Master in Biomedical Research

2022-2023

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. **These groups have expressed their interest for hosting a master student.**

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 must contact the group you are interested in, arrange an interview, and get the written acceptance of the investigator in charge of that group.

Master in Biomedical Research

2022-2023

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

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, 2023, Universitat Pompeu Fabra

Project Title: Blending Biology and Chemistry to Enable Systems Pharmacology

Project supervisor (principal investigator of the laboratory/group)
Name: Patrick Aloy
eMail: patrick.aloy@irbbarcelona.org
Group name: Structural Bioinformatics and Network Biology
Institution: Institute for Research in Biomedicine (IRB Barcelona)
Webpage of the group: https://sbnb.irbbarcelona.org

Main grant associated with this project:
Principal investigator: Patrick Aloy
Agency: Ministerio de Ciencia e Innovación
Reference/ years: 2021-2024

Brief summary of the project or current research lines of the

Large-scale small molecule bioactivity data are not routinely integrated in daily biological research to the extent of other 'omics' information. Compound data are scattered and diverse, making them inaccessible to most researchers and not suited to standard statistical analyses. We recently developed the Chemical Checker (CC), a resource that provides processed, harmonized and integrated bioactivity data on small molecules (1-3). The CC divides data into five levels of increasing complexity, ranging from the chemical properties of compounds to their clinical outcomes. In between, it considers targets, off-targets, perturbed biological networks and several cell-based assays such as gene expression, growth inhibition and morphological profiles. In the CC, bioactivity data are expressed in a vector format, which naturally extends the notion of chemical similarity between compounds to similarities between bioactivity signatures of different kinds. We showed how CC signatures can boost the performance of drug discovery tasks that typically capitalize on chemical descriptors, and we demonstrated and experimentally validated that CC signatures can be used to reverse and mimic biological signatures of disease models and genetic perturbations, options that are otherwise impossible using chemical information alone (4). We are now developing a generalized connectivity mapping, as a form of virtual phenotypic screening, to discover novel chemical or genetic modulators able to *revert* the specific signatures of disease and 'cancel out' the phenotypic traits of complex disorders.

References

1. Duran-Frigola M, et al. Extending the small-molecule similarity principle to all levels of biology with the Chemical Checker, Nature Biotechnology, 2020, 38(9):1087-1096.

2. Bertoni M, et al. Bioactivity descriptors for uncharacterized compounds, Nature Communications, 2021, 12:1-13.

3. Fernández-Torras A, et al. Connecting chemistry and biology through molecular descriptors, Current Opinion in Chemical Biology, 2022, 66:10290.

4. Pauls E, et al. Identification and drug-induced reversion of molecular signatures of Alzheimers disease onset and progression in AppNL-GF, AppNL-F and 3xTg-AD mouse models, Genome Medicine, 2021, 13:168.

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/biomed/entry/-/-/15818/adscripcion/jose-francisco-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: RTI2018-095902-B-I00 and PID2021-128721OB-I00 (2019-2024)

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 metabolism influences diverse immune responses in two pathological settings, obesity and 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 and enhance their therapeutic effectiveness in cancer and obesity. 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, CRISPR-directed deletions, gene expression, chromatin analyses, cell differentiation assays, metabolic activity, antitumor function) of primary immune cells isolated from gene-edited mice under different pathological settings.

Leading recent publications of the group:

Lunazzi et al., 2021 Journal of Immunology
Huerga Encabo et al., 2020 Journal of Experimental Medicine
Aramburu and López-Rodríguez, 2019 Frontiers in Immunology
Buxadé et al., 2018 Journal of Experimental Medicine
Tellechea et al., 2018 Journal of Immunology
Aramburu et al., 2014 Science Signaling
Berga-Bolaños et al., 2013 Proc Natl Acad Sci USA
Buxadé et al., 2012 Journal of Experimental Medicine
Ortells et al., 2012 Nucleic Acids Research

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Dissecting the role of DYRK1A kinase in neurogenesis and neuron differentiation using conditional mutant mice

Project supervisor (principal investigator of the group)
Name: Mariona Arbonés
eMail: marbmc@ibmb.csic.es
Group name: Proliferation and Differentiation of the Nervous System
Institution: Institut de Biologia Molecular de Barcelona, IBMB-CSIC
Webpage of the group: http://www.ibmb.csic.es/home/marbones/

Main grant associated with this project:
Principal investigator: Mariona Arbonés
Agency: Spanish Ministry of Science and Innovation
Reference: PID2019-105902RB-I00
years: 2020-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The neocortex is the brain region responsible for sensory perception and integration, sensory-motor transformation and learning and memory. Neocortical neurons are morphologically and functionally very heterogeneous. These neurons are generated at different rates and developmental times from progenitors located in distinct proliferative domains of the embryo telencephalon. Shortly after mitosis, new-born neurons migrate from these domains to the future cortex where they mature and project intracortically or to subcortical regions. Alterations in neuron production (neurogenesis) or neuron differentiation (acquisition of a proper fate) could lead to different disorders, including intellectual disability and autism.

In this project we aim at understanding the function of DYRK1A kinase in brain development in both, physiological and pathological conditions. *DYRK1A* is encoded by a chromosome 21 gene and its overexpression is key for Down syndrome neuropathology. Moreover, dominant loss-of-function mutations in *DYRK1A* gene are also pathogenic, causing a rare syndrome of intellectual disability and autism. We and others have shown that DYRK1A regulates brain growth in a region-specific manner by controlling neurogenesis, structural neuronal differentiation and developmental cell death.

The objectives of the project are: 1/ To extend the current knowledge about the cellular and molecular mechanisms by which DYRK1A balances proliferation and differentiation during the neurogenic phase of cortical development and 2/ to analyse *in vivo* the impact of loss-of-function *DYRK1A* mutations on the morphology and axonal projections of neocortical neurons that are thought to underpin high-level cognitive functions. The project involves the use of a variety of methodologies (advanced fluorescence microscopy, *in vivo* GFP labelling of neurons, transcriptomics and proteomics, and classical molecular biology and histological methods), and constitutive and conditional *Dyrk1a* mouse models.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: Cell cycle control: elaborating an integrative map of DNA synthesis regulators and tumour progression.

Project supervisor (principal investigator of the laboratory)
Name: José Ayté
Mail: 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: 2019-2022

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

We are ultimately interested in deciphering the mechanisms that control cell cycle progression. Inactivation of the Retinoblastoma protein (RB) leads to unregulated cell cycle progression promoting cell growth, genomic instability and aneuploidy, hallmarks of tumor progression. RB activity is achieved through binding the E2F family of transcription factors. It is well known that a tumor process is very complex, accumulating secondary mutations that eliminate the brakes to the cell cycle. Even though many regulators of the RB-E2F are known, an integrative view of all the regulatory events controlling the G1/S transition is required to anticipate putative interventions able to block proliferative processes.

The candidate will characterize the regulation of the yeast MBF complex (functional homolog of human RB-E2F). The regulated activity of this complex is also essential for the G1/S transition since cells with hyperactive MBF have genomic instability. The candidate will perform 2 whole-genomic screens searching for global regulators of MBF. We have developed a reporter strain in the laboratory that measures MBF activity in vivo as an YFP/RFP output, either on FACS or on an automated fluorescence microscope platform. This reporter strain will be introduced in a commercial yeast KO deletion library. These screenings will allow the creation of a complete map with all the MBF regulators and, by extrapolation, will establish the nodes that regulate the RB pathway.

Some recent publications from the group are:

Hummer et al. (2021) **Cell Rep.** 37:109893
Borao et al. (2021) **Int. J. Mol. Sci.** 22:12444
Salat-Canela et al. (2021) **Cell Rep.** 37: 109951
González-Medina et al. (2019) **Nucleic Acids Res.** 47:8439-8451
Knezevic et al. (2018) **FEBS J.** 285:3870-3881
Alves-Rodrigues et al (2016) **Cell Reports** 14:885-895
Eckert et al. (2016) **PLoS Genet.** 12:e1005768
Gomez-Escoda et al. (2011) **EMBO Rep.** 12:84-89
Moldon et al. (2008) **Nature** 455:997-1000

Project Title: EPIGENETIC REGULATION OF CHROMATIN STRUCTURE AND FUNCTION: 3D CHROMATIN ORGANIZATION AND LINKER HISTONES H1

Project supervisor (principal investigator of the laboratory/group)

Name: Dr. F. Azorin

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Group name: Chromatin Structure and Function

Institution: IRB Barcelona and IBMB, CSIC

Webpage of the group: https://www.irbbarcelona.org/es/research/chromatin-structure-and-function#ferran-azorin

Main grant associated with this project:

Principal investigator: Dr. F. Azorin

Agency: AEI

Reference/ years: PGC2018-094538-B-I00 (2019-2022) and PID2021-123303NB-I00 (2022-2026; under evaluation)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Epigenetic mechanisms regulate chromatin structure and function and, as such, contribute to the regulation of most genomic processes from DNA transcription, replication, recombination and repair to chromosome segregation and genome integrity/stability. In addition, altered epigenetic regulation is a common trait in many disease conditions, including cancer and neurodegenerative, cardiovascular, infectious and metabolic diseases, opening the possibility for new diagnostic and therapeutic tools. Our current understanding of chromatin epigenetics mainly involves the contribution of histone core modifications and variants, as well as non-coding RNAs (ncRNAs), to the establishment and maintenance of functional chromatin states. However, this general picture is still incomplete since it is largely missing a main chromatin component: *linker histones H1*. On the other hand, despite the *hierarchical tridimensional (3D) organization of chromatin* inside the nucleus is well established, many fundamental questions remain unanswered regarding the principles and factors that govern the establishment and maintenance of 3D chromatin structure and their functional relevance. These aspects, together with the regulation of *centromeric chromatin assembly and function*, focused our recent research.

Our main recent achievements have been:

1) *Linker histones H1*

- We have identified a novel germline specific linker histone, dBigH1, and analyze its contribution to germline and early embryo development, and the regulation of gene expression (Pérez-Montero *et al.*, (2013) Dev Cell, 26: 578; Carbonell *et al.*, (2017) Cell Rep, 21: 3178; Climent-Cantó *et al.*, (2020) Nucleic Acids Res, 48: 4147; Climent-Cantó, Carbonell, Tamirisa *et al.*, (2021) Open Biol, 11; 200408). In addition, we have unveiled an unexpected compensatory mechanism that co-regulates expression of germline dBigH1 and somatic dH1 during early embryo development (Carbonell, Henn et al., (2020) BioRxiv, doi: https://doi.org/10.1101/2020.03.21.001529).
- We have uncovered the essential role of somatic dH1 in the maintenance of genome stability by preventing the accumulation of deleterious RNA:DNA hybrids (R-loops) (Vujatovic *et al.*, (2012) Nucleic Acids Res, 40: 5402; Bayona, Casas-Lamesa *et al.*, (2017) Nature Commun, 8: 283)
- We have identified multiple post-translational modifications (PTMs) of somatic dH1 (Bonet *et al.*, (2012) J Proteomics, 75: 4124). We have found that one of these PTMs (dH1K27me2) is an early step in heterochromatin formation (Bernués *et al.*, (2021) bioRxiv, doi: https://doi.org/10.1101/2021.06.22.449135; Nucleic Acids Res, in revision))

2) *3D chromatin organization*

- We have identified a novel transcription complex, the HP1c-complex, that regulates RNApol II pausing and we have determined the 3D chromatin organization of the target genes (Font-Burgada *et al.*, (2008) Genes Dev, 22: 3007; Kessler *et al.*, (2015) Nature Commun, 6:7049; Puerto *et al.*, in preparation)

3) *Centromeric chromatin*

- We have uncovered the role of proteolysis in the assembly of centromeric chromatin (Moreno-Moreno *et al.*, (2019) Nucleic Acids Res, 47; 3395; Moreno-Moreno *et al.*, (2011) Curr Biol, 21: 1488; Moreno-Moreno *et al.*, (2006) Nucleic Acids Res, 34: 6247). We have identified a novel centromeric complex formed by the nuclear envelope (NE) component Barrier-to-Autointegration factor (BAF), the centromeric protein CenpC and the protein phosphatase PP4 that is essential for stability of centromeric chromatin and controls mitosis progression (Torras-Llort, Medina-Giró, Escudero-Ferruz *et al.*, (2020) Commun Biol, 3; 454).

Project Title: SARCOPENIA AND NUTRITIONAL ABNORMALITIES IN BRONCHIECTASIS PATIENTS: IMPLICATIONS IN THE CLINICS OF DIFFERENCES BETWEEN MEN AND WOMEN

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

Dr Esther Barreiro, MD, PhD

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

Non-cystic (non-CF) fibrosis bronchiectasis is a highly prevalent disease, since it represents the third chronic inflammatory disease of the airways after bronchial asthma and chronic obstructive pulmonary disease (COPD). Hypothesis and objectives: In bronchiectasis patients, systemic inflammation and nutritional abnormalities are relevant manifestations, which may also affect the muscle compartment. Hence, we hypothesized that the function of the respiratory and both upper and lower limb muscles may be altered in patients with bronchiectasis. The level of respiratory and limb muscle dysfunction may be associated with the degree of the patients' systemic manifestations, namely the nutritional abnormalities and systemic inflammation levels. Differences in the target parameters may exist between female and male patients. Hereafter, we further hypothesized that nutritional abnormalities, muscle dysfunction/sarcopenia, and systemic inflammation would be more severe in female than in male patients. Methods: A total of N=150 adult patients, men and women, with non-CF bronchiectasis and 20 control subjects (lung function and normal body composition) will be recruited from the outpatient Bronchiectasis Clinical Unit of the Pulmonology Department at Hospital del Mar (Barcelona). In addition, patients will have a wide-range body composition, which will allow stratification according to alterations in their nutritional status, muscle mass and function loss. In patients and control subjects, the following parameters will be determined: clinical evaluation and nutritional status, lung function, respiratory and peripheral muscle function (upper and lower limbs), and exercise capacity. In a subgroup of patients (N=20) and controls (N=10) the vastus lateralis quadriceps will be sampled. Inflammatory and nutritional parameters and damage (troponin I) will be analyzed in blood from all patients and controls, and levels of proteolysis, autophagy, apoptosis, muscle damage and regeneration, oxidative stress, cytokines, endoplasmic reticulum stress, and signaling (NF-kB and FoxO1/3 pathways), will be quantified in muscle specimens using diverse laboratory techniques. Using the corresponding statistical methods, all clinical, physiological, and biological variables and their potential relationships will be analyzed in specific stratified groups of patients. Differences between female and male patients will also be assessed.

Barcelona, January 28th 2022

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Epigenetic and metabolic functions of histone variants

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://www.carrerasresearch.org/en/Chromatin_Metabolism_and_Cell_Fate

Main grant associated with this project:
Principal investigator: Marcus Buschbeck
Agency: La Marató de TV3
Reference/ years: 257C/2019

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The modular building block of chromatin structure is the nucleosome that contains a core of histone proteins. Histone variants replace replication-coupled canonical histones and thus endow local chromatin environments with unique properties. The histone variants macroH2A are unique in having a tripartite structure consisting of a N-terminal histone-fold, an intrinsically unstructured linker domain and a C-terminal macro domain (see Figure below). Recently, we have made two major discoveries. First, macroH2A proteins have a major role in the nuclear organization mediated by the linker domain (Douet et al., 2017, JCS; Kozlowski, Corujo et al., 2018, EMBO Rep). Second, by directly binding metabolites and metabolic effector proteins through their macrodomain, they impact on the metabolic regulation (discussed in Hurtado-Bagès, 2020, Mol Metab). The challenge for us now is to understand how these molecular functions mediate cellular functions in cancer, differentiation and somatic cell reprogramming (discussed in Buschbeck and Hake, 2017, Nature Reviews MCB). On the molecular level, we are interested to understand how direct metabolite binding affects the function of macroH2A in 3D chromatin architecture.

Other projects in the lab focus on chromatin regulators as potential drug targets in blood cancers.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: **Understanding the involvement of hippocampal circuits in higher-order conditioning**

Project supervisor (principal investigator of the laboratory/group)

Name: **Arnau Busquets Garcia**

eMail: **abusquets@imim.es**

Group name:

Institution: **Institut Hospital del Mar d'Investigacións Mèdiques**

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: **ERC Starting Grant**

Reference/ years: **Highmemory project (Ref. 948217, 2021-2026)**

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Animals and humans adapt to changes in the environment encoding and storing previous experiences. Although associative learning involving a reinforcer has been the major focus in the field of cognition, other forms of learning are gaining popularity as they are likely to be both more significant and frequent in human daily choices. Indeed, associations between non-reinforcing stimuli represent the most evolutionarily advanced way to increase the chances of predicting future events and adapting an individuals' behaviour. Animals are also able to utilise these higher-order conditioning processes, but more research is needed to understand how the brain encode and store these complex cognitive processes.

This Master project will be performed in the general frame of the HighMemory project, which is investigating hippocampo-cortical circuits in higher-order conditioning processes in mouse models. These processes explain why individuals are very often repulsed or attracted by stimuli (people, places, sounds), which have no intrinsic repellent or appealing value and have never been explicitly paired with negative or positive outcomes. A possible explanation for these "ungrounded" aversions or repulsions is that these stimuli have been incidentally associated with other directly reinforced cues. This is called higher-order conditioning or mediated learning (ML). Importantly, these behavioural processes involve the hippocampus, are characterised by defined and accessible phases and involve several brain regions, making them perfect models for studying tight behaviour regulation by hippocampo-cortical projections. By using genetic (viral and chemogenetic techniques), Ca2+ imaging, and mouse behavioural (sensory preconditioning) approaches, the aim of the HighMemory project is at dissecting and characterizing, at the macro- (brain regions), meso- (cell sub-types), and micro-scales (activity changes), the causal involvement of hippocampo-cortical projections in higher-order cognitive processes.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: Epigenetic regulation of gene expression in malaria parasites

Project supervisor (principal investigator of the laboratory/group)
Name: Alfred Cortés, ICREA Research Professor
eMail: alfred.cortes@isglobal.org
Group name: Malaria Epigenetics Lab
Institution: Barcelona Institute for Global Health (ISGlobal)
Webpage of the group: https://cortesmalarialab.wordpress.com/ ;
http://www.icrea.cat/Web/ScientificStaff/Alfred-Cortes-Closas-375

Main grant associated with this project:
Principal investigator: Dissecting the initial molecular events that trigger sexual conversion and transmission in malaria parasites
Agency: La Caixa Health Research
Reference/ years: HR18-00267 (2019-2022, no cost extension until 2023).

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

The team. Our team investigates transcriptional processes, including chromatin-based epigenetic regulation, in the malaria parasite *Plasmodium falciparum*. We study the transcriptional changes underlying parasite adaptation to the conditions of their environment, with a special focus on the genes that regulate sexual conversion, the heat-shock response and solute permeability.

The project. The transmission of malaria from one human host to another occurs via mosquito vectors. In the human blood, the majority of parasites multiply asexually, but the only forms that can infect a mosquito are the sexual forms termed gametocytes. Hence, the conversion of some asexually-growing parasites into sexual gametocytes is essential for malaria transmission. Some important regulators of sexual conversion, which involves a transcriptional switch, were recently identified by us and by others, including the master regulator PfAP2-G, its upstream regulator GDV1 and an antisense long non-coding RNA. In this project we investigate the role of heterochromatin in controlling the expression of these regulators, with the aim of identifying the initial molecular event that controls sexual conversion.

Techniques. For our research we routinely use *P. falciparum* cultures, transcriptional analysis (RT-qPCR, RNA-seq and microarrays), chromatin immunoprecipitation (ChIP-qPCR and ChIP-seq), flow cytometry and genome editing with the CRISPR/Cas9 system.

Main recent publications from the team:

E. Tintó-Font, L. Michel-Todó, T.J. Russell, N. Casas-Vila, D.J. Conway, Z. Bozdech, M. Llinás & A. Cortés, 2021, “A heat-shock response regulated by the PfAP2-HS transcription factor protects human malaria parasites from febrile temperatures”, ***Nature Microbiology*** 6:1163-74.

H.P. Portugaliza, S. Miyazaki, F.J. Geurten, C. Pell, A. Rosanas-Urgell, C.J. Janse & A. Cortés, 2020, “Artemisinin exposure at the ring or trophozoite stage impacts *Plasmodium falciparum* sexual conversion differently”, ***eLife*** 9:e60058.

O. Llorà-Batlle, L. Michel-Todó, K. Witmer, H. Toda, C. Fernández-Becerra, J. Baum & A. Cortés, 2020, “Conditional expression of PfAP2-G for controlled massive sexual conversion in *Plasmodium falciparum*”, ***Science Advances*** 6:eaaz5057.

Bancells C, Llorà-Batlle O, Poran A, Nötzel C, Rovira-Graells N, Elemento O, Kafsack BFC & Cortés A, 2019, “Revisiting the initial steps of sexual development in the malaria parasite *Plasmodium falciparum*”, ***Nature Microbiology*** 4:144-154.

Kafsack, B.F.C., Rovira-Graells, N., Clark, T.G., Bancells, C., Crowley, V.M., Campino, S.G., Williams, A.E., Drought, L.G., Kwiatkowski, D.P., Baker, D.A., Cortés, A. & Llinás, M., 2014, "A transcriptional switch underlies commitment to sexual development in malaria parasites", ***Nature*** 507:248-52.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title:

Genome editing by CRISPR to mimic human mutations in *Caenorhabditis elegans*

Project supervisor (principal investigator of the laboratory)
Name: Julián Cerón Madrigal
Mail: jceron@idibell.cat
Group name: Modeling human diseases in *C. elegans*
Institution: Bellvitge Biomedical Research Institute (IDIBELL)

Webpage of the group: www.ceronlab.com and www.idibell.cat
Twitter: @ceronlab

Main grant associated with this project:
Principal investigator: Julián Cerón Madrigal
Agency: Ministerio de Ciencia e Innovación
Reference/ years: *DEVELOPMENT OF CRISPR-CAS TECHNOLOGIES IN C. elegans TO INVESTIGATE HUMAN PATHOGENIC MUTATIONS AND OTHER GENE VARIANTS, AND TO CREATE RARE DISEASE MODELS.* PID2020-114986RB-I00. From 2021 to 2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Our lab uses the powerful genetic model *C. elegans* to investigate human diseases: rare diseases (*Kukhtar et al, 2020*) or cancer (*Serrat et al, 2019*). We have broad expertise in CRISPR technologies that are being applied to model human diseases (ex. by introducing human mutations in *C. elegans*). Moreover, we have an active research line on optimizing CRISPR genome editing by creating methodologies or by using distinct Cas9 enzymes (*Vicencio et al, 2019; 2021*). Thus, a Master's research project in our lab would include molecular biology, CRISPR, and genetics training. The student will participate in any ongoing projects focused on modeling genetic diseases in *C. elegans* with the chance to explore innovative CRISPR methods.

Recent publications:

Mimicking of splicing-related retinitis pigmentosa mutations in C. elegans allow drug screens and identification of disease modifiers. Kukhtar D, et al. *Human Molecular Genetics* 2020 doi: 10.1093/hmg/ddz315.

CRISPR editing of *sftb-1*/SF3B1 in Caenorhabditis elegans allows the identification of synthetic interactions with cancer-related mutations and the chemical inhibition of splicing. Serrat X et al,
PLoS Genetics. 2019 Oct 21;15(10):e1008464. doi: 10.1371/journal.pgen.1008464

Efficient Generation of Endogenous Fluorescent Reporters by Nested CRISPR in Caenorhabditis elegans. Vicencio J et al. *Genetics.* 2019 Apr;211(4):1143-1154. doi: 10.1534/genetics.119.301965

Genome editing in animals with minimal PAM CRISPR-Cas9 enzymes. Vicencio et al, BioRxiv 2021.06.06.447255; https://doi.org/10.1101/2021.06.06.447255

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: Understanding stress adaptation

Project supervisor

Name: Eulàlia de Nadal

Mail: eulalia.nadal@irbbarcelona.org; eulalia.nadal@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: Eulàlia de Nadal

Agency: Spanish Government

Reference/ years: Dissecting Stress Adaptation Across Eukaryotes (PGC2018-094136-B-I00). Ministerio de Ciencia, Innovación y Universidades. 2018-2021

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

We aim to unravel how cells detect and respond to environmental changes. We focus our studies on the characterisation of stress signal transduction pathways, especially those regulated by MAP kinases of the Hog1/p38 family, also known as the stress-activated MAP kinases (SAPKs). Proper adaptation to stress involves the modulation of several basic aspects of cell biology, among them the cell cycle and gene expression. Using *S. cerevisiae* budding yeast as a model organism, as well as higher eukaryotic cells, we are dissecting the molecular mechanisms underlying cell response to changes in the extracellular environment and characterising the adaptive responses required for cell survival. Based on our knowledge of signal transduction and using synthetic biology, we also seek to modify cell behaviour to reprogram cell response to specific inputs/stimuli.

Research lines:

- SAPK signalling: Using quantitative data in single cells and mathematical modelling, together with mutational analyses, we study the basic signalling properties of stress-responsive MAP pathways and how to alter them.

- SAPK targets: Using proteomics, biochemistry and genetics, our main goal is to identify new targets for SAPKs and thus widen our understanding of cellular adaptation to stress. This information is expected to facilitate the characterisation of the bases of adaptation in eukaryotes.

- Cell cycle control: SAPKs act in several phases of the cell cycle to allow prompt response to extracellular stimuli and the maintenance of cell integrity. We are uncovering the mechanisms by which Hog1 and p38 SAPKs regulate the cell cycle.

- Regulation of mRNA biogenesis: SAPKs control critical steps of mRNA biogenesis and are thus key regulators of stress-responsive gene expression. Our main aim is to determine the contribution of multiple factors to overall gene expression in response to stress. We are also using genome-wide CRISPR screening to identify essential genes for stress adaptation.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Examining underlying mechanisms of the efficacy of multimodal interventions on life style factors in subjects at risk of dementia: a metabolomics approach to evaluate the gut brain axis

Project supervisor (principal investigator of the laboratory/group)

Name: Rafael de la Torre, PharmD, PhD, rtorre@imim.es and Nieves Pizarro, BsC, PhD, npizarro@imim.es

Webpage of the group:
https://www.imim.cat/programesrecerca/neurociencies/grfh/labrafa/

Institution: Hospital del Mar Medical Research Institute (IMIM), Dr Aiguader 88, 08003 Barcelona

Group name: Integrated Pharmacology and Systems Neurosciences

Main grant associated with this project:

Principal investigator: Rafael de la Torre

Agency: Alzheimer's Association

Reference/ years: 2020-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Subjects exhibiting subjective cognitive decline (SCD) and carriers of the APOE4 allele, are at an increased risk for mild cognitive impairment and dementia. Given the delay between risk exposure and disease onset, SCD individuals are increasingly considered a good target population for cost-effective lifestyle-based Alzheimer's disease prevention trials.

The PENSA study is a randomized, double-blind, controlled clinical trial that aims to evaluate the efficacy of a personalized multimodal intervention in lifestyle (diet counseling, physical activity, cognitive training, and social engagement) combined with the use of epigallocatechin gallate (EGCG) over 12 months, in slowing down cognitive decline and improving brain connectivity.

The master degree practicum will explore the underlying mechanisms that may explain improvements or deceleration in cognitive decline in SCD subjects participating in a multimodal intervention targeting life style habits. Several pathways linking the gut-brain axis will be examined (i.e. kynurenine pathway, short chain fatty acids, TMAO) following a metabolomics analysis approach.

Two biological matrices will be explored: oral fluid (saliva) and feces. Data will be correlated with plasma analysis and cognitive performance of subjects

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Synthetic Biology of Enzymatic Flagellins for Biotechnology and Biomedicine.

Project supervisor (principal investigator of the laboratory/group)

Name: Ulrich Eckhard

eMail: ulrich.eckhard@ibmb.csic.es

Group name: Structural Biotechnology and Proteolysis Lab

Institution: Department of Structural Biology, Institute of Molecular Biology of Barcelona (IBMB-CSIC), Parc Científic de Barcelona, Carrer de Baldiri Reixac, 15, 08028 Barcelona.

Webpage of the group: https://www.ibmb.csic.es/en/department-of-structural-biology-dsb/structural-biotechnology-lab-ulrich-eckhard/ and https://www.ibmb.csic.es/en/department-of-structural-biology-dsb/proteolysis-lab/

Main grant associated with this project:

Principal investigator: Ulrich Eckhard

Agency: Ministerio de Ciencia e Innovación

Reference/ years: RYC2020-029773-I (2022-2025)

Synthetic Biology of Enzymatic Flagellins for Biotechnology and Biomedicine.

We are looking for motivated students for practical work, internships, and master thesis research projects, to work with us on the development of biotechnological and biological applications based on proteolytic flagellins, a recently discovered flagellin protein family with enzymatic activity. Depending on project status, potential work packages may include: molecular cloning, gene editing, recombinant protein expression and purification, biochemical and structural characterization, functional assays, microbial imaging, structural modelling and structure-function analysis, all under the guidance and supervision of an experienced researcher in the lab. Importantly, the lab has a strong commitment to train and mentor students, and to help them take their next steps in their academic and scientific career.

About the lab: We are a research team focusing on the biological impact of enzymatically active flagella, and the possibility to alter their biochemical properties for biotechnological and biomedical applications. We are located at the *Parc Científic de Barcelona*, one of the main life science research hubs in Spain, which hosts not only over 90 companies, but also major research institutes such as the Institute for Research and Biomedicine (IRB), the Institute of BioEngineering of Catalonia (IBEC), and also our institute, the IBMB-CSIC. As part of the Structural Biology Department, we are in close contact with multiple high-profile research teams and have access to state-of-the-art research equipment and facilities, such as the Automated Crystallography Platform for robot-assisted protein crystallization and imaging, and have readily access to the various European Synchrotrons, including ESRF in Grenoble (France), Diamond Light Source in Didcot (UK), or ALBA in Cerdanyola del Vallès. Additionally, as the lab is embedded within the highly collaborative Proteolysis Lab of Prof. Xavier Gomis-Rüth, we fully profit of a well-established and a highly productive research environment.

Candidate specifications: Motivated candidates with a keen interest in Molecular Biology, Microbiology, Biochemistry, Biotechnology, and Biomedicine are encouraged to send their CV directly to Ulrich Eckhard (ulrich.eckhard@ibmb.csic.es). Fluency in English, team spirit, and good communication skills are expected.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Nanotools for super resolution microscopy of the machinery controlling cell growth

Project supervisor (principal investigator of the laboratory/group)
Name: Oriol Gallego
eMail: oriol.gallego@upf.edu
Group name: Live-cell structural biology
Institution: UPF
Webpage of the group: www.gallegolab.org

Main grant associated with this project:
Principal investigator: Oriol Gallego
Agency: Human Frontiers Science Program
Reference/ years: RGP0017, 2020-2022

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Understanding the molecular mechanisms that drive life (and those that lead to death) requires structural characterization of the protein machinery sustaining the biology of the cell, both in a healthy and in a pathological situation. However, the degree of knowledge acquired to improve human health will be determined not only by the precision of the experimental measurements but also by their proximity to a physiological context. This project aims to develop intracellular nanotools to undertake future investigations relevant for biomedicine and to implement structural biology in living cells.

Our group develops advanced methods of fluorescence microscopy that allow the study of macromolecular complexes directly in living cells. For instance, these methods can quantify protein-protein interactions and reconstruct the 3D architecture of protein complexes. We apply this new technology to study the molecular basis that control cell growth. The aim of the project is to develop new genetically-encoded nanotools to boost the power of quantitative fluorescence microscopy. In collaboration with the group of Alex De Marco, at the Monash University (Australia), we will also asses the implementation of these new nanotools in cryo-electron microscopy. During the progression of the project the student will acquire a strong expertise in gene editing tools, advanced light microscopy, image analysis and proteomics. Depending on the student's skills and interest, the project could also involve *in silico* integration of acquired data to model 3D structures of large protein complexes controlling exocytosis.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Strategies to restore or replace insulin production in diabetes.

Project supervisor (principal investigator of the laboratory/group)
Name: Rosa Gasa
eMail: rgasa@clinic.cat
Group name: Translational research in diabetes, lipids and obesity
Institution: IDIBAPS
Webpage of the group: https://www.clinicbarcelona.org/ca/professionals/rosa-gasa?from=research

Main grant associated with this project:
Principal investigator: Rosa Gasa
Agency: Instituto Salud Carlos III
Reference/ years: PI19/00896 (2020-2022)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Diabetes is characterized by an absolute (type 1 diabetes) or relative (type 2 diabetes) deficit in functional beta cell mass. Hence, regeneration and replacement of beta cells have been postulated as promising strategies to prevent and/or delay the onset or even reverse overt diabetes. One approach is to stimulate proliferation of remaining beta cells. In this line, we seek to identify extrinsic and intrinsic factors that govern beta cell proliferation during organismal postnatal life, both under physiological and pathophysiological conditions.

On the other hand, donor islet transplantation has been quite successful in providing temporary insulin independence in type 1 diabetes patients. However, donor islet scarcity makes this strategy non-viable as a broad treatment option. In this area, we seek to develop cellular reprogramming protocols to generate substitute insulin-producing cells from other somatic cell types

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: "Identification of NON-coding variants important for the development of T-cell acute lymphoblastic leukemia (T-ALL)"

Project supervisor (principal investigator of the laboratory/group)

Eulàlia Genescà-PhD
ALL Research Group
Josep Carreras Leukaemia Research Institute (IJC)
Carretera de Canyet s/n, camí de les escoles. Edifici IMPPC
08916, Badalona (Barcelona), SPAIN.
Tel: +(34) 93 557 28 08/ + (34) 93557 28 07
egenesca@carrerasresearch.org
http://www.carrerasresearch.org/ca/acute-lymphoblastic-leukemia-all-_3726 (web page needs to be updated)

Main grant associated with this project:
Principal investigator: Eulàlia Genescà
Agency: ISCIII
Reference/ years: PI19/01828 and PI19/01183, period: 2020-2022+ 2023
Renewal of the project-period: 2023-2025

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

ALL is characterized by a multistep oncogenic process leading to maturation arrest and malignant transformation of lymphoid hematopoietic precursors. T-ALL is the less common and the most complex and heterogeneous at the genetic level ALL subtype. Data generated over twenty years of genomics in T-ALL highlight the importance of using genetic techniques with high resolution in order to detect cryptic aberrations present in T-ALL and define primary genetic events that will determine acquisition of secondary genetic event necessary to transform T-cell progenitors, explaining the particular onco-genetic process in each T-ALL leukemia. Genetics plays a key role in the development of T-ALL and also has prognostic value. However, in some T-ALL leukemias no primary events have been identified although an aberrant expression of T-ALL driving transcription factors (TF) is observed. In those cases, it is feasible to argue that alterations in regulatory regions and/or in enhancers of the TFs can contribute to alter their expression.

Goal

The main goal of this project is to explore non-coding data generated in the laboratory applying cutting-edge genomic techniques such as: whole genome sequencing (WGS) and target deep sequencing (TDS), to identify point mutations and indels, and SNPa and optical genome mapping (OGM), to detect structural variants that will contribute to the development of T-ALL and/or have prognostic value.
For that we will do the following steps:

1. Identify non-coding variants with potential implication in T-ALL:
- **1.1** From NGS data
- **1.2** From structural data

2. Assess the relevance of identified variants in T-ALL
- **2.1** Functional experiments
- **2.2.** Clinical correlations

Methods

1. Analysis of NGS data and structural data provided by WGS; SNPa and OGM
2. Statistical analysis
3. Functional experiments in cell lines and in immunodeficient mice

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: ***Molecular analysis of proteins of biomedical or biotechnological 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 Lab

Department of Structural Biology

Barcelona Science Parc, Helix Building

C/ Baldiri Reixac,15-21

08028 Barcelona

Tel. 934020186 / Fax. 934034979 / e-mail. xgrcri@ibmb.csic.es / https://www.ibmb.csic.es/proteolysis

Main grant associated with this project: PID19-107725RG-00I

Principal investigator: F. Xavier Gomis-Rüth

Agency: State Research Agency (AEI), Ministry of Science and Innovation

Reference/ years: 2020-2023

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

The research group is centered on the study of proteins involved in host-microbiome interactions, including microbial virulence factors and antibiotic resistance determinants, as well as potential therapeutic targets. Such 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 an experienced member 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. This work could be continued within the frame of a Ph.D. thesis.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title

Precise RNA-based gene writing in mammalian genomes

Project supervisor
Marc Güell
Tenure Track Professor
Pompeu Fabra University

Web: http://synbio.upf.edu
Mail: marc.guell@upf.edu
Address:
PRBB – Room 704
C/. Dr. Aiguader 88
08003 – Barcelona

Main grant associated with this project:
Principal investigator: Marc Güell
Agency: Agencia Estatal de Investigación
Reference/ years: **PID2020-118597RB-I00 (2020-2022)**

Summary of project summary or current research lines

Our laboratory is focused on applied synthetic biology for therapeutic purposes. We recently developed FiCAT, a DNA-based gene writing methodology combining the precision of CRISPR and gene transfer capacity of transposases (Pallarès-Masmitjà et al, Nature Communications 2021). This DNA writing technology has provided an efficient tool for gene therapy applications which will be pushed to the clinic by the recently created spin off Integra Therapeutics (https://www.integra-tx.com/). FiCAT still requires CRISPR double stranded breaks and DNA as a template, we are now focused into developing a future technology of gene writing based on RNA and absent double stranded breaks which is inspired from retroviruses and retrotransposons. We are offering a project to develop new RNA-based gene writing technologies. The project will consist in leveraging reverse transcriptases, CRISPR systems and other retroelement components to achieve message writing in precise locations of mammalian genomes.

Project Title

Developing sensor circuits embedded in the skin microbiome

Project supervisor
Marc Güell
Tenure Track Professor
Pompeu Fabra University

Web: http://synbio.upf.edu
Mail: marc.guell@upf.edu
Address:
PRBB – Room 704
C/. Dr. Aiguader 88
08003 - Barcelona

Main grant associated with this project:
Principal investigator: Marc Güell
Agency: **ONR, DARPA - US Government**
Reference/ years: **N629092012086 (2020-2022)**

Summary of project summary or current research lines

Our laboratory is focused on applied synthetic biology for therapeutic purposes. We have had long term interest in engineering the skin microbiome. We described the first in vivo modulation of the skin microbiome composition using life bacteria (Paetzold et al, Microbiome 2019). This technology enabled the creation of the company Sbiomedic (https://www.sbiomedic.com/) who launched clinical trials on acne (Karoglan et al, Acta Dermato-Venereologica 2019) and is working in multiple indications. Specifically, Cutibacterium acnes, one of the skin microbes, has proven an excellent platform for engineering showing high engraftment power and safety. At the UPF lab, we are offering a master position in developing skin probiotics with advanced functionalities. Specifically, we are equipping skin microbes with sensing circuits and therapeutic circuits to create novel advanced therapeutics. Besides the acne indication we are working on body monitoring, hair loss and mosquito repellant.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Role of cannabinoid system in pulmonary fibrosis

Project supervisor (principal investigator of the laboratory/group)
Name: Raquel Guillamat Prats
eMail: rguillamat@igtp.cat
Group name: Lung Immunity Translational Research
Institution:
Webpage of the group: http://www.germanstrias.org/

Main grant associated with this project:
Principal investigator: Raquel Guillamat Prats
Agency: Instituto de Salud Carlos IIII (ISCIII)
Reference/ years: CP20/00133 (March 2021 to February 2026)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Idiopathic pulmonary fibrosis (IPF) is a chronic, progressive, fatal disease of unknown ethology, which equally affects men and women. It presents as a progressive worsening of dyspnoea and lung function and is associated with a poor prognosis with a median survival time of 3 to 5 years from the time of diagnosis and the five-year survival rate lies between 20% and 40%. There is no effective pharmacologic therapy for IPF, despite the recent approval of pirfenidone and nintedanib. Although these newer drugs have shown some efficacy, the poor prognosis of IPF remains unchanged. Moreover, surgical therapy with lung transplantation is only available for a small minority of patients. A challenge for biomedical research is the development of more efficient therapies.

Previous studies described pro-fibrotic effects of cannabinoid CB1 receptor and anti-fibrotic effects of CB2 receptor in pathophysiological conditions affecting liver, kidney and cardiovascular system. These receptors are activated by endogenous lipids called endocannabinoids. We hypothesize a pathophysiological implication of endocannabinoid signalling via CB1 and CB2 in IPF and propose the use of cannabinoid drugs as therapeutic agents to treat IPF. It is of crucial importance to investigate in detail the cell-specific effects of both cannabinoid receptors.

The proposal raises four key questions:

(1) Is endocannabinoid signalling involved in the activation of fibroblasts and their differentiation to myofibroblasts?

(2) Are CB1 and CB2 regulating macrophage polarization during pulmonary fibrosis?

(3) Does genetic deficiency of endocannabinoid receptors affect fibrosis development?

(4) Can we use a pharmacological drug blocking CB1 (CB1 antagonist) or activating CB2 (CB2 agonist), respectively, as a treatment for IPF?

The multidisciplinary approach will advance our current understanding of the pathology of IPF and development of more efficient and specific therapies targeting the endocannabinoid system.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: Mitochondrial metabolism and aging

Project supervisor:

Elena Hidalgo / Montse Vega
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: 2019-2022

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 related to:

(i) study cellular processes linked to healthy aging;
(ii) selection of fission yeast strains with altered lifespan;
(iii) characterization of the selected mutants, especially regarding mitochondrial homeostasis.

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:

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. 29:981.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Dynamics of stem cell surveillance in live embryos using quantitative imaging

Project supervisor (principal investigator of the laboratory/group)
Name: Esteban Hoijman
eMail: hoijman@ub.edu
Group name: Embryonic Cell Bioimaging
Institution: Program of Regenerative Medicine, IDIBELL-University of Barcelona
Webpage of the group: www.embryobioimaging.com

Main grant associated with this project:
Principal investigator: Esteban Hoijman
Agency: Spanish Ministry of Science and Innovation
Reference/ years: 2021-2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Errors in stem cells are considered the main cause of human preimplantation failures. In our group we study how early embryos can recover homeostasis by self-healing, before the formation of the immune system. We recently discovered an epithelial phagocytic program able to detect and remove defective stem cells (Nature 2021, www.nature.com/articles/s41586-021-03200-3). Using quantitative imaging of live embryos, we study single cells dynamics during tissue repair. In this project we want to elucidate the signals and mechanics regulating this protective program of the embryo, with the long-term aim of improving embryo survival.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Elucidating the cellular processes that are critical for p53 mediated tumour suppression

Project supervisor (principal investigator of the laboratory/group)
Name: Ana Janic
eMail: ana.janic@upf.edu
Group name: Cancer Biology
Institution: DCEXS-UPF: https://www.upf.edu/web/cancer-biology/

Main grant associated with this project:
Principal investigator: Ana Janic
Agency: **Obra Social Fundación la Caixa. Captació de Talent Investigador.**
Reference/ years: 01/01/2019-31/12/2021

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Mechanisms critical for tumor suppression downstream of p53 remain largely unexplored, despite their great interest for cancer biology. Recent studies, including ours, have challenged the significance of classical p53 downstream functions (of apoptotic cell death, cell cycle arrest, and cell senescence) in tumor suppression. Our hypothesis is that the p53-mediated tumour suppression relies on collective and cooperative activation of the p53 target gene network. Genetic screens and genetical modified mouse models have provided useful tools for revealing the importance of numerous p53-mediated target genes and biological functions to tumour suppression that comprise a cooperative tumour suppression network downstream of p53. The relative importance of different target genes downstream of p53 could vary based on context, such as the cell type, mutational landscape or stress placed on the cell. Different components of the p53 pathway might also have distinct roles in tumour suppression depending on whether p53 is acting to suppress spontaneous cancer initiation or cancer progression in the context of oncogenic drivers. The E3-ubiquitin ligase RNF was the most potent hits from our screens. Understanding the mechanisms, by which RNF act in healthy and cancer cells, and how mediates its tumour suppressive function is the major focus of this master project.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: From *Drosophila* development to human disease

Project supervisor (principal investigator of the laboratory/group)

Name: Gerardo Jiménez

eMail: gjcbmc@ibmb.csic.es

Group name: Gene expression and signaling

Institution: Institut de Biologia Molecular de Barcelona (CSIC), ICREA

Webpage of the group:

http://www.ibmb.csic.es/groups/gene-expression-and-signaling

https://www.icrea.cat/Web/ScientificStaff/gerardo-jimenez--canero-307

Main grant associated with this project:

Principal investigator: Gerardo Jiménez

Agency: Ministerio de Ciencia e Innovación

Reference/ years: PID2020-119248GB-I00 (2021-2024)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

During animal development, the formation of tissues, organs and actually all body structures is under strict control by signaling pathways, transcription factors and effector genes. We are investigating these regulatory processes using the fruit fly *Drosophila*, a powerful experimental model for genetic and molecular analyses. We are particularly interested in the Ras-MAPK signaling pathway and in mechanisms of transcriptional repression, which we are studying by focusing on highly conserved molecules that are also implicated in human diseases, including cancer. The student will be exposed to these projects and the use of advanced technologies such as CRISPR-Cas9 and confocal microscopy. See our web pages for further details.

We welcome applications from highly qualified students with a bachelor degree in Biology, Biochemistry or a related area. Ideally, candidates should have an average score above 2.5/4.0 (8.25/10) and be strongly motivated to do a PhD.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: **Role of human histone H1 variants in cell proliferation, gene expression and cancer progression**

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. Molecular Genomics

Webpage of the group: https://www.ibmb.csic.es/en/department-of-molecular-genomics-dmg/chromatin-regulation-of-human-and-viral-gene-expression/

Main grant associated with this project:

Principal investigator: Albert Jordan

Agency: Ministerio de Ciencia e Innovación – Plan Nacional BFU

Reference/ years: PID2020-112783GB-C21 (2021-24)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

We focus our research on the control of gene expression in human cells by chromatin organization, components and modifications. The degree of compaction of chromatin affecting a gene promoter dictates accessibility to transcription factors and RNA polymerase, and many chromatin modifying enzyme families act to overcome difficulties imposed by chromatin. DNA repeats and satellites immersed in heterochromatin are also regulated by these factors.

We investigate the role and specificity of histone H1 variants in chromatin organization and gene expression control. By RNA interference of the different human H1 variants we have found that they have different involvement in cellular processes such as cell cycle progression and gene expression. We have also described a differential role of H1 variants in pluripotency and differentiation. Currently, we are investigating the occupancy of H1 variants genome-wide by ChIP-seq (NGS) and the consequences of altering H1 levels on chromatin organization (ATAC-seq, DNA methylation, chromosome conformation-HiC, etc), with an extensive use of Genomics and Bioinformatics. Additionally, we are performing proteomics of H1 variant specific protein complexes in chromatin and nucleoplasm.

More recently we have found that depletion of multiple H1 variants in breast cancer cells induces the interferon response as a consequence of derepression of ERVs and satellites. We will investigate whether this also occurs in melanoma cells and this could help immunotherapy to fight cancer cells.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Fighting the Resistance: Visible Light Photoswtichable Antibiotics

Project supervisor (principal investigator of the laboratory/group)
Name: Xavier Just Baringo
eMail: Xavier.just@ub.edu
Group name: Just-Baringo Chem
Institution: Universitat de Barcelona
Webpage of the group: http://justbaringochem.org

Main grant associated with this project:
Principal investigator: Mercedes Amat
Agency: Ministeri de Ciència, Innovació i Universitats
Reference/ years: RTI2018-093974-B-I00 (2018-2020)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Antibiotic resistance is one of the major healthcare issues that humankind is facing at present and is becoming a growing concern as current therapies become inefficient against resistant strains.[1] Discovering new classes of antibiotics that aim at new molecular targets can be helpful; however, these will eventually face the same fate as microbes become resistant to them due to their accumulation in the environment. Thus, ***a novel approach that changes the paradigm on how we fight against bacterial infections is on high demand.***

Photopharmacology has recently appeared as a unique way of turning drugs on and off using light. ***Switching antibiotics off after their therapeutic use will render them inactive to highly diminish the chances of resistance appearing as their accumulation in the environment does not increase the evolutionary pressure on bacteria.*** Most approaches to photoswitchable drugs rely on the use of azobenzenes, which require the use of harmful UV light for their activation. However, these can be modified to cause a red-shift that allows ***activation with visible light that does not harm tissues and can penetrate deeper than shorter wavelengths***.

The introduction of photoswitch CEBA has allowed us to ***modulate the antimicrobial activity of tyrocidine A analogues using exclusively visible light***, granting spatiotemporal control under benign conditions.[3] Compounds bearing this photoswitchable amino acid become active upon irradiation with red light, but quickly turn off upon exposure to other visible light wavelengths. Critically, sunlight quickly triggers isomerisation of the red light-activated compounds into their original trans isomer, offering an ideal platform for self-deactivation upon release into the environment. Linear analogues of tyrocidine A were found to provide the best photocontrol of their antimicrobial activity, leading to ***compounds active against Acinetobacter baumannii or Streptococus pyogenes upon isomerisation***.

The student will join a ***multidisciplinary project*** to work on ongoing research than covers most stages of drug design and development, as well as state-of-the-art photoswitches currently being developed in the group, which can be used as a ***platform to develop several biomedical tools***.

References:

1. Theuretzbacher, U.; Outterson, K.; Engel, A.; Karlén, A. *Nat. Rev. Microbiol.* **2020**, *18*, 275.
2. a) Liu, Y.; Li, R.; Xiao, X.; Z. Wang, *Crit. Rev. Microbiol.* **2019**, 45, 301; b) C.-H. Huang, Y.-H. Hsieh, Z. M. Powers, C.-Y. Kao*, Int. J. Mol. Sci.* **2020**, *21*, 1061.
3. Just-Baringo, X.; Yeste-Vázquez, A.; Moreno-Morales, J.; Ballesté-Delpierre, C.; Vila, J.; Giralt, E. *Chem. Eur, J.* **2021**, *27*, 12987.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title:
HARNESSING INFLAMMATORY PATHWAYS IN ANTITUMOR IMMUNE INTERVENTION

Project supervisor (principal investigator of the laboratory)
Name: Cristina Lopez-Rodriguez
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Group name: GENIMMUNE
Institution: Universitat Pompeu Fabra, department of Experimental and Health Sciences
Webpage of the group: https://www.upf.edu/web/genimmune
https://www.upf.edu/web/biomed/entry/-/-/23934/adscripcion/cristina-lopez-rodriguez

Main grant associated with this project:
Principal investigator: Cristina Lopez-Rodriguez and Jose Aramburu
Agency: Plan Estatal I+D+i (MINECO, FEDER, EU); Worldwide Cancer Research United Kigdon
Reference/ years: RTI2018-095902-B-I00 and PID2021-128721OB-I00 (2019-2024); WWCR UK: 20-0144 (2020-2023)

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

Alterations in immune functions not only impair our organism defenses to pathogens but also underlie diseases such as cancer, neurodegenerative, cardiovascular and metabolic disorders. We focus our work on transcription regulators that control innate and adaptive immunity in different scenarios, such as inflammation, transplant rejection, tumor progression and viral infection. By uncovering circuits that tune different immune cell functions, our work can guide innovative approaches that improve antitumor immunotherapy and anti-pathogen defense.

We offer a master position in a project based on our recent identification of a unique transcription mechanism that, while promoting other inflammatory responses, limits type I interferon (IFN-I) expression to control antiviral responses and preserve hematopoietic stem cell (HSC) function (Huerga Encabo et al. 2020 J Exp Med). Natural IFN-I-repressive mechanisms are necessary since an excess of IFN-I can compromise key systems such as the regeneration of hematopoietic stem cells and certain antimicrobial defenses. On the other hand, IFN-I can induce cancer cell senescence and antitumor immunity, so enhancing these responses could be applied to improve anticancer immunotherapy.

In this project, we will apply our experience with tumor mouse models, gene-edited mice, and cutting-edge molecular and cellular biology techniques, to identify new mechanisms that can push the boundaries of IFN-I and other inflammatory responses, to boost antitumor immunity by enhancing tumor detection by immune cells and also by promoting cancer cell senescence.

Leading recent publications of the group:

Lunazzi et al., 2021 Journal of Immunology
Huerga Encabo et al., 2020 Journal of Experimental Medicine
Aramburu and López-Rodríguez, 2019 Frontiers in Immunology
Buxadé et al., 2018 Journal of Experimental Medicine
Tellechea et al., 2018 Journal of Immunology
Aramburu et al., 2014 Science Signaling
Berga-Bolaños et al., 2013 Proc Natl Acad Sci USA

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Formation and roles of microtubules in iPSC-derived neural stem cells.

Project supervisor (principal investigator of the laboratory/group)
Name: Jens Luders
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Group name: Microtubule Organization Group
Institution: IRB Barcelona
Webpage of the group:
www.microtubul.es
www.irbbarcelona.org/research/microtubule-organization

Main grant associated with this project:
Principal investigator: Jens Luders
Agency: MICINN
Reference/ years: 2022-2025

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

A process that strongly depends on the proper organization of the microtubule network is neural development. In the neuroepithelium highly polarized neural progenitor cells are vertically aligned, extending a basal process that contacts the basal lamina, and an apical process with a centrosome that is localized underneath the apical membrane. Most microtubules are arranged as an apico-basal array, and only a subset of microtubules seems to originate from the centrosome, the main microtubule organizing center. We hypothesize that generation of the microtubule network in these cells requires both centrosomal and non-centrosomal factors. In this project we will (i) characterize candidate factors for nucleating interphase microtubules, and (ii) probe the roles of these factors in highly polarized neural progenitors including their contribution to cell and tissue integrity. For this we will employ genome editing and advanced microscopic imaging of polarized progenitors in fixed and live neuroepithelium-like neural rosettes obtained by differentiation of human iPSCs in vitro.
This project will explore fundamental questions at the interface of cell biology and development, namely how non-mitotic microtubule arrays are established and how they contribute to tissue formation and integrity. These questions are also relevant in the context of disease, since defects in the microtubule cytoskeleton have been linked to various neurodevelopmental disorders.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: The insect insulin receptors tangle

Project supervisor (principal investigator of the laboratory/group)

Name: José Luis Maestro

Mail: joseluis.maestro@ibe.upf-csic.es

Group name: Nutritional signals in insects

Institution: Institute of Evolutionary Biology (CSIC-UPF)

Webpage of the group: http://www.biologiaevolutiva.org/jmaestro/

Main grant associated with this project:

Principal investigator: José Luis Maestro and Xavier Bellés

Agency: Agencia estatal de investigación. Ministerio de ciencia e innovación.

Reference/ years: PID2019-104483GB-I00 (june 2020 – may 2023)

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The projects that we are carrying out in our laboratory are related to the study of the functions of the insulin pathway in insects, in particular in processes related to reproduction, development and growth. It has recently been described that insects have two insulin receptors (InR) and that in some evolutionary lineages, such as that of cockroaches and nearby groups, a third InR has been acquired. The present project is directed to the study of the functions of the different InRs in the German cockroach, *Blattella germanica*. This is a very common domestic pest with which our group have been working for decades and for which a large amount of information (including transcriptomes generated in the group or the sequenced genome produced also with our contribution), and tools (we have found that it is very sensitive to the interfering RNA (RNAi), which is extremely useful for functional genomics studies), are available. We will pay especial attention in the analysis of the function of the new InR that appeared in this evolutionary line and the possible evolutionary fate of this new molecule: non-functionalization, subfunctionalization or neofunctionalization.

Some of the methodologies that will be used are:

-RNAi methodologies, which include cloning, synthesis of dsRNA and treatment of the animals, etc.

-Expression studies in different treatments and physiological conditions: tissue dissections, RNA extraction, cDNA synthesis and real time-quantitative PCR.

-Microscopy techniques.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Involvement of the insula in the Autism neurodevelopmental disorder

Project supervisor (principal investigator of the laboratory/group)

Name: Rafael Maldonado

eMail: Rafael.maldonado@upf.edu

Group name: Neuropharmacology

Institution: Universitat Pompeu Fabra

Webpage of the group: http://www.upf.edu/neurophar/

Main grant associated with this project:

Principal investigator: Elena Martín García

Agency: ERANET

Reference/ years: 2022-2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

We will explore the pathophysiological mechanisms underlying autism spectrum disorder (ASD). ASD is a multifactorial complex disorder involving multiple genes, environmental factors, and the interaction among these factors. We will focus our attention on the involvement of a neuromodulatory system, the endogenous cannabinoid system, in specific cell types of a crucial brain region that represents a hub of communications, the insular cortex. We will use a well-recognized genetic mouse model of ASD, the deletion of the Shank3 gene, and several complementary experimental approaches: additional genetic mouse models, behavioral and electrophysiological techniques, viral vector strategies to express and delete some genes in specific cell types in the brain, strategies to investigate the use and the transformation of energy at the cellular level and human cerebral organoids. These techniques will provide important information to clarify the specific mechanisms underlying ASD.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Bioinformatics of stop codon readthrough

Project supervisor (principal investigator of the laboratory/group)

Name:	Marco Mariotti
eMail:	marco.mariotti@ub.edu
Group name:	Comparative Genomics and Recoding lab
Institution:	Universitat de Barcelona
Webpage of the group:	https://www.mariottigenomicslab.com/

Main grant associated with this project:

Principal investigator:	Marco Mariotti
Agency:	Spanish Ministry of Science, Innovation and Universities
Reference/ years:	Proyectos de I+D+I PID2020-115122GA-I00 2021/2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Our lab employs comparative genomics approaches to study the mechanisms of gene expression and protein synthesis. We focus on programmed exceptions to the genetic code, known as “translational recoding”. In particular, we currently study stop codon readthrough, a phenomenon wherein certain stop codons are recoded to support amino acid insertion instead of causing termination. A remarkable example of readthrough is the insertion of selenocysteine, encoded by UGA (a stop codon). This special amino acid has unique biochemical properties, and it is located in the catalytic site of essential oxidoreductase enzymes in human and many other species. Specific sequence elements are located in the genes that encode for selenocysteine, functioning as signals to recode their internal UGA codon. Defects in selenocysteine encoding, either in these genes or in the pathway to synthesize and insert selenocysteine, result in various defects and diseases.

Stop codon readthrough presents a challenge for gene annotation. Due to the non-canonical meaning of stop codons, these cases are typically missed in public databases. In the lab, we work to identify cases of readthrough and understand their function, mechanism, and evolution.

The student in our group would work primarily in bioinformatics. They would analyse high-throughput data (RNAseq, Riboseq, Mass Spec) and evolutionary patterns (multiple sequence alignments) to discover and characterize cases of readthrough. The project has synergy with the experimental strategies currently developed in our lab to verify readthrough candidates, so that possible candidates emerging from the analysis may be later tested.

Call for project proposals, master in Biomedical Research practicum, 2023, UPF

Project Title: **Regeneration versus Tumor formation in Drosophila Imaginal Discs**

Project supervisor (principal investigator of the laboratory)
Name: Enrique Martín-Blanco
Mail: embbmc@ibmb.csic.es
Group name: Morphogenesis Mechanics Lab
Institution: Instituto de Biologia Molecular de Barcelona
Webpage of the group: http://www.ibmb.csic.es/groups/signalling-events-controlling-cell-migration-during-morphogenesis

Main grant associated with this project: Biomechanics of Morphogenesis: from Health to Disease.
Principal investigator: Enrique Martin-Blanco
Agency: Ministerio de Ciencia e Innovación
Reference/ years: PID2020-116273GB-I00, 2021/2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

In *Drosophila* there are well-established protocols for inducing regeneration. We took advantage of this methods to investigate if we could generate overgrowths/tumors, just by repeatedly killing and letting regenerate the *Drosophila* wing imaginal disc. We found that a death induction/regeneration protocol repeated several times results in neoplastic growth. Importantly, tissue overgrowths were not restricted to the targeted area and resulted from uncontrolled and unpatterned proliferation. Overgrowths show landmarks of tumorigenic cells and tumorigenic properties: strong ectopic expression of mitogens [Wingless (Wg)]; derangement of the basal membrane; macrophages recruitment; and loss of apico basal polarity. Preliminary data also show a loss of DNA repair capability. All in all, we have established a reliable model for the analysis of the relationships between tissue repair/regeneration and tumor formation.
The offered master project will focus in the analysis and characterization of single cell responses during regeneration vs tumorogenesis. We will explore, through genetic interference and in vivo visualization, potential conflicts between death instructions, DNA integrity surveillance and proliferative demand, as the potential causes of neoplastic transformation. Single Cell RNA seq analyses to compare regenerative and neoplastic growth will be performed in collaboration with the laboratory of Dr. Michael Boutros (DKFZ, Heidelberg, Germany).

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Genome – Phenome Analyses: From Populations to Phylogenies

Project supervisor (principal investigator of the laboratory/group)
Name: Arcadi Navarro
eMail: arcadi.navarro@upf.edu
Group name: Comparative & Evolutionary Genomics
Institution: UPF (IBE – DCEXS)
Webpage of the group: https://www.upf.edu/web/evolutionary-genomics-lab

Main grant associated with this project:
Principal Investigator: Arcadi Navarro
Agency: Dirección General de Investigación Científica y Técnica – DGICYT /// Instituto de Salud Carlos III
Reference/ years: PGC2018-101927-B-I00 / 2020-2022 /// Infraestructura de Medicina de Precisión asociada a la Ciencia y Tecnología (IMPaCT) de la Acción Estratégica en Salud 2017-2020

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The highly polygenic architecture of human traits, including complex diseases and phenotypes of relevant personal, medical, and social implications, such as longevity, suggests research approaches that recognize them as the result of complex dynamic systems that are the results of millions of years of evolution. Our group carries out two lines of research related to such complex phenotypes.

First, all these complex traits and diseases are highly intertwined and present large genetic overlap with each other (that is, there are strong genetic correlations among different conditions and phenotypes). While there have been some notable efforts on understanding the genetic architecture of human disease and its relationship to anthropometric, socioeconomic and neuropsychiatric traits, including our own studies linking antagonistic pleiotropies between early- and late-onset diseases with human aging patterns [PMID: 28812720, PMID: 31235924, PMID: 29788292], a comprehensive cross-trait analysis is still needed, and we are intensely working on it.

Second, the study of the genetic architecture of complex traits and diseases has focused, for more than 15 years, on the search for associations between genetic variation and phenotypic differences across individuals of the same species, with Genome-Wide Association Studies (GWAS) in humans as the flagship method. In recent years, however, the quest to stablish links between genomes and phenomes has been disrupted by comparative genomic approaches, including results on longevity by our own group [PMID: 29788292, PMID: 34297086]. The main advantages of large-scale comparative genomics are that (i) it affords the opportunity of focusing on the complex traits themselves (including their presence or absence in some species) rather than on relatively subtle within-species differences in each trait; and that (ii) it leverages the enormous amount of variability (both genomic and phenotypic) accumulated along evolution. We develop our own methods and apply them to variety of phenotypes relevant to human disease and evolution.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Generating Patient Registries and understanding the pathogenesis of Myotonic Dystrophy 1 trough cellular models.

Project supervisor (principal investigator of the laboratory)

Name: Gisela Nogales Gadea

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Group name: Neuromuscular Neuropediatrics Research Team

Institution: Germans Trias i Pujol Research Institute

Webpage of the group: http://www.germanstrias.org/research/neurociencias/5/investigacion-neuromuscular-y-neuropediatrica

Main grant associated with this project: DIMINUTES, Childhood and adult myotonic dystrophy: evaluation of new treatments and pathogenicity through genetic, epigenetic and molecular imaging analysis

Principal investigator: Gisela Nogales Gadea

Agency: ISCIII

Reference/ years: PI18/00713/2019-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Myotonic dystrophies (DM) are rare diseases with multiple organ involvement. Type I DM (DM1) can appear at any age, with pediatric forms being less frequent and more severe. These infant forms are devastating and have no treatment. Early onset is conditioned by the length of the CTG gene expansion -the greater the expansion, the earlier the onset- although this only explains 60% of DM1 cases and epigenetics could also influence. In addition, the number of toxic RNAs, derived from the CTG expansion, is unknown. Antisense oligonucleotides are a therapy under study, but have been little used in childhood DM1. The DIMINUTES project will generate new knowledge about DM1 pathogenicity, diagnose new DM cases and evaluate new treatments in pediatric DM1 patients, largely forgotten in these studies. The objectives are: 1) To carry out a clinical and genetic registry of pediatric DM1 patients and adults; 2) Characterize the genetics and epigenetics of pediatric and adult DM1; 3) Analyze the quantity and size of the toxic RNA. The methodology used includes multiple techniques of genetic, epigenetic, protein and RNA analysis, and molecular imaging.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Characterization of RNA binding proteins as neurogenesis regulators

Project supervisor (principal investigator of the laboratory/group)
Name: Mireya Plass
eMail: mplass@idibell.cat
Group name: Gene Regulation of Cell Identity
Institution: Bellvitge Biomedical research Institute
Webpage of the group: https://p-cmrc.cat/research/plass-group/

Main grant associated with this project:
Principal investigator: Mireya Plass
Agency: Ministerio de Ciencia, Innovación y Universidades
Reference/ years: PID2019-108580RA-I00 / 2020-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The high and complex diversity of neurons in the brain results from a tightly regulated process called neurogenesis. Although this process occurs mainly during embryonic development, it is also relevant in adulthood and is related to the development of neurodegenerative diseases. Our group is interested in understanding how neurogenesis is regulated in humans and, in particular, what the role of RNA binding proteins (RBPs) is in this process. For that purpose, we use a combination of high-throughput single-cell transcriptomics, computational methods and classic molecular biology methods to investigate the function RBPs in the differentiation and maturation of neurons from stem cells. Currently, we have generated single-cell transcriptomics data to characterize how neurogenesis happens in vitro and identify putative RBPs important in the process. The main objective of this project will be to investigate the role of one of the identified RBP during the differentiation of induced pluripotent stem cells (iPSCs) to neurons. The candidate will have the opportunity to learn cutting-edge technologies such as CRISPR/Cas9, to KO the expression of the RBP, and iPSC cell culture. The effect of the RBP on neural differentiation will be evaluated using conventional molecular biology approaches (immunohistochemestry, qPCR) as well as with single-cell transcriptomics.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: **Gene Regulation in Stem Cells, Cell Differentiation & Cancer**

Antonio Postigo
ICREA Professor
Group of Gene Regulation in Stem Cells, Cell Plasticity, Differentiation, and Cancer
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IDIBAPS -- https://bit.ly/3HsFmSJ
Twitter: @GeneRegLab

Summary of project summary or current research lines

The Gene Regulation Lab is looking for a motivated MSc student to work in the area of "Gene Regulation of Stem Cells, Cell Differentiation, and Cancer". ZEB1 and ZEB2 play key roles in both homeostasis and in different pathologies. The MSc student will have the opportunity to work in one of the several projects currently ongoing in the lab. Available projects include the study of the mechanisms regulating gene expression in stemness (normal and cancer stem cells), cellular plasticity and differentiation, inflammation, tissue regeneration, and tumor initiation and progression. The project make use a wide array of in vitro and in vivo approaches including unique transgenic mouse models and high throughput techniques (RNAseq, ChIPseq, metabolomics).

See the following three (3) links for additional information: https://bit.ly/34r2VXT / https://bit.ly/3HsFmSJ / https://bit.ly/3Jc4HAC for additional details

Requirements: BSc in Biology, Biotechnology or in any other biomedical-related discipline. Candidates with a good academic record (higher than 8.4/10), previous lab experience, and/or interested in pursuing later a PhD will receive special consideration in the selection process.

Recent Publications by the Group (as corresponding author): ***Science Advances.*** 7:abd7455 (Impact Factor: 14.1); ***Nature Commun*** 10:1364 (Impact Factor 14.9); ***Nature Commun***. 9:2424 (IF 12.2); ***Nature Commun***. 4:2650 (IF 14.9); ***Nature Commun***. 5:5660 (IF 14.9); ***Gut*** 68:2129 (IF: 23.0); ***Gut*** 66:666 (IF 23.0); ***Nucleic Acids Res*** 46:10697 (IF: 11.6), ***Nucleic Acids Res*** 46:1069 (IF:16.9) ***Cell Death Differ*** 21:247 (IF:15.8); ***EMBO J*** 36:3336 (IF 12.7); ***Clin Cancer Res*** 19:1071 (IF 12.1),

Information. To obtain additional information and/or to set up a visit to the laboratory, please send CV and the names and contact details of 2-3 researchers that have supervised the candidate during the BSc to **idibaps.postigo3@gmail.com** indicating "**Master UPF 2022-2023** " in the subject of the email.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: The Contribution of Human-Acquired Centrosome-Cilia Genes in Normal and Pathological Neural Development

Project supervisor (principal investigator of the laboratory/group)
Name: Murielle
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Group name: Development of the Nervous System in health and disease
Institution: IBMB-CSIC
Webpage of the group: https://www.ibmb.csic.es/en/department-of-developmental-biologyddb/development-of-spinal-cord-in-health-and-disease/
Main grant associated with this project:
Principal investigator: Murielle Saade
Agency: Spanish ministry of Economy, Industry and Competitiveness.
Reference/ years: RYC2018-025379-I/ 1/2020-1/2025.

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

The centrosome is a non-membranous cellular organelle, involved in key functions during brain development, where it acts to regulate processes such as; cell division, cilia formation, and cell migration. While many mutations in centrosome-associated proteins lead to diseases, often predominantly affecting the brain, the basis for this specificity is in most cases not known. Recent discoveries have revealed a potential link of human specific genes enriched in neural precursor cells with the centrosome/cilia axis and the 1q21.1 syndrome, a neurodevelopmental disorder (NDD) associated to abnormalities in head size and mental pathologies. In fact, the ch1q21 region contains a disproportionate number of genes that are ‘human-specific’ and that have arisen by evolutionary genetic mutations known as segmental duplications (SD) in the last million years. This provides a unique opportunity to: 1/ Assess the impact of structural variations (SVs) on human brain development investigating the association among the spectrum of genomic pathogenic SV and clinical manifestations of 1q21.1 NDD by developing patient-specific 3D brain organoids. 2/ Dissect the cellular mechanisms associated with the 1q21 human-specific genes at the centrosome/cilia axis. 3/ Interrogate the contribution of 1q21 human-specific genes in the evolutionary expansion of the human neocortex and understand how de novo mutations or deletions of these genes impact neural development. My previous seminal contributions and current work in the field of centrosome/cilia signaling in neural development, provide the unique scientific background and leadership capacities, to successfully address these questions of neuralspecific centrosome proteins in human brain evolution and the acquisition of cognitive abilities. As an additional fundamental benefit, this work will provide a full landscape of the genetics/biological basis of the poorly explored 1q21.1 syndrome.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Deciphering the role of HDAC11 in muscular dystrophies

Project supervisor (principal investigator of the laboratory/group)
Name: Mònica Suelves
eMail: msuelves@igtp.cat
Group name: Neuromuscular and Neuropedriatric Research Group
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: Ministerio de Ciencia e Innovación
Reference/ years: PID2020-118730RB-I00

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Histone deacetylase 11 (HDAC11) is the latest member identified of the HDAC family, it is the unique member of the class IV HDAC subfamily and globally, its functions are poorly understood. HDAC11 is highly expressed in skeletal muscle tissue and very recently, our laboratory has shown that HDAC11 genetic deficiency in mice 1) promotes a glycolytic-to-oxidative muscle fiber switch, enhances mitochondrial content and increases lipid oxidation and globally, thus resulting in increased muscle performance (Hurtado et al, 2020); and 2) accelerates the regeneration process in response to muscle injury, by acting on SCs and macrophages, and enhancing SC differentiation Núñez-Álvarez et al, 2020). Because severe muscular dystrophies, including Duchenne muscular dystrophy (DMD) and myotonic dystrophy type 1 (DM1) course with cycles of degeneration, inflammation and regeneration, HDAC11 could be involved in their progression. Currently, in the laboratory we are performing experiments to better understand the contribution of HDAC11 in these chronic muscle pathologies and during aging.

The candidates should be very motivated students. Experience in cellular and molecular biology techniques and with mice handling will be well considered. We are interested in recruiting a PhD student, so the Master project can be continued with a PhD Thesis.

Contact to Mònica Suelves (msuelves@igtp.cat) sending a motivation letter, academic records and CV

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: A nanomedicine in clinical oncology

Project supervisor (principal investigator of the laboratory)
Name: Pilar Rivera Gil
Mail: pilar.rivera@upf.edu
Group name: Integrative Biomedical Materials and Nanomedicine Lab
Institution: UPF-CEXS
Webpage of the group: https://www.upf.edu/web/nanomed

Main grant associated with this project:
Principal investigator: Pilar Rivera Gil
Agency: MICINN-AEI
Reference/ years: PID2019-106755RB-I00 / 2020-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Pancreatic cancer is a lethal disease which is expected to be the 3rd cancer death caused by 2025. 95% of the patients die within 5 years.

The reason for these dismal results is a failed diagnosis and an inefficient therapeutic strategy. NanoTarg therapeutic solution is to use an oncotarget present in tumor cells favouring tumor progression, to specifically direct a nanocapsule. Our previous results show specific targeting in xenografts (EESR approved, ongoing PCT). NanoTarg aims at nanoencapsulating and directing the therapeutic gold standard (paclitaxel) precisely to the tumour tissue and to promote its targeted release. NanoTarg will validate the therapeutic potential *ex vivo* using 3D organoids from murine models and from patients' pancreatic tumour cells, and *in vivo* using orthotopic xenografts. The oncotarget is present in other types of cancers and therefore, NanoTarg technology can be extrapolated to them. As an added value, NanoTarg introduces the concept of biomedical SERS for the detection of biomarkers, the clinical relevance of it and the challenges that might appear to this novel strategy for its implementation in clinical oncology. NanoTarg will synthesize a SERS-based sensor to correlate imbalances with enhanced proliferation, invasiveness and in general, with tumour progression.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: The PLK1/NEK9/NEK6/7 signaling axis in G2 and early mitosis

Project supervisor (principal investigator of the laboratory/group)

Name: Joan Roig Amorós

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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-cell-biology-dcb/cell-cycle-and-signaling/

Main grant associated with this project:

Principal investigator: Joan Roig

Agency: Plan Nacional de I+D, Ministerio de Ciencia, Innovación y Universidades, Spain.

Reference/ years:

2019-2021, PGC2018-096307-B-I00

2022-24, awaiting resolution

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Our group is interested in understanding how G2 and early mitosis are controlled through phosphorylation. We focus our research on the roles of the signaling axis formed by the protein kinase PLK1 and its downstream partners NEK9, NEK6 and NEK7, three related NIMA-family kinases that are activated at the centrosomes and we have shown to be 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, N. et al. (2021). *BioRxiv*. 2021.11.04.467245).

Failure to properly duplicate, mature or separate the centrosomes result in abnormal mitosis, aberrant chromosome segregation and aneuploidy, a major cause of developmental defects and abortions and one of the hallmarks of cancer cells. Using engineered animal models and genetically modified cell lines produced through CRISPR-Cas9 technology plus 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 may result in abnormal chromosome segregation and the onset of aneuploidy. We will relate our observations with clinical data with the aim of assessing the possible involvement of the studied kinases in the process of cell transformation and the apparition of cancer as well as the onset of developmental abnormalities.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: **Unraveling the cell biology of the closest relatives of animals**

Project supervisor (principal investigator of the laboratory/group)
Name: Iñaki Ruiz-Trillo/Elena Casacuberta
eMail: inaki.ruiz@ibe.upf-csic.es / elena.casacuberta@ibe.upf-csic.es
Group name: MultiCellGenome Lab
Institution: Institute of Evolutionary Biology, IBE (CSIC-UPF)
Webpage of the group: https://multicellgenome.com

Main grant associated with this project: The origin of animals; A functional and biodiversity approach
Principal investigator: Iñaki Ruiz-Trillo/Elena Casacuberta
Agency: Ministerio Español de Ciencia e Innovación
Reference/ years: PID2020-120609GB-I00 2021/2024

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

Have you ever wondered how are the protists that are most closely related to animals? Any idea how researchers develop new methodologies to convert an organism into a model organism?

In our labs we are working with different protists that are phylogenetically close to animals. For three of them, the icthyosporeans *Creolimax fragantisima* and *Abeoforma whisleri*; and the corallochytrian *Corallochytrium limacisporum,* we have been developing genetic tools, from transient, to stable transfection and soon to come Crispr/Cas9. These organisms have the potential to become important models to understand the evolution of specific cell biological features, because they have different life cycles and morphologies, from the coenocytic stage of Creolimax and Corallochrytrium to an incredible diversity of shapes and stages in Abeoforma (for pictures and videos of those taxa see:
"https://www.flickr.com/people/146564503@N06/"
"https://www.youtube.com/user/multicellgenomeLab")

A master student would join our project to deeply study these emerging models in biology, by addressing questions about their nuclear division and their cytoskeleton understanding the transitions of their different life stages. The techniques involved in the project include basic molecular biology, cell culture, transfection, microbiology, and optical and fluorescent microscopy.

Call for project proposals, master in Biomedical Research practicum, 2023, Universitat Pompeu Fabra

Project Title: Genetic characterization of therapy related myeloid neoplasms (TRMN)

Project supervisor (principal investigator of the laboratory/group)

Name: Francesc Solé
eMail: fsole@carrerasresearch.org
Group name: MDS Group
Institution: Institut de Recerca contra la Leucèmia Josep Carreras
Webpage of the group: https://www.carrerasresearch.org/en/Myelodysplastic_Syndromes

Main grant associated with this project:
Principal investigator: Francesc Solé
Agency: FIS (ISCIII)
Reference/ years: 2021-2023

Brief summary of the project or current research lines of the group (please do not include pictures or logos)

- FIS Project (ISCIII): Patients diagnosed with cancer and treated with chemotherapy and / or radiotherapy are at future risk of developing myeloid neoplasms related to therapy (TRMN). TRMNs are aggressive clonal hematologic malignancies that occur as a late complication after chemotherapy and/or radiotherapy and are associated with a very poor prognosis. TRMNs are genetically complex and are often refractory to standard therapy. In addition, cancer patients who have clonal hematopoiesis of indeterminate potential (CHIP) have an increased risk of developing TRMN. Objective: genetic characterization by whole exome sequencing (WES), targeted deep sequencing (TDS) and single cell analysis. Methodology: 50 patients (25 with complex karyotype and 25 with normal karyotype) will be studied prospectively and retrospectively at the time of diagnosis of TRMN by WES. It is expected recover peripheral blood samples from the moment of the primary tumor from approximately 10 of these patients in order to be analyzed by TDS. It is estimated that in 5 of them we will detect CHIP, which will also be analyzed by TDS. To obtain more information regarding the intratumoral heterogeneity and clonal evolution of TRMN, single cell genomic studies will be performed in bone marrow samples from 8 patients with TRMN at two different time points. Expected results: to detect the genetic changes involved in the pathogenesis of TRMN, evaluate their application in the diagnosis, prognosis and monitoring of this group of patients.

- “Dissecting the mechanisms of clonal expansion in del(5q) myelodysplastic syndrome to selectively target the disease-initiating hematopoietic stem cells”. Stiftung Carreras Foundation (2021-2023). PI: Francesc Solé

- TRANSCAN “An Integrated European Platform to conduct translational studies in Myelodysplastic Syndromes base ont the EuroBloodNet Infraestructure”. Single cell studies of patients with low risk MDS that evolved into high risk MDS and single cell studies of cases with CHIP (Clonal hematopoiesis) that evolved into MDS. PI: Francesc Solé

- “Study of clonal hematopoiesis (CHIP) in cured patients with the diagnosis of breat and ovarian cancer. Rotary Badalona Funding. PI: Francesc Solé