DCEXS-UPF (Barcelona) International PhD call 2021

The Department of Experimental and Health Sciences of the Pompeu Fabra University (DCEXS-UPF) opens a call for the academic year 2022-23, for accomplished and driven students with an excellent academic record to carry out a PhD in Biomedicine.

The research and teaching excellence of the DCEXS-UPF is widely acknowledged, for instance, the DCEXS-UPF has been awarded the "María de Maeztu" distinction and grant in 2014 and 2018. Furthermore, the DCEXS-UPF offers a unique and international research environment and cutting-edge scientific facilities, thanks to its privileged location in the Barcelona Biomedical Research Park (PRBB).

Eight PhD contracts are offered in groups led by recognized scientists performing research in biomedicine, please see below for more information on the scientific projects.

Contracts, training and advantages

Contracts will be funded by the Spanish "Researcher Training Program" as well as by the DCEXS-UPF. All positions will offer the same wage conditions, for 4 years, and fellows will be registered in the Spanish Social Security System, which provides health and occupational insurance coverage. Academic costs (except fees) are also covered.

The UPF's PhD programme in Biomedicine has been certified by the ANECA and in October 2011 it was awarded the "Mention towards Excellence". Since the academic year 2012-13, the PhD Programme in Biomedicine follows the latest regulations for doctoral studies in Spain, the so-called Royal Decree (RD) 99/2011, which were introduced to comply with the guidelines and recommendations of the European Higher Education Area (EHEA) on doctoral studies. The contents of this doctoral programme have been verified by the Catalan Agency for Quality Assessment and Accreditation with a qualification "Quality Label towards Excellence".

The PhD programme, all of whose activities are carried out in English, attracts every year a large number of international students. These activities aim at preparing students to become independent researchers pursuing a scientific career. Fellows will have access to a wide range of academic activities, as well as ad hoc training in scientific skills, and access to the PRBB Intervals programme, an interdisciplinary education programme for professionals working in the PRBB.

Requirements

Candidates must have excellent academic qualifications and good command of English. Research experience and authorship of scientific publications will be a plus.

Candidates must have obtained a University Degree and a Master's Degree in natural or medical sciences (Biology, Medicine, Biochemistry, Biomedicine, Chemistry, Physics, etc), or in other quantitative disciplines (Mathematics, Computer Science, Bioengineering, etc) within the European Higher Education System (minimum 300 ECTS), or an equivalent university degree, of at least 300 ECTS, that would allow the candidate to start a PhD thesis in their home country by September 2021 (candidates who expect to be awarded such degree by September 2021 are eligible to apply).

Candidates are advised to check that they fulfil the requirements for admission to the UPF PhD in Biomedicine as those who do not will be considered ineligible. **Please note that it is not necessary to start the admission process for the PhD programme at this stage**; if you are selected we will help you prepare your application for admission.

All candidates will be required to present their academic record.

Reference letters will be requested for **pre-selected** candidates. Also, pre-selected candidates who obtained their degree and/ or Master's in a country other than Spain will have to present the conversion of their grades to the Spanish 0-10 scale.

The DCEXS promotes diversity in an inclusive environment that welcomes applicants regardless of age, disability, gender, nationality, race, or religion.

Application

To apply, please register and send the required information and documents through the Interfolio website: http://apply.interfolio.com/85540 (except the position in Prof. Pura Muñoz-Cànoves' group, please see below for more information).

You will be able to choose one or two positions in order of preference.

Deadline for applications: May 28th 2021 at 17h CET.

Selection process and calendar

The pre-selection of the candidates will be based on academic qualifications and research experience.

Candidates will receive feedback on pre-selection before June 20th.

Pre-selected candidates will be interviewed by at least one Principal Investigator in the DCEXS facilities or via videoconference during late June and early July and will receive feedback in early September.

Contracts are expected to start from June 2022 (depending on the publication and resolution of the "Researcher Training Program" call).

Contact (for enquiries only; applications must be sent via Interfolio)

Dr Regina López, phdfellowships.dcexs@upf.edu

Universitat Pompeu Fabra Barcelona
Department of Experimental and Health Sciences

EXCELENCIA MARÍA DE MAEZTU
AGENCIA ESTATAL DE INVESTIGACIÓN
CEX2018-000792-M

Principal Investigator: Jose Aramburu and Cristina López-Rodríguez

NFAT proteins and immune cells Group

https://www.upf.edu/web/genimmune

https://www.upf.edu/web/biomed/entry/-/-/23934/adscripcion/cristina-lopez-rodriguez

https://www.upf.edu/web/biomed/entry/-/-/15818/adscripcion/jose-francisco-aramburu

Research project title

Metabolic regulation of proinflammatory immune responses

Research project summary

We use mouse models, cell and molecular biology, and bioinformatics approaches to understand the mechanisms that the immune system uses to control the defense against pathogens, metabolic diseases, and cancer.

The group's current projects include:

1) How infection and inflammatory cytokines control the stability and function of hematopoietic stem cells.

2) Influence of immune cell metabolism on their inflammatory activity in obesity.

3) Identification of pro- and anti-inflammatory modules in immune cells that can help control tumor progression.

Preferred background of candidates

The main requirements are to have completed a degree in Biology, Biomedicine or similar, and to have (or be in the process of completing) a master to meet the 300 credits necessary to access the doctorate.

The selection will be made based on these criteria:

1) Academic record of the bachelor's and master's degrees
2) Background in immunology
3) Previous experience in Cell Biology and Molecular Biology projects. We will value experience with mouse models, and techniques to analyze transcription, epigenetics, metabolism, and functional analyses of lymphocytes, macrophages and stem cells. Bioinformatics skills (R programming and use of large sequencing datasets such as RNA-seq or ChIP-seq will be a plus).
4) Interest in understanding the molecular bases of diseases
5) Strong motivation towards the scientific career and the projects of our group

Selected references

Huerga Encabo et al., 2020 *Journal of Experimental Medicine* (Pubmed ID: 31816635)
Aramburu and López-Rodríguez, 2019 *Frontiers in Immunology* (PMID: 30949179)
Buxadé et al., 2018 *Journal of Experimental Medicine* (PMID: 30327417)
Tellechea et al., 2018 *Journal of Immunology* (PMID: 29150563)
Berga-Bolaños et al., 2013 *Proc Natl Acad Sci USA* (PMID: 24043824)
Buxadé et al., 2012 *Journal of Experimental Medicine* (PMID: 22312110)

Principal Investigator: Marc Güell

Translational Synthetic Biology Research Group

https://www.upf.edu/en/web/synbio

Research project title

Precise engineering of mammalian genomes for therapeutic applications

Research project summary

Do you feel motivation to use advanced biotechnology and synthetic biology to address current medical problems? Do you want to train in developing new gene-editing technologies?

This project is ideal for a candidate who is highly motivated by applied science. This project will give the opportunity to engage with the translational side of gene editing and gene therapy.

Despite enormous progress, precise introduction of new alleles in mammalian genomes remains difficult. Our goal is to explore novel alternatives, combining molecular biology and engineering to precisely re-write genomes safely and efficiently for therapeutic purposes.

Responsibilities

- Develop new technologies for precise gene editing
- Apply new concepts of synthetic biology and genetic engineering to gene therapy
- Deploy technology to clinically relevant models on muscular dystrophy (MDC1A) and
- potentially other indications
- Interface with collaborators and stakeholders: experimental/medical partners, patient
- associations
- Integration in a multidisciplinary and international research team

Preferred background of candidates

- Degree in engineering, experimental sciences or medicine
- Basic knowledge of molecular biology
- Interest in Synthetic Biology
- Interest in applied genetic engineering and translational science
- Curiosity and motivation to develop new therapeutic biotechnologies
- Strong academic record will be appreciated
- Multidisciplinary mind to engage with multiple players of translational science (clinicians,
- patient associations, private sector, collaborators)

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Principal Investigator: Elena Hidalgo

Oxidative Stress And Cell Cycle Research Group

www.upf.edu/osccg

Research project title

Physiological fluctuations of reactive oxygen species regulate signaling cascades and alter the cellular proteostasis network – Influence on aging

Research project summary

We study how waves of reactive oxygen species such as H_2O_2, produced at the mitochondria during respiration, convey on the regulation of cellular responses both regarding signaling (driven by reversible cysteine oxidation of proteins known as H_2O_2 sensors) and toxicity (damaging proteins, lipids and DNA). Using fission yeast as a model system, the candidate will be involved in one of the following topics:

a. We have designed new and ultrasensitive probes to measure intracellular waves of H_2O_2; these genetically-encoded fluorescent reporters have to be expressed in different cellular compartments to monitor H_2O_2 gradients during physiological conditions. The final aim is to determine the peroxide concentrations in specific sub-cellular locations ruling cellular processes and leading to longevity

b. Protein aggregation has been recently appreciated as a mechanism to prevent cellular proteostasis and maintain cellular fitness. Part of our lab is interested in describing the network of chaperones controlling refolding, degradation or aggregation of misfolding intermediates caused by temperature up-shifts or by oxidative stress.

Preferred background of candidates

The main requirement for applicants is to have completed graduate studies on Biology, Biotechnology, Chemistry or Biochemistry, and a master (M.S.) (which may be unfinished). Previous research experience in yeast genetics and molecular biology will be highly appreciated.

Selected references

Boronat, S., Marte, L., Vega, M., García-Santamarina, S., Cabrera, M., Ayté, J. and Hidalgo, E. 2020. The Hsp40 Mas5 connects protein quality control and the general stress response through the thermo-sensitive Pyp1. iScience 23:101725.

Cabrera, M., Boronat, S., Marte, L., Vega, M., Pérez, P., Ayté, J. and Hidalgo, E.. 2020. Chaperone-facilitated aggregation of thermo-sensitive proteins shields them from degradation during heat stress. Cell Rep. 30:2430–2443.

Carmona, M., de Cubas, L., Bautista, E., Moral-Blanch, M., Medraño-Fernández, I., Sitia, R., Boronat, S., Ayté, J. and Hidalgo, E. 2019. Monitoring cytosolic H_2O_2 fluctuations arising from altered plasma membrane gradients or from mitochondrial activity. Nat. Commun. 10:4526.

Domènech, A., Ayté, J., Antunes, F. and Hidalgo, E. 2018. Using in vivo oxidation status of one- and two-component redox relays to determine H_2O_2 levels linked to signaling and toxicity. BMC Biol. 16:61.

Boronat, S., Domènech, A., Carmona, M., García-Santamarina, S., Bañó, M.C., Ayté, J. and Hidalgo, E. 2017. Lack of a peroxiredoxin suppresses the lethality of cells devoid of electron donors by channelling electrons to oxidized ribonucleotide reductase. PLoS Genet. 13:e1006858.

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CEX2018-000792-M

Principal Investigator: Tomàs Marquès

Comparative Genomics Lab

http://biologiaevolutiva.org/tmarques

Research project title

Patterns of epigenomic, genetic diversity and CNV in primates

Research project summary

The current knowledge of variation in primate studies have proven to be useful for the study of natural populations, but there have been certain limitations given the number of samples.

In the last year, we have generated the most complete data set of high coverage primate genomes from tenths of species with matching epigenomic data. The objective of this project will be then to study population genomics, gene regulation across the primate phylogeny comparing methylation maps and structural variation maps in a wide representation of primate samples.

Preferred background of candidates

Candidates should have a very strong theoretical background in population genetics, gene regulation and the use and analysis of next-generation sequence methods (Illumina).

Selected references

Marc de Manuel et al. “Chimpanzee genomic diversity reveals ancient admixture with bonobos” Science 2016 354 (6311), 477-481

Javier Prado-Martinez*, Peter H. Sudmant*, et al. (2013). “Great ape genetic diversity and population history.” Nature 2013 Jul 25;499(7459):471-5. doi: 10.1038/nature12228. Epub 2013 Jul 3.

Martin Kuhlwilm*, Marc de Manuel*, Alexander Nater*, Maja P. Greminger*, Michael Krützen, Tomas Marques-Bonet “Evolution and demography of the great apes.” Current Opinion in Genetics & Development 2016.

Raquel García-Pérez, Paula Esteller-Cucala, Glòria Mas, Irene Lobón, Valerio Di Carlo, Meritxell Riera, Martin Kuhlwilm, Arcadi Navarro, Antoine Blancher, Luciano Di Croce, José Luis Gómez-Skarmeta, David Juan, Tomàs Marquès-Bonet “Gene regulatory architectures dissect the evolutionary dynamics of regulatory elements in humans and non-human primates” Nature Communications (in press).

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EXCELENCIA MARÍA DE MAEZTU
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CEX2018-000792-M

Principal Investigator: Alfonso Martínez Arias

Stembryo Engineering Lab

https://www.upf.edu/web/stembryo-engineering-lab

Research project title

Mechanochemical basis of the mammalian body plan

Research project summary

We have developed a new model system to study, in vitro, the early stages of mammalian development (see refs below). The project will make use of this system to study how mechanochemical signals steer the cell intrinsic programs of gene expression that characterize the laying down of the mammalian body plan.

Preferred background of candidates

Quantitative Cell Biology/microscopy, Tissue culture, basic molecular biology

Selected references

Ghimire, S. Maintzou, V., Moris, N. and Martinez Arias, A. (2021) Human gastrulation: the embryo and its models. Dev. Biol. In press.

Moris, N., Martinez Arias, A. and Steventon, B. (2020) Experimental Embryology of Gastrulation: Pluripotent Stem Cells as a new model system. Curr. Ops Genetics and Development 64, 78-83.

van den Brink, S., Alemany, A., van Batenburg, V. Moris, N., Blotenburg, M., Vivié, J., Baillie-Johnson, P., Nichols, J. Sonnen, K., Martinez Arias, A. and Oudenaarden, A. (2020) Single cell and spatial transcriptomics reveals somitogenesis in gastruloids. Nature 582, 405-409.

Beccari, L., Moris, N., Girgin, M., Turner, D., Baillie-Johnson, P., Cossy, A.C., Lutolf, M., Duboule, D. and Martinez Arias, A. (2018) Multiaxial self organization properties of mouse embryonic stem cells gastruloids. Nature 562, 272-276.

Principal Investigator: Pura Muñoz-Cánoves

Cell Biology Group

https://www.upf.edu/web/cellbiology

Research project title

Cellular Senescence, A Novel Target To Combat And Ameliorate Duchenne Muscular Dystrophy

Research project summary

We are looking for a highly motivated and ambitious **Young researcher (pre-doctoral student)** to join our research team, working at the Department of Experimental and Health Sciences of the Pompeu Fabra University (UPF) at the PRBB, in Barcelona. We study the mechanisms underlying the loss of stem cell regenerative decline with aging or disease, and in particular the failure in proteostasis and entry into senescence of aging stem cells, as well as potential mechanisms to reverse these associated defects.
This position is financed by La Marató through a competitive grant entitled "Cellular Senescence, A Novel Target To Combat And Ameliorate Duchenne Muscular Dystrophy" (Reference: 202021).

You will be employed on the **202021_Marató de TV3** project and be part of a dedicated team of molecular and cell biologists. Your main project will combine molecular biology, mouse genetics and tissue injury-regeneration, as well as senescence approaches, to define the causes of senescence entry of skeletal muscle stem cells during Duchenne Muscular Dystrophy progression and analyze whether cellular senescence causes loss of muscle regenerative functions.

Preferred background of candidates

Highly motivated candidates with a strong interest in stem cells and aging are encouraged to apply. Degree and Master in Biomedical or biological sciences are required for applicants. We will appreciate:

- experience in either of the following areas: mouse genetics, molecular biology, stem cells
- excellent communication skills in written and spoken English
- strong analytical skills, and a problem-solving and result-oriented attitude

Email application

Applicants should submit an application containing: motivation letter and CV including contact details for two referees to Marina Raya Chamorro (marina.raya@upf.edu) and Pura Muñoz Cánoves (pura.munoz@upf.edu)

Universitat Pompeu Fabra Barcelona
Department of Experimental and Health Sciences

EXCELENCIA MARÍA DE MAEZTU
AGENCIA ESTATAL DE INVESTIGACIÓN
CEX2018-000792-M

Principal Investigator: Francisco José Muñoz López

Aging Brain and Neurodegeneration Research Group

https://www.upf.edu/web/lmp/aging-and-neurodegeneration

Research project title

Dysregulation of synaptogenesis due to the effect of amyloid -peptide on the TRPM7 and Piezo1 mechanoreceptors and CamKIIalpha signaling

Research project summary

Alzheimer's disease (AD) is due to the extracellular aggregation of the amyloid ß-peptide (Aß) into oligomers and fibrils, which are synaptotoxic leading finally to cell death. There is no specific treatments that can cure, prevent or retard the disease. Therefore, we carried out a screening in 5,154 k.o. yeasts to look for new proteins involved in AD. We found 3 genes (TRPM7, CaMKIIalpha and AIF1) that can be related with AD attending to their involvement in synaptic formation and maintenance, intracellular signalling and pro-apoptotic effects, plus one mechanoreceptor (Piezo1) found to respond to oxidative stress and Aß in our lab.

Our hypothesis proposes that oligomeric Aß (oAß) directly or indirectly (by oxidative stress) affect the physiological function of mechanoreceptors that will have deleterious effects on the growth and maintenance of the synaptic spines, and a rise in intracellular calcium. Calcium will affect: i) to CaMKIIalpha, impairing its protective role and neuronal plasticity; ii) to mitochondria increasing nitro-oxidative stress and the activation of apoptosis, where AP1 can play a key role.

Our objectives are:

1. Characterization of the effect of the oAß binding and/or the oxidative stress induced by oAß on TRPM7 and Piezo1 functions in the synaptic spines.
2. Study of the role of Calcium-Calmodulin Kinase IIalpha (CaMKIIalpha) in response to the activation of synaptic mechanoreceptors and the oAß effects.
3. Identification of the contribution of the Apoptosis-inducing factor 1 (AIF1) to oAß toxicity.

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

Preferred background of candidates

Candidates should have a degree in Sciences. The expertise in molecular biology of proteins and mRNA, gene overexpression and silencing, siRNAs, confocal microscopy, spectrofluorometry, calcium image, path-clamp, flow cytometry and in silico studies, will be positively evaluated.

Selected references

- Picón-Pagès P, Gutiérrez DA, Barranco-Almohalla A, Crepin G, Tajes M, Ill-Raga G, Guix FX, Menéndez S, Arumí-Uría M, Vicente R, Álvarez AR, Muñoz FJ. 2020. Amyloid beta-peptide increases BACE1 translation through the phosphorylation of the eukaryotic initiation factor-a. Oxidative Medicine and Cellular Longevity. 2020. 2020: 2739459.

- Picón-Pagès P, Bonet J, García-García J, Garcia-Buendia J, Gutierrez D, Valle J, Gómez-Casuso CES, Sidelkivska V, Alvarez A, Perálvarez-Marín A, Suades A, Fernàndez-Busquets X, Andreu D, Vicente R, Oliva B, Muñoz FJ. 2019. Human albumin impairs amyloid ß-peptide fibrillation through its C-terminus: from docking modeling to protection against neurotoxicity in alzheimer's disease. Computational and Structural Biotechnology Journal. 17. p. 963 – 971.

- Picón-Pagès P, Garcia-Buendia J, Muñoz FJ. Functions and dysfunctions of nitric oxide in brain. Biochim Biophys Acta Mol Basis Dis 4439(18)30452-6. 2018.

- Valls-Comamala V, Guivernau B, Bonet J, Puig M, Perálvarez-Marín A, Palomer E, Fernàndez-Busquets X, Altafaj X, Tajes M, Puig-Pijoan A, Vicente R, Oliva B, Muñoz FJ. The antigen-binding fragment of human gamma immunoglobulin prevents amyloid β-peptide folding into β-sheet to form oligomers. Oncotarget. 8:41154-41165. 2017.

- Núnez-Ollé M, Jung C, Terré B, Balsiger NA, Plata C, Roset R, Pardo-Pastor C, Garrido M, Rojas S, Alameda F, Lloreta J, Martín-Caballero J, Flores JM, Stracker TH, Valverde MA, Muñoz FJ*, Gil-Gómez G*. Constitutive Cyclin O deficiency results in penetrant hydrocephalus, impaired growth and infertility. Oncotarget 8: 99261-99273. 2017. *Co-senior authors.

- Guivernau B, Bonet J, Valls-Comamala V, Bosch-Morató M, Godoy JA, Inestrosa NC, Perálvarez-Marín A, Fernández-Busquets X, Andreu D, Oliva B, Muñoz FJ. Amyloid-β peptide nitrotyrosination stabilizes oligomers and enhances NMDAR-mediated toxicity. J Neurosci. 36:11693-11703. 2016. (IF: 5.673 Q:1 C:25)

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EXCELENCIA MARÍA DE MAEZTU
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CEX2018-000792-M

Principal Investigator: Arcadi Navarro i Cuartiellas

Evolutionary Genomics Lab

https://www.ibe.upf-csic.es/navarro

Research project title

The role of pleiotropy in the genetic architecture of human complex traits

Research project summary

Genome-wide association studies (GWAS) based on SNP-arrays, and more recently on exome and full-genome sequencing, have been the choice strategies for genome-phenome studies exploring links between genomic variants and complex diseases. Over the last decade, huge amounts of information have been gathered contributing to a better understanding of disease etiology and pathophysiology and paving the way to improved diagnosis, prognosis and treatment. Despite many advances, most disease-associated loci remain functionally elusive, limiting the medical exploitation of the knowledge stored in publicly available databases. Moreover, rather than a full assessment of the genetic architecture of complex traits and disease risk, GWAS is geared towards the exploration of differences in these traits between individuals of the same species.

As a result, once a link between a genetic variant and a given phenotype has been established, there is no simple procedure neither to (1) understand what are the detailed physio-pathological mechanisms in which this variant is involved; nor to (2) ascertain what is the relevance of that variant in the overall architecture of the trait in question.

We intend to carry out a full-fledged exploration of the pleiotropic relations of complex traits and diseases, with particular focus on evolutionary relevant traits (*e.g.*, fertility or longevity) and on the use of comparative genomics data to do deeper into the genetic underpinnings of these traits and diseases.

Preferred background of candidates

- Degree in Biology (or related Sciences) and MSc in Bioinformatics
- Demonstrable experience in dealing with R and Python.
- Working knowledge of statistical genomics.
- Experience with GWAS databases.
- Excellent communication skills in English.

Selected references

- Comparative analysis of mammal genomes unveils key genomic variability for human lifespan (https://www.biorxiv.org/content/10.1101/2021.02.09.430384v1)
- Muntané, G., X. Farré, E. Bosch, L. Martorell, A. Navarro and E. Villella. (2021) The shared genetic architecture of schizophrenia, bipolar disorder and lifespan. Hum. Genet. ePub ahead of print (doi: 10.1007/s00439-020-02213-8).
- Farré, X., N. Spataro, F. Haziza, J. Rambla and A. Navarro*. (2020) Genome-Phenome Explorer (GePhEx): A tool for the visualization and interpretation of phenotypic relationships supported by genetic evidence. Bioinformatics 36: 890–893 (doi: 10.1093/bioinformatics/btz622).
- G. Muntané, X. Farré, J. A. Rodríguez, C. Pegueroles. D. A. Hughes, J. P. de Magalhães T. Gabaldón and A. Navarro* (2018). Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. Molecular Biology and Evolution 35(8): 1990-2004 (doi: 10.1093/molbev/msy105)
- U. Martinez- Marigorta, J. A. Rodrigues, G. Gibson and A. Navarro*. (2018) Replicability and Prediction: Lessons and Challenges from GWAS. Trends in Genetics 34(7): 504-517 (doi: 10.1016/j.tig.2018.03.005)
- Rodriguez, J.A., U.M. Marigorta, D. A. Hughes, N. Spataro. E. Bosh* and A. Navarro*. 2017. Antagonistic pleiotropy and mutation accumulation influence human senescence and disease. Nature Ecology & Evolution 1(3): 0055 (doi:10.1038/s41559-016-0055)