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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: RODRIGUEZ FRATICELLI, ALEJO EZEQUIEL
Referencia: RYC2020-029004-I
Área Temática: **Biociencias y biotecnología**
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Título:

Mechanisms of blood and immune functional variation: stem cell heterogeneity and cellular memory

Resumen de la Memoria:

Blood and immune cells play a critical role in a majority of deadly diseases on a global scale. These cells are constantly being replaced through the regenerative activity of stem cells in the bone marrow, in a process termed hematopoiesis. For decades, hematopoiesis has been studied using the lineage tree paradigm, a model of bifurcating fate paths that the progeny of stem cells would make as they differentiate into mature blood cells. But recent analyses of stem cell function and identity at the single-cell level have prompted a reevaluation of this model. In the past few years, I have made a series of ground-breaking discoveries through advanced clonal analysis, revealing an unprecedented variation in the regenerative behaviors of individual stem cells in vivo and the molecular programs that drive these fates (Rodriguez-Fraticelli et al. Nature 2018; Rodriguez-Fraticelli et al. Nature 2020; Weinreb*, Rodriguez-Fraticelli* et al. Science 2020). In this updated model, hematopoiesis results from the combination of thousands of different lineage trees arising from individual stem cell clones, each defined by their unique imprinted properties (reviewed in Laurenti et al. Nature 2018, and Rodriguez-Fraticelli et al. Curr Op Hem 2021).

In my future independent career, my vision is to tackle a critical yet unresolved question: what is the role of stem cell heterogeneity in blood and immune physiology and disease? To break down this question, my independent research program will focus initially on the physiology of myeloid cells (platelets, neutrophils, monocytes, and dendritic cells). Myeloid cells play essential roles in the innate response to injury and infection, and their dysfunction contributes to a wide range of disorders, from chronic inflammation to cancer. Myeloid cells are highly variable at the single-cell level, both in their function and their transcriptome, but the mechanistic basis of this myeloid heterogeneity remains unclear. Due to their shorter lifespans, myeloid cells are more rapidly replaced by stem cells, making them more sensitive to stem cell variation and plasticity. Certain reports have even suggested that stem cells can be a source of long-term innate immunologic memory. However, the role of stem cell heterogeneity in myeloid variation, plasticity, and memory remains unknown. My preliminary data suggest that mature myeloid cells show distinct molecular profiles linked to their unique stem-cell origins, suggesting an exciting and novel mechanism that contributes to their functional variation. My research proposal is to define the cellular and molecular mechanisms of myeloid heterogeneity through quantitative stem-cell lineage tracing and single-cell functional assays. Unveiling the stem-cell origins and mechanisms of myeloid functional heterogeneity will constitute a methodological and conceptual leap forward for the study of immune and blood biology. These results will be crucial to advance the next generation of cellular therapies and improve outcomes for various diseases that are driven by myeloid cell dysfunction, including chronic inflammation and cancer. Finally, these studies will unlock an entirely new field studying the impact of HSC heterogeneity in dozens of biological contexts where blood and immune cells play a central regulatory role.
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Resumen del Currículum Vitae:

I obtained my Ph.D. in July 2014, training as a developmental cell biologist under the supervision of Dr. Fernando Martin-Belmonte and Dr. Miguel A. Alonso, experts in membrane trafficking and epithelial polarity. Through my Ph.D., I published 4 studies as a first or co-first author in well-recognized journals in the cell biology field, including the Journal of Cell Biology and Nature Cell Biology, I also contributed to several collaborations, and I created one patent. In addition, I set up many of the lab protocols and procedures, and co-supervised 6 Master and Ph.D. students, leading to my recent co-corresponding authorship in Current Biology.

I started my postdoctoral training in 2015, in the laboratory of Dr. Fernando Camargo (Boston Children s Hospital and Harvard University), an internationally recognized expert in adult stem cell biology. There, I set on a path to develop methodologies for highly-multiplexed single-cell lineage tracing in vivo to study the functional heterogeneity of stem cells. The power of these innovative methods led to many groundbreaking discoveries in the field of hematopoiesis and stem cell biology. I published 3 studies as a first or co-first author in wide-interest generalist journals (2 in Nature and 1 in Science) in addition to other studies as a collaborator (published in Cell and Cell Stem Cell). Through my collaborative work, I have been able to establish a scientific network of outstanding researchers and leaders in the stem cell field such as Allon Klein (Harvard Medical School), Darrell Kotton (Boston University), and many others.

My career achievements have been recognized through multiple invitations and oral presentations at prestigious international scientific meetings (GRC, Keystone, ASH, ISEH) as well as invitations to peer-review for very prestigious journals (Nature Cell Biology, Nature Protocols, Stem Cells, ATVB).

Ever since I started my career I have been independently funded, including prestigious postdoctoral fellowships and awards, such as the LSRF Fellowship, the ASH Scholar Award, the LLS Special Fellowship, and the NHLBI K99 award. This degree of independence has been crucial for allowing me to boldly explore the most challenging questions with cutting-edge resources to perform ground-breaking research.

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INVESTIGACIÓN

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

In addition to my research interests, I have recently become a member of the ISEH New Investigators Committee, helping organize the prestigious Annual Meeting of this society, its career development activities, and scientific outreach. I am also proud to be a devout mentor for younger students and scientists, who have since moved on to have brilliant careers of their own, with Ph.D. positions at McGill University and the University of Basel, and postdoctoral positions in Harvard Medical School and the Queen Mary University of London.
I have recently been selected to join the IRB Barcelona as an independent Group Leader to set up the Laboratory of Quantitative Stem Cell Dynamics, starting in Spring 2021. IRB Barcelona is an internationally acclaimed biomedical research interest that fosters an interdisciplinary research environment. My lab will have the central goal of defining the role and mechanisms of stem cell heterogeneity in regeneration, age-related degeneration, and cancer.

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Turno de acceso general

Nombre: BOGDANOVIC KUPESIC, OZREN
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Área Temática: **Biociencias y biotecnología**
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Título:

Programming, Inheritance and Evolution of Chromatin States

Resumen de la Memoria:

My research aims to unravel how a critical epigenome component, DNA methylation, participates in diverse developmental processes as well as in aging and disease formation, and how the impaired deposition and removal of this mark impact embryonic and germline competence and integrity. I conducted my PhD research at the Radboud University (Nijmegen, NL) where I worked on DNA methylation and MBD proteins during vertebrate embryogenesis. There I generated the first DNA methylome of a developing vertebrate embryo using massively parallel sequencing technology (Bogdanovic et al, 2011; Genome Res).

I then moved to CABD (Seville, Spain 3 years) to work with Dr. Juan Ramon Martinez Morales and Prof. Jose Luis Gomez-Skarmeta on diverse aspects of embryonic gene regulation. The highlights of my postdoctoral work at CABD include: the functional characterization of Opo protein (Bogdanovic et al, 2012; Dev Cell) and the genome-wide identification of embryonic enhancers in zebrafish (Bogdanovic et al, 2012; Genome Res). Following my time at CABD, I started a second postdoc at UWA (Perth, Australia) where I obtained the prestigious ARC DECRA fellowship to work on evolutionary conservation of enhancer DNA demethylation (Bogdanovic et al, 2016; Nat Genet co-corresponding). In this study we unraveled the mechanisms that underpin phenotypic similarities of distantly related vertebrates during the phylotypic period, which led to significant recognition of my research in the field. In 2017 I was awarded the Raine Research Prize for best biomedical publication in Western Australia, and the prestigious Millennium Science Award for significant contributions to Australian genomics research.

In 2017 I started the Developmental Epigenomics lab (www.bogdanoviclab.org) at the Garvan Institute of Medical Research / UNSW (Sydney, Australia). My lab is supported by competitively acquired funding, including grants from the Australian Research Council (DP190103852) and fellowships from NHMRC (APP1162993) and CINSW (CDF181229). We remain fascinated by the contributions of DNA methylation to embryonic development, cell differentiation and disease, and over the last three years we have made important advances in the field including: detailed genome and epigenome maps of amphioxus development (Marletaz et al, Nature co-first), zebrafish embryonic germline DNA methylomes (Skvortsova et al, 2019, Nat Commun corresponding), a novel non-CG methylation signature in zebrafish (Ross et al, 2020; Nucleic Acids Res corresponding). Other highlights include: a comprehensive review on epigenetic inheritance (Skvortsova et al, 2018; Nat Rev Mol Cell Biol corresponding) and a collaborative paper on inherited Polycomb function (Zenk et al, 2017; Science). This significant research output led to my promotion to Associate Professor in 2020.

Moving forward I aim to establish a novel research program that will capitalize on the recent development of single cell transcriptome and epigenome profiling techniques with the aim of understanding better how gene-regulatory information, and in particular DNA modifications, are programmed in the germline and reprogrammed during vertebrate embryogenesis.
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Resumen del Currículum Vitae:

I am a Laboratory Head and Associate Professor at the Garvan Institute of Medical Research and the University of New South Wales (Sydney, Australia) where I lead the Developmental Epigenomics lab. Our research aims to understand the contributions of the epigenome to embryogenesis, cell differentiation and disease. We are particularly interested in how DNA methylation patterns are established, maintained and altered during those processes.

I hold a PhD from the Radboud University (Nijmegen, NL) and have conducted my postdoctoral research at the Andalusian Centre of Developmental Biology CABD (Seville, ES) and the University of Western Australia - UWA (Perth, AU). Over the course of my career, I have consistently demonstrated research excellence and leadership in the field of developmental genetics, which is evident from my track record consisting of 37 publications indexed in WoS/Scopus and 6 bioRxiv preprints, which have collectively attracted >2400 cites (Google Scholar), and history of competitive grant funding success and award attainment. My research highlights over the last five years include corresponding author publications in Nature Communications (Skvortsova et al, 2019), Nucleic Acids Research (Ross et al, 2020) and Nature Reviews Molecular Cell Biology (Skvortsova et al, 2018), lead author publications in Nature (co-first author), Nature Genetics (Bogdanovic et al, 2016 co-corresponding), and collaborative papers in Nature (Session et al; 2016) and Science (Zenk et al 2017).

Since my PhD completion (2012), I was successful in securing external funding as Principal Investigator from National Health and Medical

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Research Council (Australia), Australian Research Council (Australia), Cancer Institute New South Wales (Australia), as well as funding from the UWA and the Garvan Research Foundation totalling > $3,86M AUD (2.45M EUR). My research success is further exemplified by 11 highly cited publications (>50 citations), and recognition of my status as a leader in the field, as demonstrated by an increasing number of invited talks (13), keynote lectures (3), and awards i.e., Millennium Science Award (2017, awarded annually for significant contributions to Australian genomics), Raine Research Prize (2016, for best biomedical paper from a Western Australian Researcher), and Vice Chancellor s ECR Award (2016, UWA).

I have so far supervised 5 PhDs, 1 MSc, 3 honours, and 3 research practice students. As a senior member of the Garvan Institute Faculty, I undertake significant institutional leadership roles, including: Advisory Board Member of the Biological Testing Facility, Co-Chair of the Misconduct Committee, and Chair of the International Staff Support Committee. On average, I review 3 manuscripts per month for top tier international journals, including: Nature, Nature Genetics, Nature Cell Biology, Developmental Cell, and others. I have recently edited a book - TET proteins and DNA demethylation , Methods in Molecular Biology and have acted as Guest Editor for Briefings in Functional Genomics. I participate in peer review for multiple funding schemes such as: ARC and NHMRC (Australia), MRC (UK), Wellcome Trust (UK), HFSP, VIDI (the Netherlands), and DFG (Germany). I have also participated in the organisation of 5 scientific meetings, including the Lorne Genome Conference - Australia s most notable genomics meeting.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: HUNEMEIER , TABITA
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Área Temática: **Biociencias y biotecnología**
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Título:

Human Genome Diversity

Resumen de la Memoria:

Human health and diversity are determined by various factors, including physiological, ecological, social, and evolutionary processes. One of the primary goals of my research program is to understand how evolutionary forces shape health and how they interact with other biological and cultural processes.
My main research achievements centred on leveraging genetic variation to dissect the evolutionary forces involved with adaptation and maintaining the extant variability in Native Americans populations. Specifically, I focused on analysing the pace and mode of natural selection in shaping these populations' evolutionary history and health. I have taken an empirical and theoretical approach in tackling these questions and using various data such as large-scale population genetics, morphological, historical, and linguist data, along with those derived from computer simulations. My future research program will build a time series of genetic datasets to study host-pathogen coevolution and reconstruct human history in South America. I envision working on pre-and post-contact specimens (including present-day populations) from South American lowlands to understand the origin and the impact of past epidemics on the genetic profiles of the autochthonous population of this continent.
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Resumen del Currículum Vitae:

I completed my PhD in Genetics at the Federal University of Rio Grande do Sul (Brazil), with 12 months of internship at University College London (UK), in 2010. I was also a post-doctorate fellow (2010-2014), with scholarships from the Leverhulme Trust (UK) and Coordination for the Improvement of Higher Education Personnel (Brazil), at the Federal University of Rio Grande do Sul, including international internships at the University College London, and the Pompeu Fabra University. My work has yielded 56 manuscripts so far, including first-authored publications in PNAS, Molecular Psychiatry, and PLoS One, and publications in PNAS and Scientific Reports for which I was the corresponding author. Besides, I have co-authored several publications in Nature, Cell, and Nature Communications. Apart from the research experience, I also have experience in securing external funding (national and international) and have five years of experience in teaching and mentoring undergraduate and graduate students. Currently, I am an Assistant Professor at the University of São Paulo, Brazil.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: BECCARI , LEONARDO
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Área Temática: **Biociencias y biotecnología**
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Título:

Transcriptional regulation of embryonic cortex development

Resumen de la Memoria:

I performed my PhD thesis in the laboratory of Paola Bovolenta (Madrid), a reference laboratory in morphogen signaling and forebrain development, where I studied the gene networks that control vertebrate forebrain patterning, focusing on the transcriptional regulation of the gene Six3.
After my thesis, I joined the laboratory of Prof. Denis Duboule (University of Geneva), a world-leading reference in the study of the transcriptional regulation of developmental genes, to acquire a solid expertise in the analysis of the transcriptomic, epigenetic and chromatin interaction profiles. Using the HoxD cluster as a paradigm, I addressed different aspects of how the interplay between chromatin architecture and enhancer activity regulates spatio-temporal gene expression and how it contributed to its evolution. I also pioneered the use of gastruloids (3D cultures recapitulating the gastrulation process) to study the transcriptional programs governing the patterning of the post occipital region of the embryo.
In January 2020, I joined the Institute NeuroMyoGene (INMG; Lyon), to establish my own research team dedicated to the study of the transcriptional mechanisms controlling embryonic cortical development, thus bringing together the expertise and research interests of my thesis and postdoc. For that, I pioneered at the Institute the use of human cortical organoids (minibrain cultures derived from pluripotent stem cells). Furthermore, I combine functional genomics (transgenesis/ CRISPR/Cas9 genome editing) and next-generation-sequencing approaches (ChIP-seq, ATAC-seq, 4C-seq, HiC, RNAseq) to study the transcriptional control of neurodevelopmental genes. With this, I aim to establish a new methodological framework that overcomes the limitations of classic model organisms for the study of developmental gene regulation, in large part due to the evolutionary divergence of the human and mouse non-coding genome. As a proof of principle, I focus on the analysis of the transcriptional regulation of the human TBR2 gene, a transcription factor that plays an important role in the cortical neurogenesis process and whose loss of function leads to important brain alterations. Currently, I am: I) deciphering the cis-regulatory code controlling TBR2 expression in neural precursors using a transgenesis screening in human cortical organoids; II) Analyzing the epigenetic and chromatin interaction profiles of the TBR2 genomic region to understand how TBR2 enhancers control its transcription during the neurogenic process; III) Studying how disruption of the 3D architecture of the TBR2 genomic landscape impacts its expression.
In the future, I aim to apply this approach to the study of other neurodevelopmental genes and to understand how mutations in the non-coding genome can impact cortex development and lead to congenital brain alterations/disorders.
The RyC program will allow me to join the Center for Molecular Biology Severo Ochoa, a world-leading multi-disciplinary institute that will provide an ideal environment to progress in my research trajectory and establish as an independent team leader in Spain.
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Resumen del Currículum Vitae:

I performed my biology degree studies at the University of Malaga. During the last two academic years, I worked at the Department of Animal Physiology, Cell Biology and Genetics, where I performed my bachelor s thesis studying the involvement of the Lysophosphatidic Acid Receptor 1 in the adult neurogenesis of the murine subventricular zone. I was awarded an Undergraduate Student Fellowship from the Spanish Ministry of Science.
After this first experience, I joined the group of Prof. Paola Bovolenta (Madrid), a reference laboratory in morphogen signaling and forebrain development. There, I addressed the study of the gene networks controlling vertebrate forebrain patterning, focusing on the transcriptional regulation of Six3. I was funded with an Undergraduate JAE fellowship from the Superior Council for Scientific Research and a Graduate Student Fellowship of the Comunidad Autónoma de Madrid. My PhD work was published in two articles as first author in Development and J Biol Chem (the latter also as co-corresponding author), a review in Mech. Dev., and in seven publications as co-author.
After my thesis, I joined the laboratory of Prof. Denis Duboule (University of Geneva), a world-leading reference in the study of the transcriptional regulation of developmental genes, to acquire solid expertise in the analysis of the transcriptomic, epigenetic and chromatin conformation profiles with the emerging next-generation-sequencing approaches. Using the HoxD cluster as a paradigm, I addressed different aspects of how the interplay between chromatin architecture and enhancer activity regulates gene expression, and how it contributed to its evolution. I also pioneered the use of gastruloids (organoids cultures recapitulating the gastrulation process) to study the transcriptional programs governing the patterning of the post occipital region of the embryo. My postdoctoral training led to three publications as first author in Genes and Dev., Nature and Dev Dyn (also co-corresponding author) one as last author in PNAS, as well as the co-authory in five other research articles.
In January 2020, I joined the Institute NeuroMyoGene (INMG; Lyon) after ranking first in an international call for junior group leaders to establish my independent research team dedicated to the study of the transcriptional mechanisms controlling embryonic cortical

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

development. I received funding for my current work from the INSERM and a joint grant from the Universities of Lyon-Ottawa. In a competitive call, I obtained a permanent research fellow position (Chargé de recherche classe normale-CRCN) from INSERM.
Since my postdoctoral stay, I have trained a total of 6 master students, three of them have performed their master thesis projects under my supervision. I have also participated in teaching activities at the Master and Biology degree programs of the University of Geneva and took part in different scientific outreach activities. Among the latter, I contributed to a divulgation blog of the RTS decouverte (TV outreach platform) and participated in a RTS radio program. Finally, I was part of the evaluation committee for the Arditi Prize to the best PhD thesis in biology (University of Geneva; 2019) and I am a member of the eLife early career reviewer panel.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

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Área Temática: **Biociencias y biotecnología**
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Título:

RNA silencing in plants.

Resumen de la Memoria:

As a graduate student, my fascination in RNA biology led me to join the laboratory of Prof. Javier Palatnik to start my PhD studies (Rosario, Argentina). The central aim of my research was to analyze and characterize plant miRNAs biogenesis, studying RNA intermediates and proteins involved in the processing machinery. During my PhD, I did not only unravel a novel miRNA processing mechanism (Bologna et al., EMBO J 2009) but I also gained expertise in several techniques after three short stays in the laboratories of Prof. Jerome Boisbouvier (Grenoble, France) and Prof. Blake Meyers (Delaware, USA) allowing me to decipher in a genome-wide scale all miRNAs processing mechanisms in Arabidopsis (Bologna et al., Genome Res 2013). Having acquired expertise in the miRNA biogenesis mechanisms, I got interested by the regulation of miRNA silencing pathway via its subcellular localization. To develop this research interest, I obtained an EMBO and a MARIE CURIE ACTIONS postdoctoral fellowships that allowed me to move to the laboratory of Prof. Voinnet (Zurich, Switzerland) to start my postdoctoral studies (Bologna et al., 2014 Annu Rev Plant Biol). During these years, I analyzed the influence of AGO1 subcellular localization on its specific functions, redefining completely the hitherto understood loading action of AGO1 on the plant microRNA pathway (Bologna et al,. Mol Cell 2018). In parallel, I have developed a new strategy, based on catalytically inactive protein version of DCL1, to analyze RNA substrates and interaction partners. This strategy allowed me to describe two DCL1 novel functions associated on transposon elements silencing regulation (Bologna et al., in preparation for Nature Plants *Corresponding). After showing how AGO1 nucleo-cytoplasmic shuttling in Arabidopsis is intrinsically programmed by the availability of its miRNA cargoes, I found that similar mechanisms may well determine the subcellular localization of piwi proteins and WAGOs in the in metazoans. It is actually this question that motivated me to move to Prof. Eric Miska laboratory (University of Cambridge, UK) to explore this question in C. elegans (Moro,.. & Bologna, in preparation for Mol Cell Corresponding). In 2019, I started my position as Junior Group Leader at CRAG Institute in Barcelona. My group, composed by two postdoctoral, two PhDs, one technician, and several undergraduate students, is already supported by numerous grants (Incoming Junior Group Leader from La Caixa Foundation, Proyecto Nacional from MICINN, MSCA, Severo Ochoa postdoctoral and predoctoral fellowships, among the others). The main research interest is to study novel nuclear functions and shuttling mechanism of eukaryotic non-coding RNA pathways. My work during my career has so far produced, a total of 20 publications (14 in Q1), including seven in which I sign as the first author or the corresponding author (six in Q1, the remaining not defined yet) (Moro,., & Bologna. STAR Protocols 2021, Corresponding). In addition, four manuscripts more to be submitted soon. In parallel, during my time at University of Rosario, ETH Zurich and Universidad Autonoma de Barcelona, not only I successfully supervised several undergraduate, PhD and postdoctoral students, but also, I continuously participated in teaching activities of underg
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Resumen del Currículum Vitae:

I am a plant RNA biologist with more than 13 years of experience in the field and, since 2019 I am leading my independent research group studying nuclear functions and shuttling mechanisms of eukaryotic non-coding RNA pathways. By combining cell biology, subcellular fractionation procedures, live-cell imaging, CRISPR/Cas9 methodology, RNA biochemistry, and high-throughput sequencing, I expected to generate a wealth of original information by unraveling novel functions for RNA pathways, making crucial breakthroughs in both metazoan and plant RNA silencing fields.
I obtained my PhD award at the University of Rosario (laboratory of Prof. Javier Palatnik), where I investigated the role and regulation of plant miRNA biogenesis. During my PhD, I also gained expertise in numerous techniques after several short stays abroad at Prof. Boisbouvier's laboratory (CNRS, Grenoble, France) and in the laboratory of Prof. Blake Meyers (DBI, Delaware, United States). Later, I moved Prof. Voinnet s laboratory (ETH, Zurich, Switzerland) to start my postdoctoral studies examining the role of DICER and ARGONAUTES proteins on Arabidopsis sRNA pathways. Lately, I continued my scientific career through a collaboration in the Prof. Eric Miska group (University of Cambridge, UK) to explore ARGONAUTES shuttling mechanism in C. elegans. Finally, in 2019, I obtained a highly competitive position as a Junior Group Leader (PI) at the Centre de Recerca en Agrigenòmica (CRAG) in Barcelona. My group is so far composed of two postdoctoral students, two PhDs students, one technician, and several undergraduate students and already supported by numerous grants.

Among the most relevant achievements in my career I highlight the following:
(1) Establishment of an independent research group at the Centre de Recerca en Agrigenòmica (CRAG). I could already set up a very competitive group, composed of several postdoctoral, PhDs and undergraduate students, which is supported by numerous grants.
(2) Awarded by several and prestigious competitive fellowships and grants from national and international organizations (MARIE

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

SKLODOWSKA-CURIE ACTIONS postdoctoral fellowship, EMBO post-doctoral long-term fellow, FEBS fellow, Incoming Junior Group Leader from La Caixa Foundation, Proyecto Nacional from Ministerio de Ciencia e Innovacion de España, Europa Excelencia 2020 from Ministerio de Ciencia e Innovacion de España, among others).

(3) Contributions to the field of plant small RNA pathways in high impact journals as first author or last author and corresponding (Molecular Cell, EMBO Journal, Genome Research, Annual Review Plant Biology, among others).

(4) Supervision of Postdoctoral, PhD, Master and Bachelor Thesis students and teaching activities of undergraduate and postgraduate courses during the last 15 years at three different universities (University of Barcelona, Spain; University of Science and Technology-ETH, Zurich, Switzerland; University of Rosario, Argentina).

(5) Establishment of an international network of collaboration with top research groups on RNA and/or Plant Biology from different countries around the world.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: BOLOGNESI , BENEDETTA
Referencia: RYC2020-028861-I
Área Temática: **Biociencias y biotecnología**
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Título:

Functional and Dysfunctional Protein Phase Transitions

Resumen de la Memoria:

The central question to my research is understanding how protein self-assembly can cause toxicity. I tackled this question by means of different approaches during my career and I now see a combination of biophysics, cell biology and genomics as the most promising strategy to understand the implications of protein self-assembly in biology and disease. With this perspective in mind, after a competitive call, I became a Junior Group Leader at the Institute for Bioengineering of Catalonia (IBEC) in 2018 to develop this research line. My group, Phase transitions in Health and Disease develops deep mutagenesis methods to map the effect of millions of mutations in yeast prions and human disordered proteins implicated in neurodegenerative diseases. On the basis of these pioneering results (Nat Commun, Curr Opin Cell Bio), I was awarded a grant of 110,000 Euros from the Ministerio de Ciencia, Innovación y Universidades and my lab is one out of only three European labs invited to take part in the Atlas of Variant Effects, the most important global initiative on predictive medicine.
This progression in the last 2 years allowed me to recruit 2 talented PhD students (with competitive predoctoral fellowships) and a lab manager to support our high-throughput approaches. This Ramon y Cajal grant will enable me to further consolidate and expand this novel research line. Besides systematically mapping how all mutations in specific protein domains affect cellular toxicity and amyloid nucleation, we have also recently proven that the quantification of genetic interactions can be used for in vivo structure determination, an exciting new avenue which will be further supported by this grant (Nat Commun, eLife - under review).
Previously, I was a Post-Doc at the CRG, Barcelona, as a Marie Curie COFUND fellow across Ben Lehner s and Gian Tartaglia s lab. Here, I carried out an interdisciplinary study proving how inappropriate liquid-liquid phase separation can cause dosage sensitivity (Cell Rep, eLife). I also collaborated on several projects addressing the role of RNA as a scaffold in protein self-assembly (Cell Rep, NARx2, Bioinformatics, RNA). At the end of my post-doc, with the perspective of establishing my own research line, I developed a deep mutagenesis approach to study intrinsically disordered proteins.
I did my PhD at the University of Cambridge, as a fellow of St. John s College (Alzheimer s Research Trust Fellowship). In the Dobson s lab, I performed a biophysical characterization of the aggregation properties of the Amyloid-Beta peptide. One of my PhD papers has highlighted a biophysical feature shared by many protein oligomers and predictive of their toxicity (ACS Chem Biol, Nat Struct Mol Biol, Angew Chem). The extent to which hydrophobic patches are exposed is an indicator of the potential harm caused by protein oligomers. This paper has been cited more than 300 times. In another first-author publication, I discovered a link between the structural properties of amyloid fibrils and the molecular mechanism driving the kinetics of their formation (ACS Chem Biol, ACS nano).
Overall, I have published 22 scientific papers (6 first author, 3 corresponding author), 16 of which in Q1 journals. I collaborate with EU and US-based labs and received recognition as outstanding female scientist (Women in Science Support Grant and LIBRA H2020 program).
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Resumen del Currículum Vitae:

RESEARCH FOCUS:
The central question to my research is understanding how protein self-assembly causes toxicity. Along my career, I have tackled this problem by combining biophysics to cell biology and genomics. While providing systematic approaches to study protein-induced toxicity, my work has radically changed our understanding of the process, shifting the focus towards oligomeric species and liquid de-mixing. My approach has now the potential to 1) reshape our understanding of protein sequence/structure/function relationships and 2) decipher how single nucleotide changes among individuals can cause disease.

CURRENT POSITION:
Junior Group Leader of the Protein Phase Transition in Health and Disease group, Institute for Bioengineering of Catalunya (IBEC); Barcelona, Spain (2018 now).

PREVIOUS POSITIONS:
Senior Post-Doctoral Fellow, Centre for Genomic Regulation (CRG), Barcelona, Spain (2015-18).
Marie Curie COFUND Post-Doctoral fellow, CRG, Barcelona, Spain (2012 15).
PhD Student, Department of Chemistry, University of Cambridge, UK (2007 12).
GRANTS and FUNDING as PI:
PRIOMUT. Deep mutational scanning of a prion-like domain to understand protein-induced toxicity (RTI2018-101491-A-I00) RETOS-MICIU, 110.000 Euros (2019-21).

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Functional and dysfunctional phase transitions in the cell project awarded by IBEC. 376.590 Euros (2018-2022)

SCHOLARSHIPS AND FELLOWSHIPS:
- WOSS Women Scientist Support Grant (2016)
- Marie Curie COFUND Fellowship, INTERPOD programme (2012)
- Alzheimer's Research Trust PhD scholarship (2007)

PUBLICATION METRICS:
- 22 published papers+1 under revision (6 first author, 4 corresponding author).
- H-index:17
- Citations: 1336

INVITED TALKS AS EXPERT (Recent/Upcoming):
Total 14 invitations. Examples:
- SEBBM Congress, Barcelona 2021
- CIG, Lausanne 2021
- University of Copenhagen, 2021
- IDP Virtual Seminar Series 2020
- University of Washington, Seattle 2020
- IRB, Barcelona 2020
- BioInfo4Women Seminars, Barcelona Super Computing Centre 2019
- IBB, UAB, Barcelona 2016

INTERNATIONAL CONFERENCES:
Total 10 Posters and 4 Selected Talks, including:
- CRISPR and Beyond: Understanding Genomes (Wellcome Genome Campus, Hinxton, UK, 2019)
- VIB Phase Transitions in Biology and Disease" (Leuven, Belgium, 2017)
- Alzheimer's Research Trust Conference (South Hampton, UK, 2010)
- FASEB Amyloid Fibrils Formation and Disease (Snowmass, Colorado, USA 2009)

ONGOING COLLABORATIONS
- Dr Priyanka Narayan (NIDDK, NIH, USA)
- Dr Broder Schmidt (University of Stanford, USA)
- Prof Ben Lehner (CRG, Barcelona)
- Prof Xavier Salvatella (IRB, Barcelona)

ORGANIZATION of SEMINARS and COURSES
- Cambridge Biophysical Colloquia Seminar Series (University of Cambridge)
- Post-Doc Symposium (CRG, Barcelona)
- Gibson cloning course (CRG, Barcelona)
- Protein Folding and Misfolding (CRG, Barcelona)

WEBTOOLS: http://s.tartaglialab.com/update_submission/321827/2fd8319ac9.

MEMBERSHIPS:
- Biophysical Society
- International Society for Computational Biology
- Atlas of Variant Effect Alliance (https://www.varianteffect.org/)
- CATCAT (https://www.catcat-celltissuebiology.cat/)

STUDENTS SUPERVISION:
- PhD Thesis: 2 ongoing (IBEC/UB)
- Master Thesis: 4 completed (UPF, UAB, University of Pavia).
- BA projects: 3 completed, 1 ongoing (UPC, UAB, University of Pavia, University of Firenze)
- Member of 4 PhD Defense Tribunals in 2020 and of 4 Thesis Advisory Committees.

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Turno de acceso general

Nombre: YANG , JAE-SEONG
Referencia: RYC2020-028880-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: jaeseong.yang@cragenomica.es

Título:

Computational and synthetic biology

Resumen de la Memoria:

My main research interests are to understand how genetic variation affects gene expression and molecular interactions, and to generate predictive models for this. To investigate how mutations can change biological phenotypes, I have developed computational and high-throughput experimental methods to quantify mutational effects. Specifically, I have focused on quantitatively unveiling regulatory information encoded in DNA sequences and their effects on protein structures and/or molecular interactions.

Unveiling key determinants of transcription/translation and developing predictors for metabolic engineering

Precise prediction of prokaryotic translation efficiency can provide valuable information for optimizing bacterial host for the production of biochemical compounds or recombinant proteins.

As a graduate student, I investigated the relationships between hundreds of 5 UTR variants and the translation efficiency of mRNAs in E. coli, by focusing on thermodynamic interactions between ribosomal complexes and mRNA. Furthermore, I studied the evolution of allosteric molecular binding sites and developed a method to modify allosteric regulation of enzymes while preserving their activities.

As a postdoctoral researcher, I systematically investigated hundreds of thousands of synthetic promoter sequences, revealing key sequences that determine transcription efficiency in mycoplasma pneumonia. Based on this data, I built prediction models for transcription and translation efficiency and as a result we engineered bacteria to effectively express a therapeutic protein to industrially relevant levels.

This increased our understanding of the processes underlying gene expression and provided an efficient design principle for optimizing various biological systems, thereby facilitating future efforts in metabolic engineering and synthetic biology.

Properties of interacting protein pairs and developing a novel high-throughput protein-protein and RNA-protein interaction detection method

Characterizing biochemical properties, such as inter-molecular interactions, are essential to quantitatively understand how biological systems work. For example, knowing which proteins and RNAs directly interact provides us with insight into underlying molecular mechanisms.

During my Ph.D. and post-doc training, I investigated protein-protein interactions from both evolutionary and structural aspects, and further developed a novel high-throughput pipeline to detect protein-protein and protein-RNA interactions at the ORFeome scale.

Summary

These achievements demonstrate my capability to lead and to conduct R&D projects in science and technology. I have started my own independent group in Centre for research in agricultural Genomics (CRAG) in Barcelona from September 2019. Using my knowledge and skill base, we will investigate heterologous gene expression in biotechnologically relevant microalgae such as Chlamydomonas and Chlorella to develop an eco-friendly synthetic engineering platform.

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Resumen del Currículum Vitae:

I obtained my Ph.D. as a computational biologist at POSTECH, South Korea. During my Ph.D. training, I actively participated in various research projects that required data interpretations, machine learning, and communication with experimental biologists, resulting in 25 articles. Among them, I was the first author of 7 publications and the second author of 7 publications. Next, I moved to Barcelona in Spain where I worked as a postdoctoral researcher at Prof. Luis Serrano s Lab (CRG). Initially, my position was supported by the European collaborative research project (PRIMES), and then I obtained a Juan de la Cierva fellowship. During this period, I developed a novel high-throughput method to investigate hundreds of thousands of synthetic promoters, revealing key sequences that determine transcription

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

efficiency in Mycoplasma pneumoniae (Nature Comm. 2017). Further, I developed another method to identify protein-protein and RNA-protein interactions at an ORFeome-wide scale (Nature Comm. 2018, Methods 2019). Later, I moved to POSTECH in Korea, working as a Research Assistant Professor with my own Research Fellow funding from the National Research Foundation of Korea.

As a Junior Group leader at the Centre for Research in Agricultural Genomics (CRAG), since September 2019, I have started my independent research group on Computational and Synthetic Biology, with the initial goal of developing a bioengineering platform for photosynthetic cell factories, using two novel methods I developed during my post-doc period.

Among the most relevant achievements in my career I highlight the following:

(1) Awarded by several and prestigious competitive fellowships from national calls (Juan de la Cierva-incorporation, Research Fellow, a junior group leader from Severo Ochoa);
(2) Contributions to the field of computational and synthetic biology in high impact factor journals (Biotechnology Adv., Nature Communications, Bioinformatics, PLoS Comput Biol., Metab Eng.,);
(3) Establishment of an international and national network about 20 research groups from 4 different countries
(4) Author of 10 free/open-source software (ConLoc, IS, OASIS, PDZNet, UTRDesigner, UTRLibrary, SAPIN, TAPAS, ELMSeq, recYnH)
(5) Supervision of PhD, Master and Bachelor Thesis
(6) Studies of bacterial transcription and translation regulation (5 papers)
(7) Studies of protein-protein and RNA-protein interactions (10 papers)
(8) Studies of Single/Multiple localized proteins and sub-organellar localization (4 papers)
(9) Structural and evolutionary analysis of allosteric regulation and catalytic sites (2 papers)
(10) Developing statistical tools for the analysis of aging data (6 papers)

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Turno de acceso general

Nombre: SANCHEZ LOPEZ, MATEO
Referencia: RYC2020-029676-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: mateoisidro@hotmail.com

Título:

Directed evolution of optogenetic technologies for cell biology and neuroscience

Resumen de la Memoria:

I did my PhD in Santiago de Compostela in the department of organic chemistry under the supervision of Prof. Jose Luis Mascarenas and Eugenio Vazquez (2008-2014). The main focus of my thesis was related with the design and synthesis fluorescent DNA binders. Thanks to a FPU scholarship I had the opportunity the perform two internships in the in the groups of Prof. Matthew Bogyo, in the Pathology Department at Stanford University, and Prof. Alice Ting in the Chemistry Department at the Massachusetts Institute of Technology. I was awarded with the best thesis award of the University of Santiago de Compostela and with the X Eli Lilly Award for the best PhD Students in organic and analytical chemistry. During my training, I gained expertise in organic synthesis, spectroscopic and biophysical techniques. However, I become fascinated with protein engineering and directed evolution techniques. Therefore, for my postdoctoral studies (2015-2020) I decided to switch fields and I joined the Ting lab, first at MIT and later in the genetics and biology department at Stanford University. As postdoc, I was funded with a long-term EMBO fellowship and I worked on the directed evolution of optogenetic technologies for cell biology and neuroscience. To build tools like SPARK and FLARE, I combined yeast genetics, FACS, protein expression, molecular biology techniques, cellular cultures and neuroscience.
I aim to combine my training as synthetic organic chemistry with molecular biology to establish my own research at the interface between chemistry and biology; using chemistry to expand our knowledge in biology and biology to create new chemistry. With this expertise in both fields along international experience in world-top universities (MIT and Stanford) for several years, I firmly believe that I am ready to take the next step in my career.

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Resumen del Currículum Vitae:

I did my PhD in Santiago de Compostela in the department of organic chemistry under the supervision of Prof. Jose Luis Mascarenas and Dr. Eugenio Vazquez Sentis (2008-2014). The main focus of my thesis was related with the design and synthesis fluorescent DNA binders. As result of my thesis, I published 17 papers (10 of them as first or co-first author) some of them among the best journal in the area (ACIE or Chem Sci). I would like to highlight that I performed the first experiments in Mascarenas lab on the use organometallic catalysts in living cells (Chem. Sci. 2014, 5, 1901). This pioneering work paved the way of an ERC adv grant project that was awarded to the group in 2013. I got awarded with a FPU scholarship and I had the opportunity to perform two brief internships in the in the groups of Prof. Matthew Bogyo, (in the Pathology Department at Stanford University), and Prof. Alice Ting (in the Chemistry Department at the Massachusetts Institute of Technology). Its worthy to mention that the projects in which I participated, were later published in top journals (JACS, Nat. Protcols). This interdisciplinary experiences allowed me to be awarded the best thesis award of the University of Santiago de Compostela and the X Eli Lilly Award for the best PhD Students in organic and analytical chemistry. During my PhD training, I gained expertise in organic synthesis, spectroscopic and biophysical techniques. However, I become fascinated with protein engineering and directed evolution methods. Consequently, I decided to switch fields for my postdoctoral studies (2015-2020) and I joined the Ting lab, initially at MIT and later in the genetics and biology department at Stanford University. As postdoc, I was funded with a long-term EMBO (2016-2017) fellowship and I worked on the directed evolution of optogenetic technologies for cell biology and neuroscience to build tools such as SPARK and FLARE.
During my postdoctoral appointment, I have gained expertise in a wide and diverse set of skills such could be yeast genetics, FACS, protein expression, molecular biology techniques, cellular cultures and neuroscience. I created a new platform in yeast for the directed evolution of faster TEV protease variants. I was able to report these results as first author in an article published this year in Nature Methods (2020,17,167). The selected mutants were incorporated into the FLARE design combined with other optimized modules which led to a much improved second generation tool (FLiCRE). In collaboration with the Deisseroth¿s lab, we applied FLiCRE to discovered a new cell type in the nucleus accumbens that drove aversion upon illumination via opsin-reactivation of the tagged neuronal ensemble; a proof of concept that demonstrates the revolutionary potential of tool. These findings will be published in Cell (in press, joint co-first). As the development of calcium integrators is still in its infancy, I engineered a new Ca2+-activated TEV protease for the transcriptionally readout of neuronal activity, this work was also recently published in PNAS (in press, first author). All these tools have the potential to revolutionized neuroscience and due to its modular nature can be adapted to other areas in biology.

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CONVOCATORIA 2020

Turno de acceso general

Nombre: BALLESTEROS MARTIN, IVAN
Referencia: RYC2020-029563-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: ivanbamartin@gmail.com

Título:

Inmunidad Innata

Resumen de la Memoria:

My research career is focused on understanding how the plasticity of the innate immune system is orchestrated and to characterize its physiological relevance. I have explored this phenomenon for more than 12 years across three main stages of my career:

-During my PhD (2008-12) at the School of Medicine Complutense University (Spain) I explored the role of microglia and infiltrating myeloid cells on stroke outcome. Mentored by Maria A. Moro
-During my first postdoctoral stay (2014-2016) at Kings College London (UK) and Memorial Sloan Kettering Cancer Institute (U.S.) I focused on the study of tissue resident macrophage development, a research interest that has greatly contributed to expand my previous understanding of innate immune heterogeneity. Mentored by Frederic Geissmann.
-In my second postdoctoral stay (2017-today) at CNIC (Spain) I explored neutrophil plasticity in homeostasis using state of the art genomics and novel murine models to characterize the biology of tissue associated neutrophils. Mentored by Andrés Hidalgo.

During my PhD at Universidad Complutense I focused on understanding how could we modulate the innate immune response following stroke to diminish brain damage. My studies identified a high degree of heterogeneity within myeloid cells (M1/M2 for macrophages, N1/N2 for neutrophils) in thee ischemic brain that was associated with stroke outcome and, more importantly, it could be pharmacologically modulated by targeting PPAR gamma activation. In addition, My research on neuroinflammation and stroke at Moro¿s Lab resulted on the publication of a total of 14 indexed research articles (4 of them as first author) and 4 review articles. Within them, I find two of these projects of special relevance: In the first one we explored the implication of the Aryl Hydrocarbon Receptor (AhR) in stroke and characterized a novel molecular pathway associated with brain damage. In the second one, I characterized a platelets-neutrophil crosstalk in stroke and identified that platelets-neutrophil interactions within the capillaries of the ischemic brain were associated with an increased infarct size.

During my stay at the Geissmann lab I focused on the analysis of macrophage development in situ in the mouse embryo. Results from this project led to the concept that colonization of organ anlagen by macrophage progenitors is followed by their fast specification into tissue macrophages, hereby generating the macrophage diversity observed in postnatal tissue.

At Andrés Hidalgo lab, I explore whether neutrophils in tissues are able to adapt to their environment and I identified that neutrophils heterogeneity in the steady state is associated with tissue specific transcriptional profiles and functions revealing that tissues co-opt neutrophils en route for elimination to induce programs that support their physiological demands. This is a novel concept in the field, as neutrophils has been classically studied as a homogeneous population with a low degree of heterogeneity.

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Resumen del Currículum Vitae:

I am an experienced researcher in the field of innate immunity. Since 2008, I contributed with a total of 27 research items, including research articles in high-impact journals (Science, Cell, Immunity, Circulation, JEM), 5 of them as leading or corresponding author (JLB, 2013; Stroke, 2014; Circulation, 2014; Science, 2016; Cell, 2020), several methods and review articles (4 as leading or corresponding author) and book chapters (3 as leading or corresponding author). My H-index is 17 and my research holds a total of 1633 citations (source: Scopus). During my career I have been granted with several fellowships, including a doctoral Grant from the
Spanish Ministry of Science (2008-12), a Marie Curie IEF fellowship from the European Commission (2017-2019) and an EMBO Short Term Fellowship (2019) to explore neutrophil epigenomics at Oxford University. I am also a Principal Investigator of a Young Investigator Grant from the Leducq Foundation, external evaluator of the PhD committee of Complutense University (2018- today) and CNIC (2019-today), Grant evaluator of the Ministry of Science, director of two Master Students projects and currently I am codirecting two doctoral PhD thesis at the laboratory of Dr. Andrés Hidalgo. I am reviewer for several scientific journals (British Journal of Pharmacology, Circulation, iScience, Journal for ImmunoTherapy of Cancer, among others). In addition, I have participated as a
teacher at the Master of Immunology of Complutense University (2019-today).

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: ALVAREZ PINTO, ZAIDA
Referencia: RYC2020-028732-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: zaidaalvarezpinto@gmail.com

Título:

Bioactive scaffolds for neural tissue engineering: in vitro platforms and in vivo therapies.

Resumen de la Memoria:

My scientific trajectory embraces a variety of scientific fields including neuroscience, material science, chemistry, tissue engineering, and regenerative medicine. During my scientific career, I have been involved in multidisciplinary activities supported by prestigious and competitive programs, actively collaborating with top experts in different fields.
My graduate studies at the Institute for Bioengineering of Catalonia and Polytechnic University of Catalonia (UPC) was highly relevant as it provided new details into the workings of biomaterials science and neural tissue engineering and allowed for further explorations into developing biomaterials that mimic physical and biochemical characteristics of the embryonic neural stem cell niche. During this period, I have published 4 first-author papers (Biomaterials, 2013; Journal of Neuroscience Methods, 2014; Biomaterials, 2014; Cerebral Cortex 2016) in the first Q1. During my postdoctoral career experience at the Simpson Querrey Institute for Bionanotechnology at Northwestern University (USA), I have been working on peptide amphiphile nanostructures functionalized with different bioactive epitopes to investigate their effects on regenerative medicine and particularly in spinal cord regeneration. I have published numerous papers during my postdoctoral career (Nature nanotechnology, 2017; Nature communications, 2017; Nano letters, 2018; Nature communications, 2018; Advanced Science; 2019; Science, 2019; Nature materials, 2020..etc).
In my current position as Research Assistant Professor, I am currently working on two manuscripts that we submitted in December 2020 to Science and Cell Stem cell. I am particularly excited about one of these projects, as it involves the development of a highly potent, novel therapy that could be easily injected before gelling in the spinal cord environment. I have designed an injectable hydrogel containing peptide amphiphile nanostructures functionalized with different bioactive epitopes and molecular mobilities, two variables that enhanced functional recovery after spinal cord injury. I then investigated the effects of these structures on vascular regeneration, axonal extension within the scaffolds, and long-term survival and integration of axons into the surrounding tissue in a mouse model of spinal cord injury. In my second work, I have designed a new laminin-based platform for the study of neural disease progression by means of iPSCs derived into neurons. This platform has potential to enhance the attachment, survival, and maturation of these cells compared to those seeded on commercially available coatings. National Institute of Health (NIH) has shown interested in the platform.
Finally, I start working on a new hydrogel-based microenvironment to mimic the native, healthy brain and spinal cord and promote functional regeneration. These microenvironments are being designed to administer combinatorial therapies that address multiple barriers to CNS repair by incorporating guidance architecture, substrate-immobilized factors, genetically encoded regulatory factors, and cell replacement.
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Resumen del Currículum Vitae:

I graduated from the University of Barcelona in 2007 with a Bachelor of Biology specialized in Sanitary Biology. I coursed a master s degree in Biomedical Engineering from University of Barcelona (UB) and Polytechnical University of Catalonia (UPC). I carried out my PhD in Biomedical Engineering studying the effect of polylactic acid scaffolds in brain regeneration at Biomaterials for Regenerative Therapies group lead by Josep Planell and Elisabeth Engel at the Institute for Bioengineering of Catalonia (IBEC) in collaboration with Alcantara s lab at the Faculty of Medicine (UB), with an IBEC fellowship for 4 years. My thesis dissertation, qualified excellent cum laude, included four publications as a first author in the first quartile journals in biomaterials and neuroscience. To start my postdoctoral career, I was awarded a Beatriu de Pinos Postdoctoral Fellowship (AGAUR, supported by the Marie Curie COFUND Action FP7 European Commission) from 2015-2017 to join Prof Samuel I. Stupp laboratory at Simpson Querrey Institute, Northwestern University, Chicago, USA. After that period, from 2017-2020, I continued as a Paralyzed Veterans of America Postdoctoral Fellow in the same lab. My work resulted in a high-impact publication in Nano letters (2018), and Advance Science (2019) in where I was the first co-author. I also collaborated in other projects aimed to characterize the effect of supramolecular materials in regenerative medicine (Nature Nanotechnology, 2017) and specifically in neural tissue systems (Nature communications, 2017; Nature Communications, 2018; Science, 2019; Nature materials, 2020). In my current position as Research Assistant Professor, I direct the lab s research portfolio around central nervous system regeneration projects using biomaterials scaffolds. During this year, I have obtained two national grants as a principal investigator. Among my additional responsibilities in my current position, I am co-directing two graduate students theses in the biomedical engineering program. I am also mentoring several undergraduate students in their research projects by assessing, reviewing and evaluating student activities and progress and provide mentorship and professional guidance to improve student productivity in the laboratory. I am consulting engineer in AmphixBio Inc to commercialize biomaterials for regenerative medicine. I am also member of INVO Forward Therapeutics which is a mentorship program to accelerate biomedical commercialization at Northwestern University. I am author of 20 published articles in SCI-

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

indexed scientific journals with more than 590 citations and h-index=13 in Google Scholar, more than 480 citations and h-index=12 in Scopus and more than 440 citations and h-index=12 in Web of Science (WoS). I also got an average of citations per year of 56 (WOS). I have given numerous oral and poster presentations in national and international conferences. I am listed on three active patents transferred to AmphixBio Inc. I have received numerous awards from European conferences and other international scientific organizations such as Young investigator Baxter Award, US.

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CONVOCATORIA 2020

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Nombre: HERRERA RINCON, CELIA
Referencia: RYC2020-029499-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: celia.herrer@gmail.com

Título:

Análisis y Modelización del Procesamiento de la Información

Resumen de la Memoria:

Siempre me he considerado una neurocientífica no convencional, destacando principalmente por la inherente transversalidad e interdisciplinaridad de todos mis proyectos. Tras doctorarme en Neurociencia por la UCM en 2014 (con una Tesis Doctoral sobre procesamiento cognitivo de la información y neuroplasticidad) me trasladé a Estados Unidos no sólo para desarrollar mi carrera como investigadora postdoctoral, sino también con el objetivo comprender profundamente diferentes procesos de comunicación celular para lograr la efectiva modelización experimental y matemática del procesamiento complejo de la información biológica. Así, comencé mi etapa postdoctoral en Febrero de 2015, uniéndome al laboratorio del brillante Prof. Michael Levin en Tufts University (Boston, MA). Considero mis años junto al Prof. Levin como los más fructíferos y apasionantes de toda mi carrera, yendo más allá de la mera aplicación de mis conocimientos en Neurociencia a la comprensión profunda de la Inteligencia Artificial y Computación Biológica no convencional. Hasta finales de 2017 trabajé explorando los algoritmos por los que el mundo biológico implementa comportamientos adaptativos complejos, y desarrollé dos modelos únicos en Xenopus para ello: embriones sin cerebro (brainless embryo; Herrera-Rincon et al., Nat. Commun. 2017; Herrera-Rincon and Levin, Commun Integr Biol 2018) y un biorreactor ponible para inducir regeneración de miembro en ranas adultas (Herrera-Rincon et al., 2018 Cell Rep.). A finales de 2017 conseguí mi primer proyecto como Investigadora Principal (IP), financiado por la prestigiosa Fundación Templeton (TWCF, Templeton World Charity Foundation, Inc.). El Proyecto (TWCF0241), titulado From microbes to minds: using a Neural-Bacteria Interface to discover a universal code for information-processing across scales of biological organization , tiene como objetivo el estudio interdisciplinar de la comunicación bidireccional neuronas-bacteria, desde la construcción de la primera plataforma inteligente cerebro-bacteria (con cultivo simultáneo de neuronas de mamífero y bacterias), al análisis masivo de los datos sobre información mutua y la modelización matemática de las interacciones en tiempo real. Tras las aportaciones científicas conseguidas con el proyecto (Herrera-Rincon et al., 2020 NPJ Regen Med; Trivedi, , Herrera-Rincon., 2021 Science Advances (under review), la Fundación Templeton me otorgó una segunda financiación (TWCF0503) para continuar mis investigaciones, reincorporándome a la UCM en Agosto de 2020 como Personal Investigador por proyecto específico. Desde entonces, trabajo aplicando los conceptos teórico-prácticos de Big Data y Biocomputación sobre los resultados experimentales obtenidos en la plataforma cerebro-bacteria, consiguiendo la primera modelización de la comunicación bidireccional y transferencia de información entre reinos biológicos (neuronas y bacterias; manuscrito en preparación, Enero 2021).
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Resumen del Currículum Vitae:

Resumen Libre de Carrera Investigadora: Seis años después de doctorarme, puedo objetivamente afirmar que mi carrera científica ha sido exitosa. En 2014, obtuve mi Título de Doctor en Neurociencias por la Universidad Complutense de Madrid (UCM; Beca Predoctoral FPI-UCM). En Febrero de 2015 me trasladé a Estados Unidos para comenzar mi etapa postdoctoral en Tufts University (Boston), en el laboratorio del brillante Prof. Michael Levin, de reconocido prestigio mundial por sus estudios sobre los mecanismos biofísicos y computacionales que dirigen la toma de decisiones dentro de poblaciones multicelulares (nombrado por muchos como la nueva bioinformática de la forma). Tras sólo dos años trabajando como estudiante postdoctoral, en 2017 conseguí mi primer Proyecto como Investigadora Principal (IP). Este Proyecto, dirigido al estudio experimental y modelización de la comunicación bidireccional entre neuronas y bacterias (TWCF0241), fue logrado en una convocatoria internacional altamente competitiva lanzada por la fundación Templeton World Charity Foundation, Inc. (TWCF), que cada año financia dos proyectos alto riesgo/alto beneficio a prometedores jóvenes investigadores para que puedan comenzar su carrera independiente. En 2019, y tras haber sido ascendida a Research Scientist II en Tufts, decidí regresar a Europa para consolidar mi carrera. Gracias a los resultados como IP, liderando un equipo multidisciplinar de distintos laboratorios en Tufts y Harvard University, la TWCF decidió prorrogar mi proyecto de investigación, otorgándome una segunda financiación para continuar mis investigaciones en la Institución Europea de mi elección. Así, en Agosto de 2020, me incorporé a la UCM como IP de un segundo proyecto (TWCF0503) con un contrato de Personal Investigador por proyecto específico. Publicaciones: Más de 15 publicaciones, incluyendo artículos como primer firmante en Nature Communications (2017), Cell Reports (2018) y Nature Regenerative Medicine (2020). Google Scholar: Índice h =8, Índice i10=7. Movilidad Internacional: Como estudiante predoctoral, realicé estancias en Universidades y Centros de Investigación nacionales e internacionales. Entre otras, Universidad de Turín (Italia; 3 meses en 2010 y 2012), Hospital Clínico San Carlos (España; 6 meses en 2013) y University of Central Florida (FL, US; 3 meses en 2013). De 2015 a 2019 he estado realizando mi investigación postdoctoral y como IP en Tufts University (MA, US). Liderazgo: Sólo en 2019, fui invitada como ponente a cuatro conferencias y seminarios internacionales, incluyendo un Special Seminar en el NIH en Marzo 2019 (Bethesda, MD) premiada con el nombramiento de Rising Star 2019 por mi relevante trayectoria como joven investigadora. Mi trabajo publicado en Cell Reports (2018) fue seleccionado por STAT-Boston

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Globe como una de las 64 mejores publicaciones científicas en Biomedicina. Mis investigaciones han sido ampliamente cubiertas por la prensa internacional, incluyendo entrevistas para WIRED o el canal científico americano PBS. En Julio 2020 fui la ganadora del Innovator Fellowship Programme, organizado por el Instituto EIT Food de la Unión Europea y dirigido a jóvenes investigadores emprendedores, por mi proyecto de innovación científica Food4Mood.

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Turno de acceso general

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Título:

The impact of multifactorial stress combination on plants

Resumen de la Memoria:

The deteriorating environmental conditions of our planet pose an increasingly dire challenge to plants. These, not only include fluctuating weather events (heat waves, cold snaps, flooding and/or drought), but also a dangerous combination of other factors, ranging from extreme soil conditions (saline, basic or acidic), coupled with a high soil content of different contaminants. Although the knowledge of the response of different biological systems to each of these individual conditions is vast, we know very little about how a combination of many of these factors, occurring simultaneously, will impact plant life on our planet and shape our future. Therefore, the goal of my PhD was to determine the responses of citrus plants to the combination of drought and heat stress to identify key hormones, metabolites and proteins that orchestrate this response. The results obtained during my PhD served as a starting point to determine which citrus rootstocks are more appropriate to grow under this stress combination, that frequently occur in Mediterranean climate and limit crop growth and yield. After my PhD, I joined the lab of one of the pioneers of stress combination in plants, Dr. Ron Mittler, (University of North Texas and University of Missouri, 2017/21), where I was pioneering in demonstrating that multifactorial stress combinations impact an ecosystem in ways that we may not be able to currently predict and that once additional factors are introduced, they could negatively interact with each other and push the system towards a rapid collapse. By using cutting-edge biotechnology such as CRISPR-Cas9, transcriptomic networks, proteomics and metabolomics, and participating in an international network (USA, Spain, Israel), we revealed that maintaining 2 critical biological processes (iron through AtNEET protein and reactive oxygen species (ROS) homeostasis), is essential for plant acclimation to multifactorial stress combinations. This novel area led me to successfully initiate my own research to further analyze the mechanisms that regulate plant responses to multifactorial stress combinations and generate biotechnological-breeding tools for developing more resilient crops in the near future. In this new stage of my career, I co-advised a PhD student, I have been awarded a grant from Plan GenT for doctors with international experience (CDEIGENT 2021) and a MSCA Individual Fellowship (H2020-MSCA-IF-2020 ID 101018642) is under review to develop my vision to enhance plant resistance to multifactorial stress combinations. Overall, my scientific impact is demonstrated by 38 scientific papers (17 first author and 1 corresponding author) and 3 book chapters, with a current H-index of 19, and over 1700 citations.

The main goals of my future research line are (i) to deeply identify key molecular regulatory pathways, networks and proteins that are involved in the plant responses to multifactorial stress combinations and (ii) to use some of the mechanisms and pathways previously identified to enhance the tolerance of plants to conditions of multifactorial stress combinations. My research program will certainly provide valuable information about key molecular/metabolic/physiological mechanisms for the regulation of plant responses to multifactorial stress combinations, that can be used to develop plants more tolerant to naturally-occurring stress conditions

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Resumen del Currículum Vitae:

Global warming, climate change and environmental pollution present plants with unique combinations of different abiotic and biotic stresses. Although much is known about how plants acclimate to each individual stress, little is known about how they respond to a combination of many of these factors (multifactorial stress combination). My main research line is focused on (i) the study of molecular plant responses to multifactorial stress combinations and (ii) the use of plant biotechnological tools to improve the yield and survival of plants subjected to multifactorial stress combinations.

During my PhD (Universidad Jaume I), I studied plant responses to the combined effect of two stresses using molecular biology and plant physiology and biochemistry. The impact of my predoctoral research was recognized by the Extraordinary PhD Award (UJI) and Cum Laude PhD (International Mention). During my postdoctoral period at University of North Texas and University of Missouri (USA, 2017-2021), I was pioneering in demonstrating that multifactorial stress combinations impact an ecosystem in ways that we may not be able to currently predict and that once additional factors are introduced, they could negatively interact with each other and push the system towards a rapid collapse. This novel area of stress combination led me to successfully initiate my own research to further analyze the mechanisms that regulate plant responses to multifactorial stress combinations and generate biotechnological-breeding tools for developing more resilient crops in the near future. In this new stage of my career, I have co-advised undergraduate and MSc students and a PhD student, and I have been awarded a grant from Plan GenT for doctors with international experience (CDEIGENT 2021) to develop my vision to enhance plant resistance to multifactorial stress combinations.

Overall, my scientific record was recognized by the Francisco Sabater Award 2019 given by the Spanish Society of Plant Physiology to the best young plant biologist, serving as the Spanish candidate for the FESPB Young Plant Scientist Award, that will be awarded in the conference Plant Biology Europe 2021. My multidisciplinary background, leadership, capacity of adaptability, productivity, and research

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

vision will significantly contribute to the innovation of the Spanish Plant Biotechnology field, and the Ramon y Cajal contract is, certainly, the ideal opportunity to reinforce and lead my research program.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

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Título:

Adjustment of plant development through regulation of plant transcriptomes

Resumen de la Memoria:

I am a biologist with expertise in both computational and experimental biology. Since the beginning of my scientific career, I have been interested in understanding how different environmental signals are molecularly integrated by plants to coordinate development, a research interest addressed both during my PhD and Postdoc. During my PhD, in the laboratory of Elena Monte at the Centre for Research in Agricultural Genomics (CRAG; Barcelona), I studied the role of a specific subfamily of transcription factors controlling gene expression in response to light stimulus, and in coordination with other environmental and/or internal cues. After my PhD, I moved to the laboratory of Paula Duque at the Instituto Gulbenkian de Ciência (IGC; Lisboa) pursuing my interest on alternative splicing (AS) and its role shaping plant development, a yet understudied process in plants. Importantly, the Duque lab has provided the first functional links between AS and ABA-mediated plant stress responses. During this period, my research is uncovering novel and exiting roles for AS in controlling cell expansion at the interplay of light and stress responses. Moreover, my collaborative work with researchers at the Centre for Genomic Regulation (CRG; Barcelona), has provided the plant research community with novel bioinformatic resources for the study of AS. The relevance of the laboratories in which I have developed my career in their respective plant research areas (photobiology and AS), and presenting my work in different scientific meetings covering these topics, have increased my international scientific network by interacting and collaborate with researchers at the forefront of each scientific area. Moreover, both laboratories have provided me an environment in which I could follow my personal scientific interests, greatly contributing to develop my scientific independence and maturity.

During my PhD and current postdoc I have published 11 articles, six of them as first-author, including top international journals such as Current Biology, Nature Communications and Genome Biology, and another first-author article has been submitted. Importantly, I am first and co-corresponding author in my latest papers at Genome Biology and Plant Physiology, highlighting my increasing role as senior author. Moreover, the two main studies from my postdoc are currently under preparation.

I have also received diverse and substantial funds. After my PhD, I got three postdoctoral fellowships: EMBO Long-Term Fellowship, Marie Skłodowska-Curie Individual and the Postdoctoral Fellowship awarded by Fundação para a Ciência e a Tecnologia (FCT; Portugal, which I had to decline). More recently, I obtained a major national grant from FCT (the equivalent to the Spanish Plan Estatal) as the Principal Investigator, with an associated budget of 231.000 euros.

In summary, I have a track record of solid scientific production at all stages of my career and have proven to be able to attract highly competitive funding. Also, I believe that the research line I want to investigate in the near future, focused on the role of AS at the interplay between different environmental signals affecting growth, is strongly sustained by both my theoretical and technical multidisciplinary background gained during my scientific career.
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Resumen del Currículum Vitae:

My research interests have been centered on understanding how plants adapt their transcriptomes to adjust their development in response to different environmental signals. These interests have brought me to develop my scientific career in two different and excellent research groups, which have also provided me with a multidisciplinary theoretical and technical background. First, as a PhD student, where I focused my research on the control of gene expression by transcription factors. Second, as a postdoctoral researcher, I am currently investigating the role of a post-transcriptional mechanism, alternative splicing (AS), in controlling mRNA levels. The studies performed at both laboratories shared the same framework: understanding how plants react molecularly to environmental cues. My career began in 2009 as a MSc student in the laboratory of Elena Monte at CRAG (Centre of Research in Agricultural Genomics; BCN). In this laboratory I also conducted my PhD studies, which ended in 2015. The results of these studies have been published in eight different articles, four of them as a first author, and include top international journals such as Nature Communications and Current Biology. It is important to mention that another article from my PhD with me as a first author has been submitted. During this period, I have also participated in different scientific meetings which have allowed me to meet and stablish international collaborations with some of the most relevant researchers of the plant photobiology field. In addition, in this laboratory I had the satisfactory opportunity of co-supervising different undergraduate and one MsC student.

After finishing my PhD., I moved to the laboratory of Paula Duque at IGC (Instituto Gulbenkian de Ciência; Lisboa) pursuing my interest on

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ESTATAL DE
INVESTIGACIÓN

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

AS and its function regulating plant development. To this end I applied to three different Postdoctoral Fellowships, all with successful outcomes. These fellowships include the EMBO Long-Term and Marie Skłodowska-Curie Action, two of the most prestigious postdoctoral programs. Moreover, I stablished a collaboration with researchers at CRG (Centre for Genomic Regulation; BCN), which have a long trajectory on quantifying AS in animals. This has allowed me to create important bioinformatic resources for the study of this process in plants, which in comparison to other organisms were very limited. Moreover, in the context of this collaboration we have recently published a paper in Genome Biology in which I am first and co-corresponding author. Importantly, I also have these two roles in my latest paper, accepted in Plant Physiology, underscoring my increasing role as senior author. Noteworthy, the two main studies from my postdoc are currently under preparation. The dissemination of the results from my postdoctoral studies includes talks in international meetings, although my goals on this front were obviously affected by the covid-19 pandemic. During this period, I also obtained a major national grant from Fundação para a Ciência e a Tecnologia (FCT-Portugal; the equivalent to the Spanish Plan Estatal) as the Principal Investigator, whit an associated budget of 231.000 euros. This grant is allowing me to develop my personal research interest on the role of AS in plant growth in response to environmental signals, which is in line with my general research interests and is contributing to build the foundational data on which I will construct my independent research grou

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

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Título:

Comparative Stem Cell Dynamics: time and space in self-organizing tissues

Resumen de la Memoria:

I am fascinated with the molecular and cellular mechanisms by which stem cells differentiate. Throughout my career, I ve been studying gene regulation in space and time using interspecies comparisons and in vivo and in vitro models.
The main scientific achievement of my PhD project was to identify a previously unforeseen role for Notch signaling in the distinction between embryonic and extraembryonic structures in the blastocyst - the first cell fate decision in embryonic development. My work showed that a mechanism involving Notch signaling and Hippo activity promotes embryo viability and ensures the proper development of the embryo (Rayon, T. et al. Dev. Cell 2014). I then investigated the regulation of the Cdx2 gene in the extraembryonic ectoderm and pluripotent stem cells. I found that there are distinct mechanisms that regulate Cdx2 expression in the blastocyst, the postimplantation embryo, and trophoblast stem cells (Rayon, T. et al. Sci. Rep. 2016). Altogether, I was able to show how two signaling pathways directly regulate gene expression and describe the regulatory logic of an important cell fate decision.
I contributed to identifying totipotency features in freely circulating reprogrammed cells (in vivo iPS) (Abad, M. et al. Nature 2013). In vivo iPS were generated in Manuel Serrano s lab from mice in which the Yamanaka factors were transiently induced. I assessed whether these circulating iPS cells could differentiate into, or show some features related to the trophectoderm. We were able to demonstrate that in vivo iPS cells, when challenged, could express trophectoderm markers and contribute to the trophectoderm. These studies showed how reprogramming in vivo can produce totipotent cells.
In 2016 I started my postdoc at Francis Crick Institute in London funded with an EMBO long-term fellowship. I investigated the molecular mechanisms that encode time, a major unanswered question in developmental biology. I found that mouse neural progenitor cells differentiate more than twice as fast as those in humans and showed that global temporal mechanisms arise from cell-intrinsic processes. The interspecies differences in the pace of motor neuron differentiation corresponded to differences in protein turnover (Rayon et al., Science 2020). This work has pioneered the search for mechanisms that control tempo using in vitro systems and places protein turnover at the heart of developmental tempo.
I ve also contributed to two additional high impact publications in the lab. One where we discovered that stem cells in the post-implantation embryo acquire axial identity before becoming neurons in the spinal cord (Metzis et al., Cell 2018). The other is an atlas of the developing spinal cord in mouse embryos (Delile et al., Development 2019).
As an independent investigator, I intend to gain a mechanistic understanding of developmental timing. My programme of research intends to molecularly characterize and modulate developmental pace across species and determine its role in brain evolution. In the long-term, deconstructing tempo in self-organising systems will allow the design of strategies to speed up or reduce the speed of biological processes to improve organismal lifespan.

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Resumen del Currículum Vitae:

I m an experimental biologist expert in stem cells and development.
During my PhD I studied early mouse development and the evolutionary origin of pluripotency, and I collaborated in projects with other lab members as well as collaborators in the institute and abroad. Overall, I published two first-author papers, contributed to three additional research papers, one review from the lab, and four extra papers with other labs. With all this work, I acquired expertise on mouse genetics, early pre-implantation development, gene regulation and mouse stem cells. During this formative phase, I did my first international stay at Veronique Azuara s lab at IRDB (Imperial College, London, UK). I attended international conferences, and I was selected to give talks about my work. This toolkit set the foundations of my interests, critical thinking and skills in research.

In 2015 I was awarded an EMBO long-term fellowship to work at the Francis Crick Institute (London, UK) under the supervision of James Briscoe. For my postdoc, I expanded my developmental skills by working with human embryos and developing stem cell models amenable for quantitative and temporally resolved assays and from mouse and human stem cells, as well as by closely working in a multidisciplinary group with physicists and engineers. My main project studied what sets the pace of embryonic development during motor neuron formation. My work has identified a global temporal scaling, where protein stability corresponds to developmental timing in mouse and human. I have published this work recently as first and co-corresponding author in Science (Rayon et al., 2020). During my postdoc at the Francis Crick Institute, I have widened my knowledge and progressed in my career towards a senior role. Aside from developing new techniques in the lab. I ve led my own project, written project proposals, reviewed papers and projects for the AEI and supervised

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

students. Likewise, I ve trained my soft skills by organising a group retreat in 2017, establishing a seminar series entitled StemFate with Vicki Metzis (2016-17), and attending the EMBO lab leadership course (2019).

In addition to my research activities, I am very committed to science dissemination and open access. I highlight preprints - manuscripts posted on a repository- at preLights, and I have been appointed in 202 to become a board member of the Spanish Society for Developmental Biology (SEBD).

Overall, I believe that along my short scientific career I have demonstrated my technical expertise and my analytical and critical skills. This expertise combined with my capability to lead projects, signing as a co-corresponding author in two of my publications, my ability to supervise students successfully, and my ability to obtain funding for fellowships put me at the right career stage to establish an independent research group under the Ramon y Cajal Fellowship program.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

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Título:

Understanding how function, stability, and interactions interconnect with the structure and sequence of proteins

Resumen de la Memoria:

During my scientific career, I have been devoted to understanding how function, stability, and interactions interconnect with the structure and sequence of proteins. I carried out my Ph.D. at the University of Granada under José Manuel Sánchez Ruiz and Beatriz Ibarra Molero's supervision. My doctoral work combined experimental and bioinformatics approaches to tackle fundamental questions in protein folding, evolution, and design. Specifically, (i) I demonstrated how proteins are far more robust than expected and can accommodate several ionizable residues in their hydrophobic core. (ii) I developed a method that combines evolutionary and structural information to design protein hyperstability. (iii) I studied the evolutionary relation between primary and promiscuous activities in proteins.
After having acquired a solid biophysical background during my Ph.D., I was motivated to understand how proteins function and interact in a cellular context. Following this aim, I moved overseas for a postdoctoral position in the lab of Emmanuel Levy at the Weizmann Institute of Science, where I obtained a Koshland postdoctoral fellowship. During my postdoctoral research, I developed a broad research direction aimed at characterizing the potential of mutations to create promiscuous self-interactions. I selected twelve distinct proteins to ascertain the generality of my results, and I undertook a comprehensive characterization of the impact of mutations on their structure and their capacity to self-interact in vitro and in vivo. Through this research I demonstrated that point mutations at the protein surface frequently create new self-interaction patches that can drive the proteins infinite folded-state self-assembly. At the same time, I found this potential to be buffered chemically by hydrophilic residues.
Overall, I hold a multidisciplinary research background with an important record of first-author scientific publications in top journals (such as Nature, Cell, Angewandte Chemie, Plos Comp Biol). I am also corresponding and co-corresponding author of two more scientific articles (Garcia-Seisdedos, et al. BioRxiv 2020). My Ph.D. training as a biophysicist together with my postdoc research where I gained expertise structural systems biology and mastered powerful methodologies such as the use of robotics, high-throughput microscopy, yeast genomics, and gene editing tools place me in a unique position to elucidate the role of supramolecular assemblies in evolution and disease, which is my long-term goal. Lastly, I will bring the host center the opportunity to establish new scientific collaborations and import new scientific perspectives.

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Resumen del Currículum Vitae:

I graduated from the University of Salamanca, where I obtained a University degree in Biology (2005) and Biochemistry (2007). I was very keen to study how proteins work and evolve to build up the cell's exquisite machinery, and driven by this motivation, I moved to the University of Granada to start my Ph.D. in the group of Jose Manuel Sanchez Ruiz. My Ph.D. work combined experimental and bioinformatics approaches to address the design of tailor-made enzymes. In this period, I was a lecturer of two subjects, "Physical Chemistry" and "Introduction to Chemistry" of the Chemistry and Chemical Engineering degrees.
After my Ph.D., I decided to complement my expertise in protein biophysics with a cell and systems biology perspective, and study how proteins "talk to each other," making life possible. That is, to study how they interact and how they function in the context of the cell. With this aim, I joined Emmanuel Levy's group at the Weizmann Institute of Science, where I was awarded a Koshland postdoctoral fellowship. There, I demonstrated that point mutations commonly drive proteins to self-assemble in their folded form into supramolecular assemblies. This discovery has wide-ranging implications in terms of protein evolution, structural, and cell biology. For example, it implies that the membrane-less protein bodies characterized in cells in recent years are the tip of an iceberg of mesoscale protein assemblies.
In short, over my career, I have acquired a multidisciplinary background, with expertise ranging from structural and protein biophysics to systems and cell biology. I have spent almost eight years working in world-class international institutions such as Ecole Polytechnique, Max Plack Institute CBG, TU Dresden, and the Weizmann Institute of Science, in which I currently hold a Research Assistant position. I have achieved a strong academic record, gathering six first-author works published in top scientific journals (Nature, Cell, Angewandte Chemie, Structure, Plos Comp Biol, etc.), and one second-author work (Sci. Data). Furthermore, this year, I will be the first and corresponding author of two additional research articles (one of them, Garcia-Seisdedos et al. BioRxiv, was already submitted to PNAS), and the second author in one article, under submission.
I have had very relevant participation as a researcher in scientific projects funded by highly competitive agencies (ERC, ISF, Spanish Ministry of Science). Additionally, I have been the PI of 2 projects awarded by the I-CORE (Israeli Centers of Research Excellence) and Azrieli Institute for Systems Biology. My application for the ERC Starting Grants 2020 program as a PI reached Step 2, being perceived as highly innovative. I have presented my work in 25 high-profile research conferences (GRC, GRS, FEBS, ILANIT/FISEB), participating as a

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

speaker/invited speaker in more than half of them. I have helped organize a joint symposium on chemical and molecular engineering between the Weizmann Institute and the MPI of Molecular Physiology. I have been a reviewer for Cell. Lastly, I have mentored four master students (Saphira G., Freud S., Nahum S., and Abraham A.) who were part of the Chemistry and Life Sciences Master programs at the Weizmann Institute of Science.

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

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Título:

Structural basis of antibody recognition mechanism by immunomodulatory endoglycosidases

Resumen de la Memoria:

I completed my Ph.D. in Chemistry at the Universidad Autonoma de Madrid, Spain, funded by the Formación Personal Universitario (FPU) fellowship, and under the supervision of Prof. Jose Luis Chiara (Instituto de Química Orgánica General, CSIC, Spain; 2011). I performed the synthesis of a new type of glyco-clusters and studied their interactions with lectins, employing an array of biochemical and biophysical techniques. During a pre-doctoral internship in the USA, I was first introduced to macromolecular X-ray crystallography and became strongly interested in the study of catalytic and substrate recognition mechanisms of Carbohydrate Active Enzymes (CAZymes). With this in mind, I moved to the USA, where I developed my postdoctoral career at two highly renowned institutions, Boston Biomedical Research Institute and University of Maryland, School of Medicine, under the supervision of Prof. Eric J. Sundberg (USA, 2010-2016). My research was focused on two different projects: the study of bacterial endoglycosidases, and the design of monoclonal antibodies with enhanced effector functions. In 2016, I returned to Spain and joined Prof. Marcelo E. Guerin laboratory at CIC bioGUNE, funded by Juan de la Cierva-Incorporación fellowship. Nowadays, I am working on several research lines related to understanding the mechanism of substrate recognition by CAZymes. Among others, I am studying: (i) the molecular mechanism of N-glycan recognition of bacterial endoglycosidases in order to engineer enzymes with novel specificity that can be used in biotechnology to remodel monoclonal therapeutic antibodies, (ii) the molecular mechanism of substrate/membrane association of CAZymes involved in the biosynthesis of structural components of the mycobacterial cell envelope, and (iii) the structural basis of O-glycan recognition by enzymes from human gut bacteria in order to understand its beneficial effect in human health. Recently, I have been awarded with the highly competitive and renowned Marie Sklodowska-Curie Individual Fellowship from the European Commission in order to understand the molecular basis of the mechanism of substrate recognition of two endoglycosidases used in glycan remodeling of antibodies, EndoS and EndoS2. Altogether, during my scientific career, I trained in Organic Chemistry, Biochemistry, Biophysics and Structural Biology, in the form of X-ray crystallography and Cryo Electron Microscopy. This multidisciplinary background has enormously contributed to give me a vast understanding of multi-step enzyme-catalyzed processes in the cell, enzymatic activities, macromolecular interactions, and catalytic and inhibitory mechanisms in order to become an independent researcher and consolidate my scientific career in the fields of Glycobiology, Enzymology and Immunology. In that sense, the aim of my future research plan is focused on understanding the molecular mechanism of substrate recognition by bacterial CAZymes which assist pathogens to evade the host immune response. Understanding the mode of action of these specific enzymes will allow to customize the glycan remodeling of therapeutic antibodies for cancer treatment or other glycoproteins involved in autoimmune diseases. I am now ready and prepared for the next step in the progression towards a successful academic research career, in the form of an independent research position.
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Resumen del Currículum Vitae:

My interest in Glycobiology began as a Ph.D. student at the Universidad Autónoma de Madrid, working in the synthesis of multivalent glyco-clusters at the Instituto de Química Orgánica General, CSIC, Spain (2006-2010) under the supervision of Dr. José Luis Chiara. After finishing my Ph.D. studies, I started my postdoctoral career abroad in two highly renowned institutions, the Boston Biomedical Research Institute and the University of Maryland, School of Medicine in the USA under the supervision of Prof. Eric J. Sundberg (2010-2016). In 2016, I returned to Spain and joined the Structural Glycobiology Lab, led by Prof. Marcelo E. Guerin at CIC bioGUNE. Recently, we have moved the laboratory to the IIS Biocruces Bizkaia, where I am currently developing my research projects. My background is highly multidisciplinary, combining Organic Chemistry, Biology, Biophysics and Structural Biology. During my scientific career I successfully ensured my own funding, including the Formación Personal Universitario (FPU) Ph.D. fellowship from MICINN (2006-2010), the Juan de la Cierva-Incorporación Post-doctoral fellowship from MINECO (2016-2018), the Bizkaia Talent Post-doctoral fellowship (declined), and more recently, the Marie Sklodowska-Curie Individual Fellowship (MSCA-IF) Post-doctoral fellowship from the European Commission. My research career has been also funded by contracts from R01 projects of the NIH.

The results of my work certainly have implications not only in fundamental aspects of Glycobiology and Enzymology, but also in the application of this knowledge in areas including biomedicine and biotechnology. As a consequence, I have contributed 19 publications (8 as first author, 3 as second author, 2 as corresponding author) in top-ranking journals including Nature Communications (3 articles as first author, 1 as corresponding author), Proceedings National Academy Sciences USA (1 article as first author), ACS Central Science (1 article as first author), Chemistry A European Journal (3 articles, 1 as first author), Advanced Functional Materials (2 articles, 1 as first author), ACS Chemical Biology, the Journal of Biological Chemistry (2 articles), Biochemistry, Glycobiology (1 review article as co-corresponding author), and Methods in Enzymology between others. Of note, my publications in specialized journals are receiving increasing numbers of citations,

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

and I currently have an H-index of 8. Moreover, I also contributed with two patent applications, one obtained during my Ph.D. studies in the Universidad Autonoma de Madrid, Spain (ES236046B1), and an international patent, during my Post-doctoral stage at the University of Maryland, School of Medicine, USA (PCT/US2014/066197). Throughout my scientific career, I have participated in R+D+I International (3, including 2 R01 NIH projects, R01AI149297 and R01AI090866) and national projects (8). I have also attended 14 international, including 7, and national conferences, including 7. In addition, I have mentored 3 Master students and I am the thesis co-director of a Ph.D. student, Mikel Garcia-Alija, funded with a La Caixa Fellowship. Collectively, after 10 years of postdoctoral experience, I acquired the scientific maturity required to conduct an independent scientific career.

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Turno de acceso general

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Título:

Innovative genome engineering approach for the design of synthetic genetic circuits with potential impactful applications in biotechnology and biomedicine

Resumen de la Memoria:

Throughout my scientific career I have focused on incorporating cross-functional concepts and cutting-edge technologies into my research, and as such I have gained a unique multidisciplinary background demonstrated in my extensive experience in molecular biology, microbiology, biochemistry, immunology and cellular biology. I have made unprecedented strides and important original contributions to different biological fields, from environmental microbiology to microbial pathogenesis, infectious diseases, and genome engineering.

Early in my career I explored the mechanisms underlying microbial adaptations to the environment. During my Ph.D. thesis research in Eduardo Díaz laboratory at the Biological Research Center (CIB-CSIC), I applied a multifaceted approach of basic microbiology, genetics, biochemistry, bioinformatics, and structural biology and pursued this research through the discovery of complex molecular mechanisms by which bacteria recognize and degrade environmental pollutants. My Ph.D. research work included 3 first author publications in prestigious journals, showcased several novel findings for the field, and constituted a model approach to understand the complex regulatory network controlling the expression of catabolic genes in microorganisms.

After receiving my Ph.D. in Biochemistry and Molecular Biology, I joined Victor Nizet laboratory at University of Californian San Diego (UCSD) to extend my perspectives as microbiologist and decided to utilize my postdoctoral training to explore bacterial pathogenesis with equal focus on the bacteria adaptation in the host and the host response to the infection. As part of my postdoctoral training, I have studied and led collaborative projects on the fundamental mechanisms of pathogenesis for several important human pathogens. Remarkably, I described a novel pathogenic property of the pathogen Streptococcus pyogenes and its interactions with human macrophages. My findings were published in Nature Microbiology and highlighted by several nationwide scientific posts and local news. Most recently, after been promoted to the project scientist position at UCSD, I was independently spearheading several different projects, including the one of CRISPR/Cas9 bacterial genome editing to combat public health problem of antibiotic resistance, sponsored by an individual UCSD-TIGS grant (TATA Institute for Genomics and Society), and published in Nature Communications.

To experience the differences of research between the scientific academia and the pharmaceutical settings, and motivated by the COVID-19 crisis, I am currently providing my expertise in molecular biology, microbiology and infectious diseases to the development of novel RNA platforms for vaccines, in particular to combat the worldwide problem of SARS-Cov-2.

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Resumen del Currículum Vitae:

I hold a Degree in Microbiology (2003) by the Pontificia University Javeriana (Colombia) and a Doctor degree in Molecular Biology and Biochemistry (2012) by the University Complutense of Madrid. I was Predoctoral FPI fellow at the CIB-CSIC (2008-2012) under the supervision of Dr. Eduardo Díaz. During my Ph.D research in the environmental microbiology field, I applied a multifaceted approach of basic microbiology, genetics, biochemistry, bioinformatics and structural biology to identify and address the molecular mechanisms by which bacteria recognize and degrade environmental pollutants. Along my Ph.D I published three first author articles (two in JBC and one in mBio), and contributed as co-author in one additional article in JBC, as well as in a reference Review article in the field. In addition to my publications, my work was presented in several national and international scientific meetings and highlighted with grants awarded and best presentation prizes.

Following my breakthrough Ph.D research, I was awarded by the American Society for Biochemistry and Molecular Biology (ASBMB) with a grant to study fundamental host-pathogen interactions at the Scripps Research Institute in the US. Then, I decided to expand my scientific perspectives and joined the prestigious Victor Nizet Laboratory at the University of California San Diego (UCSD). As Postdoctoral Fellow at UCSD, I studied the fundamental mechanisms of pathogenesis for several devastating human pathogens. Simultaneously, I acquired expertise in cellular, immunological and genome engineering approaches to unrevealed specific cellular mechanisms of the innate immune system to recognize and fight against the pathogens. My research contributions include the leader role on the discovery of a new property of Streptococcus pyogenes virulence. Due to the significance of my research, my findings were published in the journal Nature Microbiology, and went on to garner widespread attention in both the scientific and mainstream media. I established several collaborative research initiatives across the UCSD campus and with other American institutions to further contribute as co-author of 7 more articles in prestigious journals, such as PNAS, Frontiers in Microbiology, Journal of Innate Immunity, Journal of Immunology and infection and Immunity. Due to the influence of my work in the field I wrote a Review article as the first author in the journal Future Microbiology, which

AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

highlighted my discoveries together in the context of the most important scientific literature in the field. As yet further evidence of the importance of my work, I was recently invited to author a chapter entitled GAS encounter with host macrophages , which was published in the essential lab protocol series Methods in Molecular Biology by Springer Nature. Most recently, I was promoted to the position of project scientist at UCSD and received an individual Research Grant from the Tata Institute for Genetics and Society (TIGS). As project Scientist at UCSD, I have led different projects, including the role of Cas9 in Streptococcus pyogenes pathogenesis -whose findings were published as corresponding senior author in Frontiers of Microbiology-, and the discovery of a new genetic CRISPR/Cas9-based technology for genome engineering in prokaryotes. These findings were published as first author in Nature Communications, and I am an inventor on the disclosed intellectual property with multiple applications in biomedicine and b

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AYUDAS RAMÓN Y CAJAL
CONVOCATORIA 2020

Turno de acceso general

Nombre: DE SANTIS , SILVIA
Referencia: RYC2020-029726-I
Área Temática: **Biociencias y biotecnología**
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Título:

GLIA-MRI: untanGLing Inflammation with Advanced Magnetic Resonance Imaging

Resumen de la Memoria:

My journey in research started with a PhD in physics, during which I studied water diffusion dynamics in complex system using diffusion-weighted Magnetic Resonance Imaging (MRI), a technique that I immediately fell in love with. During my early postdoctoral years, I focused on pushing the boundaries of diffusion MRI to investigate brain microstructure through the development of more specific models, able to account for different relevant aspects of the cerebral tissue composition. My early achievements granted me international visibility and recognition, and I was able to get my first personal grant, planting the seed for an independent career.
In my more senior postdoctoral research, driven by a growing interest in neurobiology and a desire to amplify the impact of my results, I decided to leave my comfort zone to acquire complementary skills that I felt were needed to achieve true ground-breaking research in biosciences. In fact, I developed a precise translation of diffusion parameters into biological variables by demonstrating that specific tissue compartments, such as axons and other cells subtypes, leave a characteristic signature in the diffusion MRI measurements, allowing their quantitative description (i.e. axon diameter or density, reactive glia, etc.). I started applying the methodology I developed to answer important questions about the brain, like the impact of alcohol use, the evolution of brain microstructure along the lifespan and the interplay between myelination and axonal loss in early multiple sclerosis. However, the achievement which better represents my trajectory is the development of an innovative MRI strategy to image glia morphology during an inflammatory reaction in grey matter. Now, I want to bring this discovery to the next level, developing a multidisciplinary approach to look at neuroinflammation non-invasively and in a translational way, with the aim of generating innovative biomarkers of brain status potentially useful in both basic research and clinical applications.
The combination of my technical background with experience in neurobiology and clinical applications has made me a rather unique profile, and sets me on a strong path to have a real impact in biosciences. All in all, the GLIA MRI lab is expected to bring basic neuroscience closer to the clinic, ultimately improving the way brain disorders are diagnosed and treated.
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Resumen del Currículum Vitae:

My career started with a BSc in Physics, followed by a MSc in Biophysics at Sapienza University of Roma, which included a 4-months internship at University College of London. On graduating, I was awarded a PhD scholarship in Physics at Sapienza (1 of only 12), during which I studied diffusion dynamics in complex biological media and made my enter in the field of neuroscience. Before submitting the thesis, I secured a post-doctoral position in CUBRIC, Cardiff, supported by the EU-funded CONNECT Consortium, during which I specialized in white matter imaging under the supervision of Prof. D.K. Jones. In my second year of postdoc I was awarded the prestigious Sir Henry Wellcome Fellowship, which offered me the unrivalled opportunity to develop my own project at the best facilities across Europe (Tel Aviv University with Prof. Y. Assaf and Maastricht University with Prof. A. Roebroek), where I proposed a strategy to fully characterize water dynamics in brain white matter, aiming at identifying relevant biomarkers of brain status in health and disease. Using this framework, I designed an innovative application in the field of addiction; my project ADDICT - Advanced Diffusion Dynamics to Investigate Cerebral Tissue - was awarded a 2016 NARSAD Young Investigator award from the Brain and Behavior Foundation. This grant marked a major transition in my career: it allowed me to join the prestigious Institute of Neuroscience of Alicante (INA) as junior researcher. In 2017 I started at the INA an ambitious project, founded by the EU through a Marie Sklodowska-Curie fellowship, to use advanced MRI to look at inflammation markers in brain grey matter, under the mentorship of Dr. S. Canals. In 2019, I was awarded the prestigious SEJI grant from Generalitat Valenciana, which allowed me to start my independent group, focusing on developing and applying non-invasive techniques to look at neuroinflammatory markers in health, ageing and disease with a translational focus.
From 2016, I teach advanced MRI theory & application for the master in Neuroscience of the INA, where I also supervise master students, and co-supervise PhD students. I have published 1 book chapter and 29 full papers in peer-reviewed international journals, some of them in top journals like Science Advances and JAMA Psychiatry. I have made >40 international presentations and organized a workshop for the 2017 SENC meeting. I acted as guest editor for the journal Neuroscience. I routinely review papers for high impact journals and, importantly, I was chosen to review prestigious grants for the Wellcome Trust, McGill University, Spanish Ministry of Health. I have on-going collaborations (all led to joint papers) with researchers in Maastricht University, Cardiff University, Policlinico Tor Vergata in Rome, Uniklinik Mainz and ZI Mannheim, and a particularly close collaboration with the Multiple Sclerosis group of the Harvard Medical School in Boston. In 2019 I started an ambitious project with the R&D startup company QMENTA, for integrating the methods I develop into a state¬of-the-art cloud platform to store, process and visualize medical images.

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Referencia: RYC2020-029773-I
Área Temática: **Biociencias y biotecnología**
Correo Electrónico: ulrich.eckhard@gmail.com

Título:

Structural Biochemistry of Proteolytic Enzymes

Resumen de la Memoria:

My research career started with the biochemical and structural characterization of clostridial collagenases, one of the few protease families capable of degrading bona fide collagen. During my PhD with Prof. Hans Brandstetter at the University of Salzburg, I solved the longstanding puzzle of clostridal collagenases by structural biochemistry, highlighted by first-author publications in Nature Structural & Molecular Biology and The Journal of Biological Chemistry, and witnessed by a total of six (co-)first authorships on clostridial collagenolysis. In 2012, I shifted my research focus to the analysis of proteases and proteolytic networks by mass spectrometry, and joined the Protease Degradomics Lab of Prof. Chris Overall at the UBC Centre for Blood Research in Vancouver, Canada, where I also raised my first competitive post-doctoral fellowship. In a highly-interdisciplinary and international setting, I performed cutting-edge degradomics research, witnessed by 20 publications, including first authorships in Nature Communications, Cell Reports and Matrix Biology, and co-authorships in Cell Signaling, Blood, and Nature Methods.

In 2016, I returned to Europe and joined the lab of Prof. Maria Selmer at the renown Structural Biology Department of Uppsala University. We aimed to understand how structure and function are intertwined in the evolution of new protein variants, e.g., how Atlantic and Baltic herring accommodate environmental changes, and how promiscuous protein functions represent a crucial evolutionary advantage (latest co-author paper just accepted at eLife). I then secured competitive funding from the Engelhorn Foundation to intensify my work on proteolytic flagellins, the very first flagellum-embedded enzyme family (Eckhard et al. 2017, Nat Commun), and performed an in-depth biochemical characterization (Eckhard et al. 2020, Sci Rep). In October 2019, I joined the Proteolysis Lab of Prof. F. Xavier Gomis-Rüth at IBMB-CSIC in Barcelona as a Beatriu de Pinós fellow, where I continue my research on hydrolytic enzymes and extend my skill-set to cryoEM. Notably, I am already fully immersed in single particle reconstruction in one of my projects. Finally, I am currently awaiting the reviewer comments of my first-author manuscript at PNAS, where we passed editorial reviewing.

My ultimate career goal is to lead a multidisciplinary and international research group using structural biology, mass spectrometry, and systems biology to study proteolytic systems in health and disease. I want to unravel dysregulated pathways and elucidate the proteins and protein complexes involved. In close collaboration with both academia and biotech, I want to develop innovative treatment strategies and new therapeutics such as exosite-targeting small molecule drugs, and to design data-driven and evolution-guided enzymes for biomedicine and biotechnology. 31 peer-reviewed publications, 18 of them as (co-)first author, and post-doctoral fellowships from three different countries prove my ability to secure competitive funding and to lead, execute, and manage research projects in international and multidisciplinary environments, underlining my research capacity. I am confident that the support of the Ramón y Cajal program would represent the final building block to kick-off my own lab and to establish myself as an innovative and fully independent investigator.
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Resumen del Currículum Vitae:

=EDUCATION=
During my training at the Universities of Salzburg and Linz, I received two Excellence Scholarships and completed Bachelor and Master programs in both Biology and Molecular Biology. Furthermore, my PhD supervisor was awarded the Kurt Zopf Publication award (10k EUR) for my first author publication on bacterial collagenolysis in NSMB.

2007-2011: Doctor of Natural Sciences. University of Salzburg, Austria.
2006-2011: Master of Science, Molecular Biology. Universities of Salzburg & Linz, Austria.
2005-2007: Master of Science, Biology. University of Salzburg, Austria.
2004-2006: Bachelor of Science, Molecular Biosciences. Universities of Salzburg & Linz, Austria.
2001-2005: Bachelor of Science, Biology. University of Salzburg, Austria.

=POST-DOCTORAL RESEARCH EXPERIENCE & FUNDING=
Since 2012, I have performed post-doctoral research in four different countries and acquired competitive fellowships from the Michael Smith Foundation for Health Research (124k CAD; 2013-2016), the Peter and Traudl Engelhorn Foundation (135k EUR; 2017-2019), and the Beatriu de Pinós COFUND program (144k EUR; 2020-2023).

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CONVOCATORIA 2020

Turno de acceso general

Since 10/2019: Post-doctoral fellow in the Proteolysis Lab of Prof. Gomis-Rüth at IBMB-CSIC, Barcelona, Spain.
2017-2019: Post-doc at the Department of Biosciences with Prof. Hans Brandstetter, University of Salzburg, Austria.
2016-2017: Researcher in the Structural Biology Lab of Prof. Maria Selmer, Uppsala University, Sweden.
2012-2016: Post-doc in the lab of Prof. Chris Overall at the UBC Centre for Blood Research, Vancouver, Canada.

=TEACHING & MENTORING=
I have always enjoyed teaching and supervising students, and was involved in academic training at three different Universities. Throughout my career, I frequently participated in academic decision bodies for teaching reforms and hiring committees. I was the day-to-day supervisor of two Erasmus+, six Master and four PhD students, and designed laboratory rotations covering molecular biology, biochemistry, proteomics, and structural biology, providing both theoretical foundation as well as experimental supervision. Furthermore, I have mentored many levels of scientists, from high school to Ph.D. students, as well as international visiting scientists.

=PUBLICATIONS (Status: 01/2021)=
Over the last 13 years, I published 31 articles, 18 as (co-)first author (e.g. Nature Structural & Molecular Biology, Cell Reports, Nature Communications), and 13 as co-author (e.g. Nature Methods, Blood, Science Signaling, Nature Ecology and Evolution). With a total of 1175 citations and a cumulative Impact Factor of >240, this leads to a current H-index of 19 and an i10 of 25 on Google Scholar, and a Scopus H-factor of 17. Furthermore, I frequently act as a reviewer for e.g. The FEBS Journal, Molecular & Cellular Proteomics, Journal of Molecular Biology, and the Journal of Proteome Research. Currently, I have a first-author publication under review at PNAS, and just yesterday (16.01.2021) we got the acceptance note from eLife for one of my co-author contributions at Uppsala University.

=CONFERENCES & WORKSHOPS=
13 oral and 11 poster presentations at >20 scientific conferences. Selected participant at 10 international workshops on proteomics and structural biology, and 8 invited talks in academia (e.g. University of Waterloo, Canada) and Industry (e.g. Novo Nordisk, Måløv, Denmark).

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Área Temática: **Biociencias y biotecnología**
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Título:

Structural studies of multi-subunit machineries associated with disease

Resumen de la Memoria:

Since the beginning of my career I have been interested in understanding how the cell works and which are the molecular mechanisms that allow such an elaborate system to survive and thrive. The complexity of the cell and the presence of thousands of macromolecular complexes with their specific modifications and functions has always fascinated me. In this regard, the set of tools provided by the structural biology field allows us to "visualise" these machineries and to understand how they interact with other cellular components, how they are modified at different moments of the cell cycle or how they are altered during pathological disorders.

My research trajectory has focused in analysing macromolecular complexes using a combination of structural biology tools (X-ray crystallography and cryo-EM), protein biochemistry, biophysics and molecular biology methods. Likewise, in order to provide a cellular perspective to our molecular approaches, during my career I have participated in continuous international collaborations with reference groups in the cell biology field. My career focus has gradually evolved from the initial analysis of single proteins and subunits to the complex study of macromolecular machineries engaged with nucleic acids. During this process, I have progressively expanded my knowledge into those technologies required to answer the biological questions in front of me and I have kept up-to-date with novel methods in the structural biology field and beyond.

My research line is now focused in the field of DNA-dependent RNA transcription and associated factors. I am currently a postdoctoral researcher in the group of Dr. Alessandro Vannini where we have recently elucidated for the first time the structural details of both yeast and human RNA Polymerase (Pol) III machineries. These structures shed light into the fundamental process of transcription initiation, highlighting the relevance of some regions in the opening of the DNA bubble and rationalising the effect of mutations observed in several pathologies. As part of the dissemination of my work, I have successfully published my results in high impact factor journals. Currently, I am leading an independent project studying a poorly-understood function: the targeting of retrotransposons to transcription factors associated with RNA Pol III in S. cerevisiae. This on-going work has already provided the first structure deciphering the specificity of binding and opening the door for the development of editing tools.

In the future, I not only plan to continue my research in protein-DNA machineries, but also plan to expand into the field of human endogenous retrotransposons. Considered for years as "junk" DNA, in recent years several studies have reported an association between the reactivation of these retrovirus-like elements and the development of disease, including cancer and neurological disorders. Interestingly, the over-expression of associated proteins has also been found during embryogenic development. In the light of the recurrent pandemics occurring since the advent of the XXI century, studying the molecular basis of human endogenous retrotransposons could provide an invaluable tool to understand the relevance of these mobile elements.

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Resumen del Currículum Vitae:

After obtaining a Master's Degree, in 2008 I joined the group of Dr. Aitor Hierro at the CIC-bioGUNE as a PhD student. During my PhD, I used structural biology, biochemical and biophysical techniques to address the molecular mechanisms behind the process of vesicle tethering. To fund my research I was awarded a PhD Fellowship by the Basque Government in 2009. As a result of my PhD work, I published 2 research articles in Q1 journals as first or co-first author (Structure, 2013; PNAS, 2010) and another paper as co-author. The publication in PNAS was recognised as the most-relevant article of September 2010 by the SEBBM, highlighting the relevance of our research.

After this experience, I decided to continue my career abroad to get new perspectives from the international research community and to improve my knowledge in state-of-the-art techniques such cryoEM. With this in mind, in 2014 I joined the group of Dr. Alessandro Vannini at the ICR (London, UK) as a postdoctoral researcher. In 2015, I was awarded a Marie Sklodowska-Curie Individual Fellowship by the European Commission, which funded my independent research for 2 years. During this stage, I have been highly productive and I have developed 3 well-defined independent projects focused in the study of the fundamental function of RNA transcription using cryoEM. This research has led to the publication of 3 articles in D1 journals, two of them as first or co-first author. In my 2018 Nature paper we provided the first high-resolution structure showing how the RNA Polymerase III enzyme opens DNA and initiates RNA synthesis together with other transcription factors. The impact of this research was highlighted by the publication of the results in Nature (featuring at the journal cover) and its wide press distribution (i.e. BBC news). Likewise, this research was selected for the Diamond Light Source Annual Review 2018/2019 and it was chosen as one of the ICR main achievements of 2018. In my most recent co-first author publication in Nature Communications, we determined the structure of the human RNA Pol III, and rationalised the effect of point mutations linked to cancer and neurological disorders. In the last stage of my postdoc, I started a new research line where I supervised an Erasmus and a PhD student. This on-going

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CONVOCATORIA 2020

Turno de acceso general

project is providing key details about the molecular mechanism of retroelement integration, which will be useful for the development of tailored genetic editing techniques for RNA Pol III genes.
As a recognition of my independent research, I have participated in several international conferences and I have been invited as speaker to congresses in France and UK. Likewise, I have participated as teacher or coordinator in several outreach activities and, in 2019, I was the organiser of a symposia at the XLII Congress of the SEBBM. The involvement in a multi-disciplinary community provided me with the scientific judgment, professional connections and most recent technical knowledge that is required to pursue a career as a principal investigator. I believe my expertise in state-of-the-art cryoEM tools will be an excellent contribution to the development of this technique in the Spanish research community and the 5-year support by a Ramón y Cajal program will provide a perfect basis to establish my independent research line and create new collaborations.