primary cilia, a cellular structure organized by the centrosome that has important signaling functions in development and organogenesis as well as during tissue maintenance. A project tackling this subject and investigating the role of the NEK8 kinase in the context of developmental ciliopathies of the nephronophthisis type could also be considered.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Stop-Codon Readthrough as a Source of Novel Protein Architectures
Project supervisor (principal investigator of the laboratory/group)
Name: Maria Luisa Romero Romero
eMail: maria.romero@iqac.csic.es
Group name: Protein Evolution and Design
Institution: Institute of Advanced Chemistry of Catalonia-CSIC
Webpage of the group: https://romeroromerolab.org

Main grant associated with this project:
Principal investigator: Maria Luisa Romero Romero
Agency:
Reference/ years: Consolidación investigadora (CNS2025-166261)/ 2 años, Ramon y Cajal atracción de Talento (RYC2023-043865-I)/5 años

Brief summary of the project or current research lines of the group

How do protein complexes evolve from genetically separate subunits into single, fused polypeptides? This project explores this question by examining whether mechanisms like transcriptional stop codon readthrough (SCR) can serve as evolutionary intermediates, alongside traditional DNA sequence changes. Building on our previous work identifying SCR hotspots in bacteria (Romero-Romero et al., 2024 Nat comm), we will systematically analyze these events to determine which can yield stable, functional, and folded fused proteins.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Decoding Human-Specific Drivers of pMN Generation Using Primate Organoids

Project supervisor (principal investigator of the laboratory/group)
Name: Murielle Saade
eMail: msabmc@ibmb.csic.es
Group name: centrosome-cilia in normal and pathological neural development
Institution: Instituto de Biología Molecular de Barcelona (IBMB-CSIC)
Webpage of the group: https://www.ibmb.csic.es/en/department-of-cells-and-tissues/a-newvision-of-centrosome-cilia-in-normal-and-pathological-neural-development/#lab-presentation

Main grant associated with this project:
Principal investigator: Murielle Saade
Agency: MINCINN
Reference/ years:
1.- REF: CNS2023-144942 Proyectos de Generación de Conocimiento 2022, "EXPLORING MOLECULAR COMPLEXITY IN NEURAL DELAMINATION AND RELATED DISORDERS". PI Murielle Saade (200,000 €)
2.- REF: PID2022-140285NB-I00 "1q21.1 NEURODEVELOPMENTAL DISORDERS: IN SEARCH FOR THE BIOLOGICAL BASES OF THE DISEASE". PI Murielle Saade (300,000 € + 4-year PhD Fellowship (Spanish FPI)

Brief summary of the project or current research lines of the group Humans exhibit a unique combination of an enlarged nervous system and exclusive bipedal locomotion, which is supported by a substantially increased number and subtypes of spinal motor neurons (MNs) relative to other species. MN progenitors (pMNs) expand through distinct division modes, including symmetric proliferative (PP), asymmetric neurogenic (PN), and symmetric neurogenic (NN) divisions, ultimately shaping the size and complexity of the human spinal cord. While much of our knowledge stems from non-primate vertebrate models, human-specific mechanisms underlying pMN expansion remain poorly understood. This project hypothesizes that centrosome- and cilia-dependent pathways regulate pMN proliferation, fate specification, and tissue growth in humans. Using human and macaque 3D spinal cord organoids, combined with RNA sequencing, super-resolution microscopy, live imaging, and genome-engineering approaches, we aim to (i) compare pMN subtype generation, (ii) characterize species-specific pMN division modes, and (iii) elucidate the cellular and molecular mechanisms driving pMN expansion, focusing on the centrosome–cilia axis. Preliminary data validate the reproducibility of human spinal organoid platforms and the feasibility of reporter-based tracking of pMN division modes. This work will provide critical insights into human-specific spinal cord development, advancing our understanding of motor neuron generation, growth, and the evolutionary underpinnings of complex motor behaviors.

Project Title: New Genes in Iron Metabolism: The IRP/IRE Regulatory System

Project supervisor (principal investigator of the laboratory/group)

Name: Mayka Sanchez
eMail: msanchezfe@uic.es
Group name: Iron metabolism: regulation and diseases
Institution: Universitat Internacional de Catalunya (UIC) Campus Sant Cugat
Webpage of the group: https://researchgroups.uic.es/ironmetabolism/

Main grant associated with this project:

Principal investigator: Dr. Mayka Sanchez
Agency: MICIU
Reference/ years: GENERACION CONOCIMIENTO- project- PID2025-175115OB-I00 (2026-2029). Molecular And pathophysiological mechanisms of new Rare anemias and new genes controlled by the Iron metabolism regulatory systEm (MARIE)

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

This research project offers a high-impact opportunity to explore the IRP/IRE regulatory system, a fundamental post-transcriptional mechanism governing cellular iron homeostasis. Under the expert supervision of senior postdoc Dr. Pedro Fuentes, the student will investigate the functional impact of novel IRP targets—such as Ppp1r1b—on cellular iron metabolism, specifically examining their role in transferrin-mediated uptake and the regulation of key iron proteins. Integrating advanced RNA biology with cutting-edge molecular and celular techniques, the student will master a diverse experimental toolkit including cloning, RNA EMSAs, and luciferase assays to validate RNA-protein interactions, as well as ribosome profiling to monitor translational efficiency. These molecular insights will be complemented by robust functional assays and cellular imaging, utilizing Western blot, immunoprecipitations, immunofluorescence, and flow cytometry to quantify the cellular "iron interactome." This project provides an ideal environment for a Master student to contribute to translational discoveries while gaining expertise in the sophisticated regulatory networks that maintain cellular health. Our lab seminars are in English.

Project Highlights & PhD Opportunities

1. Expert Mentorship: Close guidance by senior postdoc Pedro Fuentes within a high-output research group.
2. Cutting-Edge RNA Biology: Hands-on experience with ribosome profiling, RNA EMSAs, and luciferase reporter assays.
3. Advanced Imaging & Analytics: Proficiency in confocal immunofluorescence, cloning, and flow cytometry.
4. PhD Continuation: Outstanding students will have the possibility to continue with a PhD project. Success is contingent on performance during the 6-month training stay and CV excellence to qualify for: Internal University Predoctoral Contracts or Competitive National predoc contracts (e.g., AGAUR Joan Oró).

Application Process

Interested candidates should contact Dr. M. Sanchez via email msanchezfe@uic.es. Please provide a motivation letter, and a complete and extensive CV including:

5. Academic Records: Graduate marks using the 1-10 Spanish system. Lab experience.

Foreign Applicants: Must include the official Ministry of Science and Universities grade equivalence (Declaration of Equivalence of Average Grades). You can process this via the official portal: Solicitud de notas medias (universidades.sede.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Gene circuits to program time in bacteria: exploring tools and applications

Project supervisor (principal investigator of the laboratory/group)
Name: Javier Santos Moreno
eMail: javier.santos@upf.edu
Group name: Synthetic Cell Programming lab
Institution: UPF - MELIS
Webpage of the group: santosmorenolab.org

Main grant associated with this project:
Principal investigator: Javier Santos Moreno
Agency: ERC Starting Grant - EU
Reference/ years: 101114955 / 2024-2029

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

In the Synthetic Cell Programming lab (santosmorenolab.org) we focus on designing and building synthetic gene circuits that allow us to program the behaviour of microbes, a requirement for using them to tackle health and environmental challenges. In that regard, programming cells to operate autonomously over time can enable applications in which external control (e.g. through inducers) is not possible or desirable.

In the past we built synthetic molecular oscillators based on CRISPR interference (CRISPRi) in bacteria (*Santos-Moreno et al. 2020, Nat Commun 11:2746*), and we used them to control the biosynthesis of the bacterial capsule in an oscillatory manner (*Rueff et al. 2023, Nat Commun 14:7454*). We are currently working of alternative tools and circuit designs that allow us to program temporal actions to occur in a discrete – rather than oscillatory – manner.

You will contribute to the assessment and characterization of molecular tools (e.g. CRISPRi, transcription factors, recombinases…) that enable the construction of synthetic gene circuits to program temporal tasks in *E.* coli cells. Besides, you will participate in exploring potential applications of temporal circuits, such as biocontainment, bioproduction or molecular recording. The range of techniques and equipment you will have access to includes *in silico* gene circuit design, advanced cloning, microplate reader measurements, automated pipetting robot, flow cytometry, fluorescence microscopy, or microfluidics, among others.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Engineering skin bacteria: tools for safe and cross-interactive strains

Project supervisor (principal investigator of the laboratory/group)
Name: Javier Santos Moreno
eMail: javier.santos@upf.edu
Group name: Synthetic Cell Programming lab
Institution: UPF - MELIS
Webpage of the group: santosmorenolab.org

Main grant associated with this project:
Principal investigator: Javier Santos Moreno
Agency: Plan Generación Conocimiento - AEI
Reference/ years: PID2024-157699OA-I00 / 2025-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

In the Synthetic Cell Programming lab (santosmorenolab.org) we aim to engineer human skin bacteria for diagnostic and therapeutic applications. Indeed, skin conditions affect ~25% of the world population, and engineered microbes constitute an innovative approach to tackle human diseases. *Cutibacterium acnes* is the most abundant skin bacterium and stably colonizes the follicles, where its presence generally correlates with healthy skin. *C. acnes* is therefore an ideal chassis for medical applications, but its engineering has been hampered by unsuccessful DNA delivery into the bacterial cytoplasm and a resulting lack of molecular tools to program its behaviour.

In the past, we managed to significantly improve the delivery of DNA into *C. acnes* cells (*Knödlseder et al. 2024, Nat Biotechnol 42:1661-1666*), and this allowed us to establish the first molecular toolbox to engineer this bacterium – including promoters, reporters, CRISPRi, recombinases, transcription factors… (*Nevot et al. 2025, Cell Systems 16: 101169*). Besides, we provided a proof-of-concept demonstration of the potential of this bacterium for medical purposes by developing strains that secrete anti-acne and anti-oxidant proteins (*Knödlseder et al.*) (*Nevot et al.*). We are currently working of new tools that allow us to engineer strains that are safer for prospective deployment on the human skin, and that interact with other members of the human microbiome, e.g. by limiting the growth of pathogenic bacteria or by cross-talking with other human commensals.

You will contribute to the assessment and characterization of molecular tools (CRISPR editing, unstable plasmids, antimicrobials…) that enable the construction of *C. acnes* strains with diagnostic or therapeutic potential. The range of techniques and equipment you will have access to includes *in silico* plasmid design, advanced cloning, anaerobic cultivation, automated pipetting robot, flow cytometry, or fluorescence microscopy.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Understanding the role of metabolically diverse cancer cell populations on colorectal cancer progression

Project supervisor (principal investigator of the laboratory/group)
Name: Carlos Sebastián Muñoz
eMail: csebastian@ub.edu
Group name: Metabolic Dynamics in Cancer
Institution: University of Barcelona, Institute of Biomedicine of the University of Barcelona (IBUB)
Webpage of the group: https://sites.google.com/view/carlossebastianlab/home

Main grant associated with this project: *Functional mapping of spatiotemporal changes in cellular metabolism during tumorigenesis*
Principal investigator: Carlos Sebastián
Agency: Agencia Estatal de Investigación
Reference/ years: PID2023-149228OB-I00, 2024-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Regulation of cellular metabolism is a fundamental trait of all living organisms. For long considered a housekeeping process mainly aimed to convert nutrients into energy and biomass, it is becoming increasingly evident that metabolism is actively involved in the control of many physiological processes. The overarching goal of our laboratory is to understand the role of metabolism as a regulator of stem cell fate, tissue homeostasis, and tumorigenesis, and the functional interplay between metabolic reprogramming and other genetic and epigenetic programs involved in these processes. We focus on colorectal cancer and our main research lines include:

1. Metabolic regulation of stem cell fate during tissue homeostasis and tumorigenesis
2. Metabolic heterogeneity and evolution of cancer
3. Metabolic crosstalk in the tumor microenvironment

To carry on these objectives, we employ stem cell cultures, 3D-organoids systems, genetically modified mouse models, tumor samples, patient-derived organoids and unique genetically encoded metabolic reporters.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Orphan mtDNA-regulatory proteins: Molecular basis of disease

Project supervisor (principal investigator of the laboratory/group)
Name: Maria Solà
eMail: maria.sola@ibmb.csic.es
Group name: Structural MitoLab
Institution: CSIC
Webpage of the group: https://ibmb.csic.es/en/department-of-structural-and-molecular-biology/mitochondrial-macromolecules/

Main grant associated with this project:
Principal investigator:Maria G. Solà Vilarrubias
Agency:MInisterio de Ciencia, Innovacion y Universidades (MICIUN)
Reference/ years: PID2024-160731NB-I00 / 2025-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Our group investigates the structural basis of the molecular mechanisms that regulate mitochondrial DNA (mtDNA) maintenance and gene expression. We have determined several structures of mitochondrial transcription factor A (TFAM/mtTFA), which activates transcription and compacts the mitochondrial genome, and addressed the mechanisms underlying both processes. These analyses where extended to mtDNA-packaging homologues, including Abf2p from *S. cerevisiae* and Gcf1p from *C. albicans*. We also solved the structures of the transcription termination factor mTERF and the replicative helicase Twinkle, and examined how disease-associated mutations in the single-stranded DNA-binding protein mtSSB affect its DNA-binding properties. We are currently working on proteins associated with mitochondrial disease, aiming to define the structural, functional, and mechanistic bases of mtDNA transcription and transmembrane trafficking-dependent regulation of mtDNA. Ultimately, the long-term goal of this work is to establish a foundation for the development of therapeutic strategies to treat mitochondrial disease.

The project offers the opportunity to work on mtDNA regulatory proteins associated with mitochondrial diseases, a group of rare and largely orphan disorders, aiming at understanding the alteration of the functional mechanisms. The targets are involved in mtDNA transcription or in transmembrane trafficking dependent - mtDNA regulation. The successful candidate will gain hands-on experience in cloning techniques, generation of disease-related and functional mutants, protein purification and biochemical and biophysical characterization. Depending on interest and progress, the project may also include protein crystallization and/or structure determination. Overall, this is a highly experimental project that provides broad, practical training in molecular and structural biology.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: **Application of NGS in the study of clonal evolution of low risk Myelodysplastic syndromes**

Project supervisor (principal investigator of the laboratory/group)
Name: FRANCESC SOLE
eMail: fsole@carrerasresearch.org;Group name: MDS GROUP
Institution: INSTITUT DE RECERCA CONTRA LA LEUCEMIA JOSEP CARRERAS
Webpage: https://www.carrerasresearch.org/en/research/myelodysplastic-syndromes

Main grant associated with this project:
Principal investigator: FRANCESC SOLE
Agency: ISCIII. FIS PROJECT; Reference/ years: 2026-2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

Myelodysplastic syndromes (MDS) are a group of highly heterogeneous haematological diseases characterised by ineffective haematopoiesis and an increased risk of progression to acute myeloid leukaemia (AML). Based on this risk, MDS are stratified into 5 groups (very low risk - low risk - intermediate risk - high risk - very high risk) according to the criteria of the Revised International Prognostic Scoring System (IPSS-R), based on haematological parameters and cytogenetic alterations [1].
The life expectancy of untreated patients with high-risk MDS is less than 1 year. For this reason, studies in this subgroup focus on the search for treatments that delay progression to AML and prolong life. At the opposite end of the spectrum, patients with low-risk MDS often follow an indolent disease course, so the focus of this subgroup is to improve quality of life. However, according to a molecular study of 1914 patients categorised as very low/low risk according to the IPSS-R, the 32% progressed to high-risk or AML. The median time to progression to high-risk was 22 months, while the median time to progression to AML was 29 months [2]. These results highlight the need to identify patterns associated with the progression of low-risk MDS to predict possible progression and apply early intervention.
The following conditions must be met for the diagnosis of primary MDS: persistent and clinically unexplained cytopenia; dysplasia of at least 1 of the myeloid lines; cytogenetic and/or molecular evidence of clonal haematopoiesis. It is suggested that soon, molecular patterns may be identified to help establish a diagnosis of MDS in patients with cytopenias, as is currently the case for certain types of cytogenetic alterations [3]. In this regard, thanks to the implementation of sequencing techniques in recent years, such as Next Generation Sequencing (NGS), numerous somatic mutations present in more than 80% of MDS patients have been identified. This technology helps to increase the accuracy of diagnosis and classification of this pathology, participates in prognostic evaluation, response to treatment and in the identification of patients who are candidates for a particular treatment [4]. The use of NGS for the study of low-risk MDS patients can be used to identify alterations that confirm the good prognosis expected in this subgroup or indicate a worse prognosis that helps predict progression.

Objectives
The main objective of the project is to improve the management of low-risk MDS patients:
- Define the molecular profile of patients with low-risk MDS.
- Assess the influence of the acquisition of additional molecular alterations.
- Compare the molecular profile of patients who progress versus those who do not progress.
- Correlate the molecular profile with clinical data.
- Predict overall survival and transformation-free survival based on the mutational profile.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Deciphering HDAC11-mediated metabolic reprogramming in fibroadipogenic plasticity

Project supervisor (principal investigator of the laboratory/group)
Name: Mònica Suelves
eMail: msuelves@igtp.cat
Group name: Badalona Neuromuscular Research Group (GRENBA)
Institution: Germans Trias i Pujol Research Institute (IGTP)
Webpage of the group: http://www.germanstrias.org/research/neurociencies/5/recerca-neuromuscular-i-neuropediatrica

Main grant associated with this project:
Principal investigator: Mònica Suelves
Agency: Duchenne Parent Project Spain
Reference/ years: DUC001

Brief summary of the project or current research lines of the group:
(please do not include pictures or logos and do not exceed this page)

Muscular dystrophies are rare diseases characterized by progressive muscle weakness, fibrosis, and intramuscular fat infiltration, which significantly reduce patients' quality of life and can lead to premature death. Unfortunately, these pathologies are incurable and patients only receive palliative therapies to delay symptoms and disease progression. Despite substantial progress in the understanding of the pathobiology of fibro/adipogenesis, the causes of fibro-fatty tissue deposition in chronic dystrophies are not well understood. Nevertheless, accumulating evidences support 1) FAPs (fibro/adipogenic progenitors) are the major precursors of fibrogenic and adipogenic cells in dystrophic muscles, 2) there is a connection between FAPs plasticity and metabolism, 3) progressive metabolic changes occur during the dystrophic process, being alterations in lipid metabolism very critical. Based on previous results of our group (Hurtado et al, 2020; Núñez-Álvarez et al, 2021; Odria et al, Life Sciences, 2026) we envision HDAC11 as a new therapeutic target to reduce fibro-fatty deposition and enhance muscle regeneration. Currently, we are analyzing the impact of HDAC11 deficiency on 1) dystrophic FAP and muscle cells and their ability to differentiate and generate fibro-adipogenesis and improve muscle differentiation, respectively, 2) impact on cellular communication between FAP and muscle cells and 3) metabolic activity regulating mitochondrial lipid oxidation. The identification of new anti-fibroadipogenic therapeutic targets (such as HDAC11) may have great relevance not only for the treatment of muscular dystrophies, but also for the treatment of other chronic diseases.

The project includes to perform:

- Cell cultures of primary and immortalized mouse/human cells
- Determination of proliferation, apoptosis and differentiation capacities of muscle and FAPs cells
- Molecular biology experiments (DNA/RNA/protein extraction, qRT-PCR, Western Blots)
- Histology, immunohistochemistry and microscopy analysis
- Metabolic analysis

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Lipid-modified proteins and their role in neurodegenerative diseases

Project supervisor (principal investigator of the laboratory/group)
Name: Gemma Triola
eMail: gemma.triola@iqac.csic.es
Group name: Chemical Biology
Institution: Institute for Advanced Chemistry of Catalonia (IQAC-CSIC)
Webpage of the group:
https://www.iqac.csic.es/research/departments/biological-chemistry/chemical-biology/

Main grant associated with this project:
Principal investigator: Gemma Triola
Agency: AEI
Reference/ years: PID2024-162523NB-I00; 2025/2028

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

S-acylation is the covalent attachment of fatty acids to cysteine residues in proteins via a thioester bond. This modification is reversible and regulated by enzymes (around 23 protein acyl transferases (PAT-DHHC) and at least 5 thioesterases). Until recently, it was thought that palmitic acid was the main fatty acid attached to proteins, and as a result, this modification was also known as protein palmitoylation. It is now clear that proteins can be modified with a wide range of fatty acids (shorter, longer, unsaturated, etc), but the consequences of this heterogeneity in regulating protein function and diseases remain unknown.[1,2] Moreover, the substrate specificity of the PAT-DHHCs and the thioesterases is also not clear. We work towards the development of tools and methods enabling the study of S-acylated proteins and the role of these diverse lipid modifications in the pathogenesis of diseases, such as cancer and rare neurodegenerative disorders. To do this, we combine techniques from different disciplines, including organic chemistry, cell biology, biochemistry, and mass spectrometry.

1. Busquets-Hernández C, Ribó S, Gratacós-Batlle E, Carbajo D, Tsiotsia A, Blanco-Canosa JB, Chamberlain LH, Triola G. Quantitative analysis of protein lipidation and acyl-CoAs reveals substrate preferences of the *S*-acylation machinery. Chem Sci. 2024 Jul 9;15(32):12845-12855. doi: 10.1039/d4sc02235a.
2. Busquets Hernández C, Tsiotsia A, Pipitò L, Chamberlain LH, Greaves J, Triola G. Different chains for different gains: How acyl chain diversity shapes S-acylated protein function. Prog Lipid Res. 2025 Nov;100:101354. doi: 10.1016/j.plipres.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Microbial Metabolism as a Mechanistic Driver of Infertility in Patients with Endometriosis

Project supervisor (principal investigator of the laboratory/group)
Name PI: Mireia Valles-Colomer Name co-supervisor: Viviana Rossi
eMails: mireia.valles@upf.edu, viviana.rossi@upf.edu
Group name: Microbiome Research Group
Institution: Department of Medicine and Life Sciences (MELIS-UPF)
Webpage of the group: https://www.upf.edu/web/microbiome

Main grant associated with this project:
Principal investigator: Mireia Valles-Colomer
Agency: Biocodex Microbiota Foundation Women's Health Grant 2026
Reference/ years: 3 years

Brief summary of the project or current research lines of the group

Endometriosis is a chronic, progressive, and estrogen-dependent gynecological disease affecting up to 10% of reproductive-age women. It is characterized by the ectopic growth of endometrial-like tissue, driven by heightened estradiol signaling and progesterone resistance. These processes enable endometrial cells to survive, proliferate, and establish lesions outside the uterus, creating an inhospitable uterine environment for embryo implantation. Although the pathophysiology of endometriosis remains incompletely understood, it is increasingly recognized as multifactorial, with emerging evidence implicating the gut and vaginal microbiomes. Microbiome dysbiosis may exacerbate inflammation, accelerate lesion progression, and impair fertility. However, inflammation alone cannot fully explain the disease, and the functional role of microbial metabolism in endometriosis remains largely unexplored. Microorganisms in the gut and vaginal microbiomes influence systemic and local sex hormone levels, thereby directly affecting reproductive physiology. In this study, we investigate the gut and vaginal microbial metabolism of bioactive compounds, particularly sex hormones, as a key driver of endometriosis progression and manifestation. Moreover, we will also tackle the contribution of the gut microbiome in the gut-brain axis, producing neuroactive compounds that communicate with the hypothalamic-pituitary-gonadal (HPG) axis and other brain regions, ultimately regulating gonadal hormone production and pain sensitization. The overarching goal of this project is to elucidate microbiome-driven, metabolism-based mechanisms underlying endometriosis. Specifically, we will conduct a clinical study to identify the main microbial functional alterations in the vaginal and gut microbiome of endometriosis patients compared to healthy controls across the menstrual cycle (proliferative phase vs secretory phase). Blood, fecal, and vaginal samples will be collected (metagenomics, metabolomics, inflammatory biomarkers assay, hormonal characterization) together with extensive high-quality metadata. Overall, this project integrates the establishment of a deeply phenotyped cohort diagnosed with high-accuracy standardized methods, with high-resolution sequencing techniques and cutting-edge bioinformatic tools, to ultimately contribute to advancing our knowledge of microbiome-based mechanisms in endometriosis, and lay the basis for more personalized and effective clinical management of this debilitating condition.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Redefining Hormonal Regulation in Breast Cancer: Interplay Between Signaling Pathways, Epigenetic Regulators, and Cellular Mechanics

Project supervisor:

Name: Guillermo P. Vicent; eMail: gvmbmc@ibmb.csic.es; Group name: Chromatin and gene regulation; Institution: Molecular Biology Institute of Barcelona (IBMB); Webpage of the group: https://ibmb.csic.es/en/department-of-structural-and-molecular-biology/chromatin-and-gene-regulation/

Main grant associated with this project:

Principal investigator: Guillermo P. Vicent; Agency: Ministerio de Ciencia e Innovación; Reference/ years: Ref# PID2022-137045OB-I00 (2023-2026). Currently under renewal for the 2026–2029 period.

Brief summary of the project or current research lines of the group:

Breast cancer remains one of the leading causes of cancer-related morbidity and mortality in women worldwide (World Health Organization, Breast Cancer, 2025; Kim et al., 2025). The majority of tumors are hormone receptor–positive (HR^+) and depend on the coordinated activity of estrogen receptor alpha ($ER\alpha$), progesterone receptor (PR), androgen receptor (AR), and glucocorticoid receptor (GR) for proliferation and survival (Kim and Lukong et al., 2025). Although endocrine therapies target $ER\alpha$ effectively, intrinsic and acquired resistance continue to limit long-term benefit. A major limitation is that current therapeutic approaches still follow reductionist models centered on single ligands and receptors, even though mammary tissues are exposed to complex and fluctuating mixtures of estrogens, progestins, glucocorticoids, and androgens across daily and menstrual rhythms (Lonard et al., 2012). We and others have now shown that **hormonal signals in hormone-responsive breast cancer cells are far more interconnected than previously appreciated**. Thus, without models that integrate hormonal, epigenetic, and mechanical dimensions, we cannot fully understand how HR^+ tumors adapt transcriptionally to selective pressures or environmental cues.

To directly address these critical gaps, we will employ high-throughput sequencing (RNA-seq, ChIP-seq, ATAC-seq) to profile transcriptional and chromatin dynamics, RIME (Rapid Immunoprecipitation Mass Spectrometry of Endogenous Proteins) to define protein interactomes, and 3D spheroid models and patient-derived xenografts (PDXs) from Vall d'Hebron Institute of Oncology, Barcelona to compare fast (<5 years) versus slow (5–10 years) relapse cases, by:

i) Defining key features of **multi-receptor crosstalk and its transcriptional consequences** in HR^+ breast cancer;

ii) clarifying canonical and non-canonical contributions of **the epigenetic regulator EZH2** to hormone-dependent transcription and resistance; and

iii) providing mechanistic insight into how **ECM stiffness** influences hormone signaling, nuclear organization, and hormone-dependent gene regulation.

Starting hypothesis: We hypothesize that hormonal, epigenetic, and mechanical cues interact to shape transcriptional states in breast epithelial cells, and that endocrine therapy resistance in hormone receptor-positive tumors arises when either these signals or the regulatory mechanisms that coordinate them become disrupted.

Call for project proposals
Master in Biomedical Research practicum, 2027
Department of Medicine and life Sciences, Universitat Pompeu Fabra

Project Title: Host-microbiota crosstalk in cancer and ageing-related disease

Project supervisor (principal investigator of the laboratory/group)
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Group name: Intercellular Communication in Cancer and Ageing
Institution: Hospital del Mar Research Institute
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https://www.imim.cat/programesrecerca/cancer/en_intercellular_communication.html

Main grant associated with this project:
Principal investigator: Patrick-Simon Welz
Agency: Agencia Estatal De Investigación (AEI)
Reference/ years: PID2023-146053OB-I00 / 2024-2027

Brief summary of the project or current research lines of the group (please do not include pictures or logos and do not exceed this page):

The research of our laboratory focusses on deciphering how colorectal cancer or neurodegenerative disease are altering daily dynamics in host-microbiota crosstalk, and how, in turn, disturbed daily microbiome rhythms are promoting pathogenesis. We combine various omics approaches (metagenomics, transcriptomics, metabolomics) with *in vivo* experimentation in mouse models of disease to study host-microbiome interaction. Skills and techniques that can be learned during the internship include mouse genetics, molecular biology techniques (PCR, western blot, etc.), histopathology, omics data mining, and the theoretical background on colorectal cancer or Alzheimer's disease, chronobiology, and host-microbiota communication.