ERC Grantees at U.PORTO

SERVIÇO DE INVESTIGAÇÃO E PROJETOS

U.PORTO

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Title

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Format

Electronic

EUROPEAN RESEARCH COUNCIL (ERC)

Created in 2007 to foster the highest quality research, the European Research Council (ERC) provides attractive funding to support researchers across all fields of science with innovative ideas to form a team and pursue high-risk/high-gain frontier research in every domain in Europe.

The ERC is a flagship component of Horizon Europe, the European Union's Research Framework Programme for 2021 to 2027.

ERC CORE GRANT SCHEMES

ERC Starting Grants (StG) for early-career, emerging research leaders (2-7 years after PhD - up to €1.5M for a period of 5 years)

ERC Consolidator Grants (CoG) for researchers who are already independent (7-12 years after PhD - up to €2M for a period of 5 years)

ERC Advanced Grants (AdG) for established researchers (up to €2.5M for a period of 5 years)

ADDITIONAL FUNDING SCHEMES

ERC Proof of Concept (PoC) for ERC Grant holders only. Bridging the gap between research - earliest stage of marketable innovation (up to €150.000)

ERC Synergy Grants (SyG) for teams of 2-4 established leading scientist PIs (up to € 15M for a period of 5 years)

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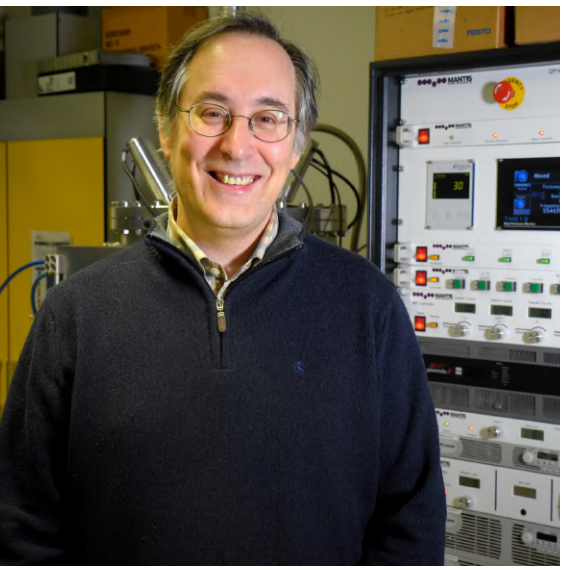
Adélio Miguel Magalhães Mendes



FUNDING SCHEME
Advanced Grant (AdG)

PROJECT ACRONYM
BI-DSC

RESEARCH DOMAIN
Physical Sciences & Engineering

HOSTING INSTITUTION
FEUP

TIMEFRAME
2013-2018

FUNDING AWARDED
1 989 300,00€

PROJECT TITLE
Building Integrated Dye Sensitized Solar Cells

In the last decade, solar and photovoltaic (PV) technologies have emerged as a potentially major technology for power generation in the world. So far the PV field has been dominated by silicon devices, even though this technology is still expensive.Dye-sensitized solar cells (DSC) are an important type of thin-film photovoltaics due to their potential for low-cost fabrication and versatile applications, and because their aesthetic appearance, semi-transparency and different color possibilities.This advantageous characteristic makes DSC the first choice for building integrated photovoltaics.Despite their great potential, DSCs for building applications are still not available at commercial level. However, to bring DSCs to a marketable product several developments are still needed and the present project targets to give relevant answers to three key limitations: encapsulation, glass substrate enhanced electrical conductivity and more efficient and low-cost raw-materials. Recently, the proponent successfully addressed the hermetic devices sealing by developing a laser-assisted glass sealing procedure.Thus, BI-DSC proposal envisages the development of DSC modules 30x30cm2, containing four individual cells, and their incorporation in a 1m2 double glass sheet arrangement for BIPV with an energy efficiency of at least 9% and a lifetime of 20 years. Additionally, aiming at enhanced efficiency of the final device and decreased total costs of DSCs manufacturing, new materials will be also pursued. The following inner-components were identified as critical: carbon-based counter-electrode; carbon quantum-dots and hierarchically TiO2 photoelectrode. It is then clear that this project is divided into two research though parallel directions: a fundamental research line, contributing to the development of the new generation DSC technology; while a more applied research line targets the development of a DSC functional module that can be used to pave the way for its industrialization.

Ana Costa Xavier de Carvalho

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
ACTOMYO

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

TIMEFRAME
2015-2021

FUNDING AWARDED
1 499 989,00€

PROJECT TITLE
Mechanisms of actomyosin-based contractility during cytokinesis

Cytokinesis completes cell division by partitioning the contents of the mother cell to the two daughter cells. This process is accomplished through the assembly and constriction of a contractile ring, a complex actomyosin network that remains poorly understood on the molecular level. Research in cytokinesis has overwhelmingly focused on signaling mechanisms that dictate when and where the contractile ring is assembled. By contrast, the research I propose here addresses fundamental questions about the structural and functional properties of the contractile ring itself. We will use the nematode C. elegans to exploit the power of quantitative live imaging assays in an experimentally tractable metazoan organism. The early C. elegans embryo is uniquely suited to the study of the contractile ring, as cells dividing perpendicularly to the imaging plane provide a full end-on view of the contractile ring throughout constriction. This greatly facilitates accurate measurements of constriction kinetics, ring width and thickness, and levels as well as dynamics of fluorescently-tagged contractile ring components. Combining image-based assays with powerful molecular replacement technology for structure-function studies, we will 1) determine the contribution of branched and non-branched actin filament populations to contractile ring formation; 2) explore its ultra-structural organization in collaboration with a world expert in electron microcopy; 3) investigate how the contractile ring network is dynamically remodeled during constriction with the help of a novel laser microsurgery assay that has uncovered a remarkably robust ring repair mechanism; and 4) use a targeted RNAi screen and phenotype profiling to identify new components of actomyosin contractile networks. The results from this interdisciplinary project will significantly enhance our mechanistic understanding of cytokinesis and other cellular processes that involve actomyosin-based contractility.

Hélder José Martins Maiato

GRANT 1

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
PRECISE

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

TIMEFRAME
2011-2015

FUNDING AWARDED
1 485 097,00€

PROJECT TITLE
Spatiotemporal regulation of chromosome segregation fidelity

At any given moment, 250 million cells are dividing in the human body through an essential process known as mitosis. Inaccuracy of mitosis leads directly to aneuploidy (gain or loss of chromosomes), a hallmark of several cancers and birth defects. Mitotic fidelity is controlled by the spindle assembly checkpoint (SAC), a signaling pathway that delays the progression of mitosis to ensure that all chromosomes are attached to mitotic spindle microtubules (MTs). Central to this activity, the kinetochore (KT), a minute structure on each replicated sister-chromatid, promotes the rapid turnover of MTs to correct potential attachment errors during early mitotic stages. Upon anaphase onset, the KT then switches to bind MTs with higher affinity, so that the energy derived from their depolymerizing plus ends helps driving chromosome motion to the poles. While the molecular basis of the KT-MT interface is only now starting to be elucidated, how the multiple KT activities are regulated throughout mitosis remains unknown. Here we propose to dissect from a molecular perspective how the interaction between spindle MTs and KTs controls chromosome segregation fidelity in space and time. For this purpose we will combine the power of biochemical analysis and genome-wide RNAi screens with the detailed functional investigation of already identified candidate genes using state-of-the-art live cell microscopy and pilot laser microsurgery tools in animal cells. Additionally, we have in place all the necessary conditions to investigate the physiological significance of chromosome segregation errors and evaluate respective outcomes using unique mammalian model systems. With this synergistic approach we aim to unveil the molecular routes of aneuploidygenesis and their implications to human health.

GRANT 2

FUNDING SCHEME
Consolidator Grant (CoG)

PROJECT ACRONYM
CODECHECK

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

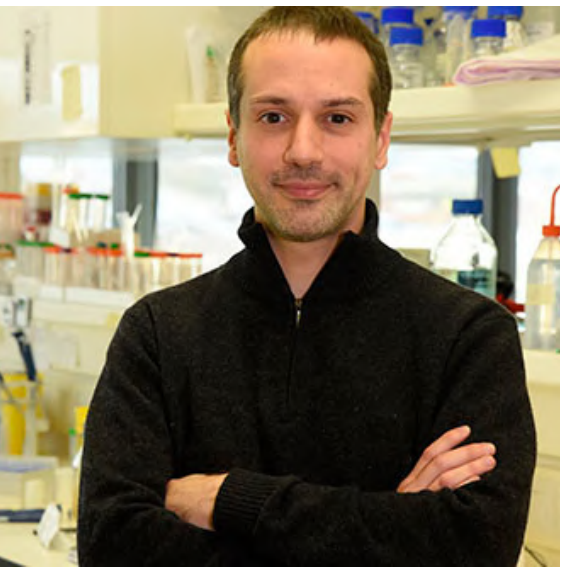
TIMEFRAME
2016-2021

FUNDING AWARDED
2 323 468,00€

PROJECT TITLE
CRACKING THE CODE BEHIND MITOTIC FIDELITY: the roles of tubulin post-translational modifications and a chromosome separation checkpoint

During the human lifetime 10000 trillion cell divisions take place to ensure tissue homeostasis and several vital functions in the organism. Mitosis is the process that ensures that dividing cells preserve the chromosome number of their progenitors, while deviation from this, a condition known as aneuploidy, represents the most common feature in human cancers. Here we will test two original concepts with strong implications for chromosome segregation fidelity. The first concept is based on the "tubulin code" hypothesis, which predicts that molecular motors "read" tubulin post-translational modifications on spindle microtubules. Our proof-of-concept experiments demonstrate that tubulin detyrosination works as a navigation system that guides chromosomes towards the cell equator. Thus, in addition to regulating the motors required for chromosome motion, the cell might regulate the tracks in which they move on. We will combine proteomic, super-resolution and live-cell microscopy, with in vitro reconstitutions, to perform a comprehensive survey of the tubulin code and the respective implications for motors involved in chromosome motion, mitotic spindle assembly and correction of kinetochore-microtubule attachments. The second concept is centered on the recently uncovered chromosome separation checkpoint mediated by a midzone-associated Aurora B gradient, which delays nuclear envelope reformation in response to incompletely separated chromosomes. We aim to identify Aurora B targets involved in the spatiotemporal regulation of the anaphase-telophase transition. We will establish powerful live-cell microscopy assays and a novel mammalian model system to dissect how this checkpoint allows the detection and correction of lagging/long chromosomes and DNA bridges that would otherwise contribute to genomic instability. Overall, this work will establish a paradigm shift in our understanding of how spatial information is conveyed to faithfully segregate chromosomes during mitosis.

José Carlos Ribeiro Bessa



FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
ZPR

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

TIMEFRAME
2016-2021

FUNDING AWARDED
1 497 520,00€

PROJECT TITLE
The Pancreas Regulome: From causality to prediction of non-coding mutations in human pancreatic diseases

Several human pancreatic diseases have been characterized, being the diabetes the most common. Like others, this genetic disease is related to disrupted non-coding cis-regulatory elements (CREs) that culminate in altered gene expression. Although Genome Wide Association Studies support this hypothesis, it's still unclear how mutations on CREs contribute to disease. The translation from the "non-coding code" to phenotype is an exciting and unexplored field that we will approach in this project with the help of the zebrafish as a suitable animal model. We aim to uncover the implications of the disruption of pancreas CREs and how they contribute to diabetes in vivo. For this we will study transcriptional regulation of genes in zebrafish. The similarities between zebrafish and mammal pancreas and the evolutionary conservation of pancreas transcription factors (TF) make it an excellent model to approach and study this disease. In this project we will characterize the zebrafish insulin producing beta-cell regulome, by determining the active CREs in this cell type and their bound TFs. Then we will compare this information with a similar dataset recently available for human beta-cells, to define functional orthologs in these species. Selected CREs will be tested by in vivo gene reporter assays in zebrafish, focusing on those functionally equivalent to human CREs where risk alleles have been associated with diabetes or those regulating genes involved in diabetes. Later these CREs will be mutated in the zebrafish genome to validate their contribution to diabetes. Finally we will translate this to predict new human disease-associated CREs by focusing on the regulatory landscape of diabetes-associated genes, without the need of having countless patients to uncover them. With this project we will create a model system that will allow the identification of new diabetes-associated CREs, which might have a great impact in clinical management of this epidemic disease.

Manuel António Moreira Alves

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
ELASTIC-TURBULENCE

RESEARCH DOMAIN
Physical Sciences & Engineering

HOSTING INSTITUTION
FEUP

TIMEFRAME
2012-2018

FUNDING AWARDED
994 110,00€

PROJECT TITLE
Purely-elastic flow instabilities and transition to elastic turbulence in microscale flows of complex fluids

Flows of complex fluids, such as many biological fluids and most synthetic fluids, are common in our daily life and are very important from an industrial perspective. Because of their inherent nonlinearity, the flow of complex viscoelastic fluids often leads to counterintuitive and complex behaviour and, above critical conditions, can prompt flow instabilities even under low Reynolds number conditions which are entirely absent in the corresponding Newtonian fluid flows. The primary goal of this project is to substantially expand the frontiers of our current knowledge regarding the mechanisms that lead to the development of such purely-elastic flow instabilities, and ultimately to understand the transition to so-called "elastic turbulence", a turbulent-like phenomenon which can arise even under inertialess flow conditions. This is an extremely challenging problem, and to significantly advance our knowledge in such important flows these instabilities will be investigated in a combined manner encompassing experiments, theory and numerical simulations. Such a holistic approach will enable us to understand the underlying mechanisms of those instabilities and to develop accurate criteria for their prediction far in advance of what we could achieve with either approach separately. A deep understanding of the mechanisms generating elastic instabilities and subsequent transition to elastic turbulence is crucial from a fundamental point of view and for many important practical applications involving engineered complex fluids, such as the design of microfluidic mixers for efficient operation under inertialess flow conditions, or the development of highly efficient micron-sized energy management and mass transfer systems. This research proposal will create a solid basis for the establishment of an internationally-leading research group led by the PI studying flow instabilities and elastic turbulence in complex fluid flows.

Nuno Miguel Cardoso Santos

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
EXOEARTHS

RESEARCH DOMAIN
Physical Sciences & Engineering

HOSTING INSTITUTION
CAUP

TIMEFRAME
2009-2014

FUNDING AWARDED
928 090,00€

PROJECT TITLE
EXtra-solar planets and stellar astrophysics: towards the detection of Other Earths

The detection of more than 300 extrasolar planets orbiting other solar-like stars opened the window to a new field of astrophysics. Many projects to search for Earth-like planets are currently under way, using a huge battery of telescopes and instruments. New instrumentation is also being developed towards this goal for use in both ground- and space-based based facilities. Since planets come as an output of the star formation process, the study of the stars hosting planets is of great importance. The stellar-planet connection is strengthened by the fact that most of the exoplanets were discovered using a Doppler radial-velocity technique, where the gravitational influence of the planet on the star and not the planet itself is actually measured. This project aims at doing frontier research to explore i) in unique detail the stellar limitations of the radial-velocity technique, as well as ways of reducing them, having in mind the detection of Earth-like planets and ii) to develop and apply software packages aiming at the study of the properties of the planet-host stars, having in mind the full characterization of the newfound planets, as well as understanding planet formation processes. These goals will improve our capacity to detect, study, and characterize new very low mass extra-solar planets. EXOEarths further fits into the fact that I am currently Co-PI of the project for a new high-resolution ultra-stable spectrograph for the VLT. The results of this project are crucial to fully exploit this new instrument. They will be also of extreme importance to current state-of-the-art planet-search projects aiming at the discovery of other Earths, in particular those making use of the radial-velocity method.

Nuno Miguel De Oliveira Lages Alves

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
TEC_Pro

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

TIMEFRAME
2015-2021

FUNDING AWARDED
1 491 749,00€

PROJECT TITLE
Molecular control of self-renewal and lineage specification in thymic epithelial cell progenitors in vivo

The development of vaccines for the treatment of infectious diseases, cancer and autoimmunity depends on our knowledge of T-cell differentiation. This proposal is focused on studying the thymus, the organ responsible for the generation of T cells that are responsive against pathogen-derived antigens, and yet tolerant to self. Within the thymus, thymic epithelial cells (TECs) provide key inductive microenvironments for the development and selection of T cells that arise from hematopoietic progenitors. As a result, defects in TEC differentiation cause syndromes that range from immunodeficiency to autoimmunity, which makes the study of TECs of fundamental, and clinical, importance to understand immunity and tolerance induction. TECs are divided into two functionally distinct cortical (cTECs) and medullary (mTECs) subtypes, which derive from common bipotent TEC progenitors (TEPs). Yet, the genetic and epigenetic details that control cTEC/mTEC lineage specifications from TEPs are unsettled. My objectives are to identify TEC progenitors and their niches within the thymus, define new molecular components involved in their self-renewal and lineage potential, and elucidate the epigenetic codes that regulate the genetic programs during cTEC/mTEC fate decisions. We take a global approach to examine TEC differentiation, which integrates the study of molecular processes taking place at cellular level and the analysis of in vivo mouse models. Using advanced research tools that combine reporter mice, clonogenic assays, organotypic cultures, high-throughput RNAi screen and genome-wide epigenetic and transcriptomic profiling, we will dissect the principles that underlie the self-renewal and lineage differentiation of TEC progenitors in vivo. I believe this project has the potential to contribute to one of the great challenges of modern immunology – modulate thymic function through the induction of TEPs - and therefore, represents a major advance in Health Sciences.

Pedro Leão

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
FattyCyanos

RESEARCH DOMAIN
Physical Sciences & Engineering

HOSTING INSTITUTION
CIIMAR

TIMEFRAME
2018-2022

FUNDING AWARDED
1 462 938,00€

PROJECT TITLE
Fatty acid incorporation and modification in cyanobacterial natural products

Known, but mostly novel natural products (NPs) are in high demand – these are used in drugs, cosmetics and agrochemicals and serve also as research tools to probe biological systems. NP structures inspire chemists to develop new syntheses, and NP biosynthetic enzymes add to the metabolic engineer's toolbox. The advent of next generation DNA-sequencing has revealed a vastly rich pool of NP biosynthetic gene clusters (BGCs) among bacterial genomes, most of which with no corresponding NP. Hence, opportunities abound for the discovery of new chemistry and enzymology that has the potential to push the boundaries of chemical space and enzymatic reactivity. Still, we cannot reliably predict chemistry from BGCs with unusual organization or encoding unknown functionalities, and, for molecules of unorthodox architecture, it is difficult to anticipate how their BGCs are organized. It is the valuable, truly novel chemistry and biochemistry that lies on these unexplored connections, that we aim to reveal with this proposal. To achieve it, we will work with a chemically-talented group of organisms – cyanobacteria, and with a specific structural class – fatty acids (FAs) – that is metabolized in a quite peculiar fashion by these organisms, paving the way for NP and enzyme discovery. On one hand, we will exploit the unique FA metabolism of cyanobacteria to develop a feeding strategy that will quickly reveal unprecedented FA-incorporating NPs. On the other, we will scrutinize the intriguing biosynthesis of three unique classes of metabolites that we have isolated recently and that incorporate and modify FA-moieties. We will find the BGCs for these compounds and dissect the functionality involved in such puzzling modifications to uncover important underlying enzymatic chemistry. This proposal is a blend of discovery- and hypothesis-driven research at the NP chemistry/biosynthesis interface that draws on the experience of the PI's work on different aspects of cyanobacterial NPs.

Reto Gassmann

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
DYNEINOME

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
IBMC

TIMEFRAME
2014-2019

FUNDING AWARDED
1 367 466,00€

PROJECT TITLE
Cytoplasmic Dynein: Mechanisms of Regulation and Novel Interactors

The megadalton cytoplasmic dynein complex, whose motor subunit is encoded by a single gene, provides the major microtubule minus end-directed motility in cells and is essential for a wide range of processes, ranging from the transport of proteins, RNA, and membrane vesicles to nuclear migration and cell division. To achieve this stunning functional diversity, cytoplasmic dynein is subject to tight regulation by co-factors that modulate localization, interaction with cargo, and motor activity. At present, our knowledge of the underlying mechanisms remains limited. An overarching goal of this proposal is to gain an understanding of how interactions with diverse adaptor proteins regulate dynein function in space and time. We choose the nematode C. elegans as our model system, because it will enable us to study the biology of dynein regulation in the broad context of a metazoan organism. The nematode's versatile genetic tools, its biochemical tractability, and the powerful molecular replacement technologies available, this makes for a uniquely attractive experimental system to address the mechanisms employed by dynein regulators through a combination of biochemical, proteomic, and cell biological assays. Specifically, we propose to use a biochemical reconstitution approach to obtain a detailed molecular picture of how dynein is targeted to the mitotic kinetochore; we will perform a forward genetic and proteomic screen to expand the so-far limited inventory of metazoan dynein interactors, whose functional characterization will shed light on known dynein-dependent processes and lead to novel unanticipated lines of research into dynein regulation; we will dissect the function and regulation of the most important dynein co-factor, the multi-subunit dynactin complex; and finally we will strive to establish a novel C. elegans model for human neurodegenerative disease, based on pathogenic point mutations in a dynactin subunit.

Rita Covas

FUNDING SCHEME
Consolidator Grant (CoG)

PROJECT ACRONYM
COOPERATIVE PARTNER

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
ICETA (CIBIO)

TIMEFRAME
2020-2024

FUNDING AWARDED
1 999 335,00€

PROJECT TITLE
Partner choice and the evolution of cooperation

Cooperation represents an evolutionary puzzle because natural sCooperation poses an evolutionary problem because natural selection is thought to favour cheaters over co-operators. However, theory and studies in humans show us that co-operators are preferred over cheaters as social and sexual partners. Partner choice may therefore provide a powerful explanation for the evolution and stability of cooperation, alongside kin selection and self-serving benefits, but we lack an understanding of its importance in natural systems. Recent studies showing that animals have a preference for associating with more cooperative individuals are promising but were mostly conducted in artificial captive conditions, making the evolutionary implications of partner choice hard to assess. Manipulating cooperation in the wild to test the fitness consequences of partner choice is the leap that is required to understand whether or not partner choice provides an evolutionary explanation for cooperation. I will pursue this goal using a long-term study that I established on a highly cooperative wild bird, the sociable weaver Philetairus socius. New methodological developments now allow us to conduct large-scale experiments in the wild, and detailed tracking of individual for several years will allow us to quantify the fitness consequences of choice. Specifically, here I will: i) use a new conceptual framework to test whether cooperation is repeatable (a pre-requirement for partner choice); ii) use state-of-the-art technology to manipulate cooperative behaviour and measure the resulting patterns of social and sexual partner choice; iii) use physiological measures and lifetime reproductive success to examine the fitness benefits arising from partner choice and the underlying mechanisms for both co-operators and the individuals that associate with them. Ultimately, the project will provide a novel and robust evaluation of the roles of social and sexual selection for the evolution of cooperation.

Susana Soares

FUNDING SCHEME
Starting Grant (StG)

PROJECT ACRONYM
BeTASTy

RESEARCH DOMAIN
Life Sciences

HOSTING INSTITUTION
LAQV/REQUIMTE

TIMEFRAME
2022 - 2027

FUNDING AWARDED
1 499 791,00€

PROJECT TITLE
New Molecular and Cell-based Approaches to assess Food Astringency and Bitterness

Taste properties are vital to humans: they impact human survival, nutrition, health and well-being. The problem of unpleasant taste properties, namely bitter- or astringent-tasting compounds is emerging in many diverse research fields. Beyond the obvious interest in food science, nutrition, and in the improvement/selection of crops, also human taste disorders and drug discovery domains could also benefit from research on astringency and bitterness. Crossing the boundaries among different fields, BeTASTy goes beyond the current state-ofthe-art of food-oriented research to respond to the prominent challenges on astringency and bitterness. This proposal will provide an in-depth mechanistic and functional understanding of the MAIN PHYSICAL-CHEMICAL-EVENTS triggering the physiological and neural perception of astringency by an innovative approach considering the main oral key pieces namely salivary proteins, epithelia and emphasizing the role of mechanoreceptors on that sensation. BeTASTy will also unveil how, for some compounds, astringency and bitterness CAN GO TOGETHER by an innovative all-in-one model. Additionally, the individual features that account for sensory differences will be deepened by a pioneering approach based on human organoids and electroencephalography. The final goal will be the creation of cutting-edge CELL-FREE BIOSENSORS based on the identified orally active mechano- and bitter taste receptors to assess astringency and bitterness, respectively, and by overcoming the main drawbacks of the existing (cell-based) ones. Endowed with a truly differentiated and disruptive character, this groundbreaking project will engage food chemistry, biochemistry, neuroscience, sensory analysis and biotechnology fields of research to outdo the state-of-the-art. Only an ambitious and multidisciplinary proposal will yield scientific breakthroughs on the BIOCHEMICAL-NEURALPERCEPTUAL TRIAD EVENTS of these taste properties which will eventually enable to tailor them.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