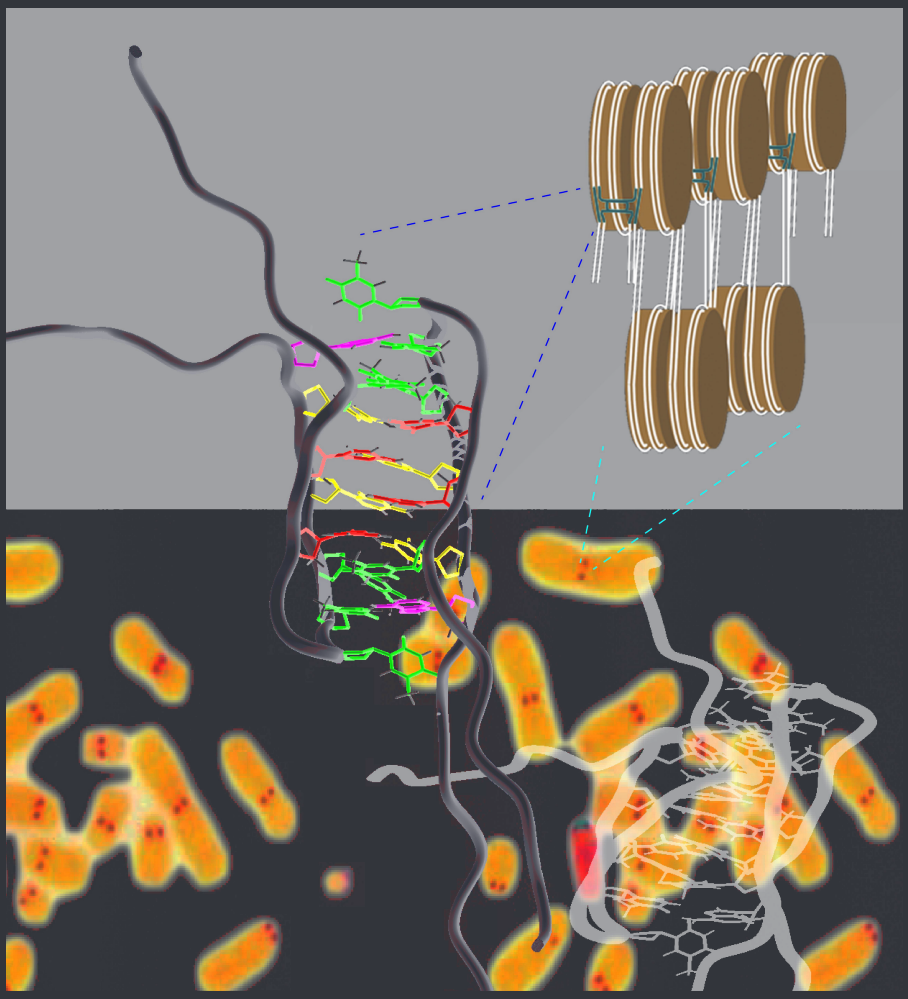
Biofísica

Magazine

May - Aug. 2015
issue #2

life version at
http://biofisica.info/



Cover image:
Courtesy of C. González

EDITORS:
Jesús Salgado
Jorge Alegre-Cebollada
Xavier Daura
Teresa Giráldez

SBE - Sociedad de Biofísica de España

http://www.sbe.es/

Biofísica
SBE Magazine

CONTACT

SBE - Sociedad de Biofísica de España
Secretaria SBE, IQFR-CSIC,
C/Serrano 119, 28006 Madrid
Email: sbe_secretaria@sbe.es
WEB: http://www.sbe.es

Biofísica
SBE Magazine

In this issue

Biofísica Magazine

EDITORIAL

Is Science at a "critical point"?

4 Comments

Jesús Salgado, *ICMol (Valencia)*

Science is living a glorious moment. It is recognized as a crucial ingredient for human prosperity, like it never was before. It is present in all aspects of modern life, from politics to mass media to education, as it never was before. However, not all that we hear today about Science is positive. Aside from recurrent bad news about funding constraints, there are growing rumours warning that something may be failing in Science. It can be argued that this is just part (or consequence) of the present *critical time* in history characterized by an overlap of a few interconnected *crisis*, affecting economy, demography, politics, market, communication, energy, climate... And Science would just be one more thing to add to the list [1].

But what are the specific ingredients of the Science critical point? Just attending to recent debates in the Scientific Community, we can identify a few:

- A crisis of the traditional Scientific Career, with a tremendous imbalance between the numbers of trainees (PhD students and postdocs) and available senior Scientist positions as a most prominent symptom [2,3].
- A crisis of the traditional Publishing System, which can be related to a number of causes and consequences. Among the causes are the impact of a still erupting communications revolution, which has accelerated the dissemination of ideas and scientific results, and the irruption of new media (Open-Access Journals, Online meetings, Social networks...). Among the consequences are a poor adaptation of traditional peer reviewing [4,5] to this new scenario and a preoccupating increase of scientific misconduct [6].
- A crisis of traditional Funding Systems, which although can profit from the available crowd of ever renewing young scientists, to select Excellence of the highest level, it is also rising concerns about efficiency and low capacity to choose quality, instead of quantity, or creativity, rather than safe projects [2,7].

The paradox, in this *best-time-ever* of Science, is that it is increasingly loosing reputation.

Although these three crisis have already been identified [2], none of them appears easy to solve. Science, like economy, operates globally, but decisions are still taken at National and Regional levels. Additionally, each of these problems may have special colours depending on the region and depending on particular economical or social circumstances. For example, the career crisis (and the postdoc overflow), far from facilitating the dissemination of Science, is contributing to centrifuge most talented Scientists from economically deprived regions and to concentrate them in the strongest economical poles. Thus, competition is having very different consequences in different parts of the world. Competition is essential for the emergence of Excellence, which in turn is the drive for the advancement of Science, but the economical context can strongly distort its potentially positive effects.

On the other hand, without a consensus definition of excellence, with questionable metrics to value Science (and Scientists) and with inefficient reviewing, how much excellence fails to be identified? And how much fake excellence may get finally funded, despite a tough filtering system? Apart from pure fraudulent work, which probably (still) does not reach preoccupating levels, low significance recurring work may easily hid behind apparently great projects and high impact publications. The urge to increase publication records, fuelled by fierce competition for projects and positions and greased by a huge list of available Journals incentivizes low risk research, easier and faster to produce and publish. But less trivial, risky and uncommon ideas, which have been historically behind the biggest steps in Science, are demotivated by the dominant system [2]. In parallel, Scientists are pushed to disseminate their achievements in mass media and to quickly explore translational research, altogether contributing to create false expectations.

The paradox, in this *best-time-ever* of Science, is that it is increasingly loosing reputation. The difficulties to develop a career in Science, well known by students, are demotivating many of the best to choose research as a profession. The publishing inflation is becoming difficult to handle by obsolete peer reviewing and inefficient evaluation systems, in turn facilitating fraud and increasing mistrust in Science. There are reasons to think that these negative perceptions may already be leaking into the Society. There should be a solution to these problems, and Science itself should be able to find it.

Jesús Salgado

Instituto de Ciencia Molecular – ICMol

Universitat de València

C/ Catedrático José Beltrán 2, 46980 Paterna (Valencia), Spain.

E-mail: jesus.salgado@uv.es

References

1. Woolston C. "Online debate erupts to ask: is science broken?". *Nature*, **2015**, 519: 393. DOI:10.1038/519393f
2. Alberts B, Kirschner MV, Tilghman S, Varmus H. "Rescuing US biomedical research from its systemic flaws". *PNAS*, **2014**, 111: 5773. DOI:10.1073/pnas.1404402111
3. Powell K. "The future of the postdoc". *Nature*, **2015**, 520: 144. DOI:10.1038/520144a
4. Nature's peer review debate. This include 22 articles of analyses and perspectives from leading scientists, publishers and other stakeholders.
5. Bohannon J. "Who's Afraid of Peer Review?". *Science*, **2013**, 342: 60. DOI:10.1126/science.342.6154.60
6. Fanelli D. "How Many Scientists Fabricate and Falsify Research? A Systematic Review and Meta-Analysis of Survey Data". *PLoS ONE*, **2009**, 4: e5738. DOI:10.1371/journal.pone.0005738
7. Li D, Agha L. "Big names or big ideas: Do peer-review panels select the best science proposals?". *Science*, **2015**, 348: 434. DOI:10.1126/science.aaa0185

Biofísica Magazine

REPORTAGE

From Tenerife to King George Island: An Antarctic Adventure

Teresa Giraldez, *Centro de Investigaciones Biomédicas de Canarias – CIBICAN, Universidad de La Laguna (Tenerife)*

Endotherm ("warm-blooded") animals -such as humans- as well as warm ectotherm animals, function physiologically at temperatures ranging approximately from 17 to 42ºC. We, endotherms, achieve this thanks to our biological thermostat, which ensures that, regardless of the outside world temperature, membranes and proteins in our cells are always maintained at their optimal temperature.

However, life also occurs at the extremes, where not all animals are able to control their internal temperature. For instance, invertebrates in the Antarctic Sea live all year long at temperatures around -1ºC, which would be harmful for us. Even so, and due to evolutionary adaptations, they are able to perform all their physiological functions as efficiently as their relatives of warmer environments. How is this possible?

Life below zero

A crucial physiological mechanism that must adapt is the transmission of bioelectrical signals in neurons and excitable cells, which are responsible for most of the physiological responses and behaviour. In excitable cells, action potentials are generated by specific proteins responding to changes in voltage across the cell membrane, i.e., voltage dependent ion channels. Sodium channels open during the depolarizing phase, whereas potassium channels are responsible for repolarization. In fact, the fine-tuning of the latter gives shape and determines duration of action potentials, which is key to allow firing of subsequent spikes. Generation of action potentials is temperature dependent, due to the higher Q10 values (rate of change for a 10ºC temperature increase) of voltage dependent channels. This means that ion channel proteins from Antarctic organisms would have similar gating kinetics to channels from organisms living at warmer temperatures! What are the evolutionary adaptations of these channels that make them able to

sustain electrical activity at temperatures that are harmful for animals living in more temperate climates?

There is one place on Earth where this question can be addressed:

Antarctica

Antarctica is dedicated entirely to Science. Uninhabited by humans, it belongs to no country. It is also the coldest and windiest place on Earth!

As part of an exciting scientific and personal adventure, I teamed up with my colleagues Patricio Rojas, María Pertusa and Bernardo Morales from the Universidad de Santiago de Chile – USACH to present a research proposal to the Antarctic Institute of Chile – INACH.

Antarctica *black and white*, somewhere at King George Island.

We proposed to study electrical signalling and to characterise biophysically voltage-gated potassium channels in *Nacella Conccina*, an Antarctic limpet. Within the framework of the Antarctic Treaty System, and associated to the Chilean Ministry of Foreign Affairs, INACH encourages the development of scientific research and innovation in Antarctica. Several projects are selected each year through a competitive call to perform research at any of the seven Chilean scientific Bases in Antarctica. One warm day, great news arrived to Tenerife from Santiago de Chile: our project had been granted. Our adventure had officially begun!

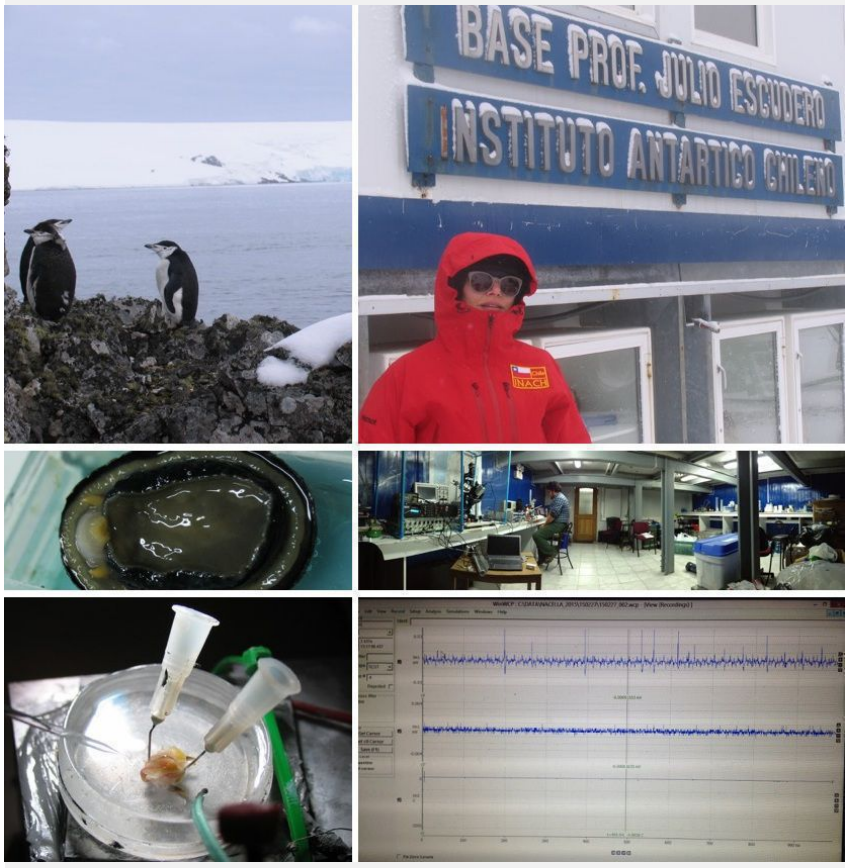
As a scientist, going to Antarctica is a dream. Protected by the Antarctic Treaty, it is the only place on Earth that belongs to no country, is not inhabited by humans and is dedicated entirely to Science. Interestingly, it is also the coldest and windiest place on Earth! Getting there is not easy. There are no regular flights and weather conditions are often extreme and unpredictable. Not surprisingly, countries closer to the White Continent have easier access to working there. With my lab settled in Tenerife, more than 10000 km away from the Antarctic Circle, one could think that the chances to participate in a research project in Antarctica would remain a life-lasting scientific wish. However, serendipity and good fortune are often cited as key factors in making science...

Building a electrophysiology lab in uninhabited land

On February 19th, 2015 I took off from Los Rodeos airport with a backpack full of small electrophysiological gadgets and my brain plenty of excitement. Final destination: **Scientific Base Julio Escudero, King George Island** (62°12'57"S 58°57'35"W, Antarctica). First stop was Santiago de Chile, where I was joined by my colleague Patricio Rojas. After a couple of days, used to gather last minute gear and to acquire technical outerwear, we flew together to Punta Arenas (Chile). The larger equipment (microscopes, amplifiers, etc.) had been sent South in three large boxes a week earlier.

In Punta Arenas, the spirit of the Antarctic explorers is alive at every corner. The INACH building used to be the post office from where Scott and Shackletton sent letters during their explorations and the Antarctic wind blows from the Strait of Magellan. Traditionally, there were only two ways of travelling to King George Island from Punta Arenas, both arranged for the scientists by the INACH: by boat (crossing for five days the turbulent Drake Passage) or by Hercules planes from the Chilean Air Force. A third option is now available thanks to a charter airline (Aerovías DAP), which was the one scheduled for us.

We arrived to King George Island on February 23rd. My first impression was bewildering. Huge volcanic rocks covered with ice and snow, untouched; a striking contrast of black and white. It was summer, so temperatures were not very cold (around 0ºC). We were received by the Chief of Escudero Base, Javier Arata, who drove us to the Base. Our laboratory was in the basement, and the dorms in the first floor. Our equipment boxes were already there, waiting to be opened. We had arrived to the white continent to do science.



Top-left: Chinstrap penguins in front of Nelson island's glacier. **Top-right:** Teresa at the entrance of Base Escudero. **Middle-left:** The limpet (white stuff is the head). **Center-right:** Panoramic view of the lab. **Bottom-left:** Limpet head ready to be recorded. **Bottom-right:** "Reading the limpet's mind".

We spent the following two days building two electrophysiology setups that we would use to record extracellular signals. Temperature was controlled using a homemade device consisting on an Arduino board and a peltier. This system

would allow us to study the spontaneous firing of Nacella concinna's buccal ganglia, a neuronal structure responsible of control of mouth musculature.

A *cool* nervous system

Time in the laboratory was combined with numerous field trips along Fildes Bay, in search for limpets. They are fairly easy to get at the rocky intertidal zone. We recorded extracellular spikes in the buccal ganglia, after applying slow temperature ramps ranging from 2 to 15 °C. Although our analysis is still undergoing, our results show three types of firing patterns: high rate at low temperatures, high rate at high temperature, and temperature independent. Regardless of the firing frequency, most recorded units decreased their activity at temperatures higher than 17 ±1 °C, suggesting that the nervous system of this organism is not adapted to live in Pacific or Atlantic coasts where other taxa from the same genus are found. Moreover, opposite spike polarity was observed in different units, suggesting that the generation of some action potentials occurs outside the ganglia. Further analysis is still needed to strengthen our conclusions.

Apart from the electrophysiological recordings, we also extracted many tissue samples for further work in our respective labs back home. Transcriptome data, published only last year (Fuenzalida, et al. Mar Genomics. 2014;18 Pt B:89-91) reveals the expression of voltage and calcium activated potassium channels, several ligand activated channels and other channels from the TRP family that are expressed in thermo-receptors of both invertebrates and vertebrates. In our laboratories, we will now extract RNA from Nacella tissue to clone the potassium channels that will be expressed in heterologous expression systems and characterized biophysically.

More things one can do at King George Island

A view of Fildes Bay including Base Escudero (blue, left), Chilean navy base (blue, right), Frei base (chilean air force, red). Farther, the Russian scientific base Bellinghausen.

But this was not the only science being made at Escudero Base. There were around 30 other scientists from Chile, Brazil, Venezuela and Portugal, from diverse scientific fields: Marine Biology, Geology, Physics... The base was organized and maintained by INACH staff: the chief of Base, a logistics operator, two boatmen and four craftsmen. We were fed by two cooks. The atmosphere was fantastic!

Outside the Base, many Antarctic animals can be seen. Penguins would be our usual companions in

our way to catch Nacella. We also saw many sea lions, Weddell seals, elephant seals and skuas. Some afternoons we would walk along the beach to enjoy the silence and beauty of such wild landscape.

We had also time to visit some of the other six Bases in the Island: Artigas (Uruguay), Bellinghausen (Russia) and Great Wall (China). Other Bases such as King Sejong (Korea) or Arctowski (Poland) are only accessible by boat or helicopter.

On march 11th, after carefully packing our equipment again, we waved Antarctica goodbye while getting into a DAP plane which would fly us back to Punta Arenas. We carried our computers full of recordings to analyse and many RNA and tissue samples. In our hearts, the wish to come back someday and the words at Scott memorial rumbling into our heads:

> *To strive, to seek, to find, and not to yield...*

Teresa Giráldez

Centro de Investigaciones Biomédicas de Canarias – CIBICAN

Universidad de La Laguna, Facultad de Medicina

Campus Ciencias de La Salud s/n, 38071

San Cristóbal de La Laguna, Santa Cruz de Tenerife.

E-mail: giraldez@ull.edu.es

Biofísica Magazine

BEYOND BIOPHYSICS

Chemistry and Biophysics

Conversation with Jesús Jiménez-Barbero

Jesús Salgado, *ICMol (Valencia)*

Professor Jesús Jiménez-Barbero.

Chemistry and Biophysics are close relatives. As *the science of molecules*, Chemistry has always been present in Biophysics, and both disciplines have shared methods, theories, achievements... and scientists. Chemistry and Biophysics have also common sub-disciplines, like (bio)polymer science, colloidal science, enzymology, or structural Biology, and in more recent times they contribute together to the development of molecular simulations, nanoscience, drug discovery, systems biology,...

To discuss about these connections I *chat* with a great Chemist and Biophysicist: Jesús Jiménez-Barbero. Educated as Organic Chemist, specialized in Structural Glycobiology, and expert on NMR, Professor Jiménez-Barbero has been Director of the Department of Chemical and Physics Biology of the Centre for Biological Research – CIB (CSIC) in Madrid and has been appointed recently as Scientific Director of CIC bioGUNE, Bizkaia (Spain). He served as President of the International Carbohydrate Organization (2012-2014) and is the current President of the Spanish Royal Society of Chemistry – RSEQ since 2012. He also acts as Manager of the General Subdirectorate for Research Projects in Chemistry (Ministry of Economy and Competitiveness, Government of Spain). These positions place him at a privileged lookout point to observe multidisciplinary Science.

We should strengthen collaboration between Chemistry and Biophysics. After all, many of us are players in the two teams!

Do not fall in the trap of *names*

Jesús Jiménez-Barbero prefers a Science with diffused borders between disciplines. "I do not know what I am", he confesses. One of his determinations, as President of RSEQ, is to tear down borders between the classical fields of Chemistry:

> *In modern Science we should just take what we need, no matter the field where it comes from. This eventually softens the lines between disciplines. We should in fact get rid of those borders. Classifying us within areas, disciplines and fields imposes limits and barriers, and this may be used for exclusion.*

He admits, that defining fields of work can still make some sense for the sake of organizing them, like with University degrees, for example. But when doing research, we must be permeable to the concepts, the methods, the language of the whole body of Science, with no much attention as to where they come from.

Chemistry meets Biophysics at the frontier with Biology

There is an internal debate within Chemistry about the position it occupies in today's Science. By synthesizing new molecules, Chemists create and solve their "own problems". But Chemistry also walks out to search for attractive problems, and it finds them at the interface with other disciplines. Modern Chemistry cares about energy, environment, health and of course Biosciences. At the interface with Biology is where Chemistry finds most connections with Biophysics: It is "Chemistry at the frontier with Biology", as Jiménez-Barbero prefers to name it.

Linus Carl Pauling (Feb. 28, 1901 – Aug. 19, 1994)**, frontier chemist and pioneer biophysicst**. [Linus Pauling holding a molecular model. 1950s] © Ava Helen and Linus Pauling Papers. Oregon State University Library.

This broad field includes Chemical Biology, which is about modifying and handling molecules outside and inside cells. It is also the playground for Structural Biology and Molecular Recognition. Linus Pauling, for example, was an *early frontier chemist* and one of the fathers of Structural and Molecular Biology. "In the study of molecular interactions Chemistry and Biophysics find their strongest synergy. Biophysics is of course also related to Physical Chemistry and overlaps as well with Nano-molecular sciences, but this all happens at the frontier with Biology", Jiménez-Barbero stresses.

Multidisciplinary Science

Chemistry and Biophysics need, and embrace, multidisciplinarity. They both look at problems from many different perspectives. However, while we should not hide behind the walls of disciplines, we cannot ambition to be experts on everything. "We are not in Leonardo's times. Collaboration is essential, as the way to reach far outside our own background knowledge". From his intense career dedicated biomolecular interactions, Jiménez-Barbero knows well how important it is for a chemist working close to spectroscopists, microbiologists, cell biologists.
Multidisciplinarity should generate attraction and be inclusive. It should be a way to integrate

knowledge and expertise from others disciplines into yours. But Jiménez-Barbero also recognizes the risks and dangers of multidisciplinarity Science, which one should be ready to overcome. This means being prepared to speak and understand the multiple "languages" of the Science. Frontier disciplines may also have difficulties to fit within the classical areas of Science, which may end up with underestimation and even exclusion. By being multidisciplinary you may feel yourself as a stranger within your mother field! Furthermore, the difficulties to assess multidisciplinary work might turn into disadvantage when competing for positions and financial support. Is it more difficult for multidisciplinary projects to get funded?, I ask. "In Spain, this can still be an issue, but the biggest problem is the scarcity of available funds, specially in recent years. This is really what makes it difficult for everyone". And he ends this enlightening conversation with a desire: "We should strengthen collaboration between Chemistry and Biophysics. We have a lot to win on that. After all, many of us are players in the two teams!"

Jesús Jiménez-Barbero
Scientific Director
CIC bioGUNE
Parque Tecnológico de Bizkaia, Edif. 801A-1º
48160 Derio- Bizkaia (Spain)
E-mail: jjbarbero@cicbiogune.es

Jesús Salgado
Instituto de Ciencia Molecular – ICMol
Universitat de València
C/ Catedrático José Beltrán 2
46980 Paterna (Valencia), Spain.
E-mail: jesus.salgado@uv.es

Biofísica Magazine

COOL BIOPHYSICS

The race towards the human proteome

Jesús Vázquez, *CNIC (Madrid)*

While current genomics approaches allow the eventual analysis of all human genes, the ability to analyze all their protein products has traditionally been considered a utopian dream. Proteins cannot be amplified like genes, and mass spectrometry (MS) —the most powerful approach for protein analysis— is hampered by the large dynamic range of human protein concentrations. However, these limitations are already being overturned by the remarkable advances made in MS in the past few years, in terms of sensitivity, mass accuracy and, above all, speed.

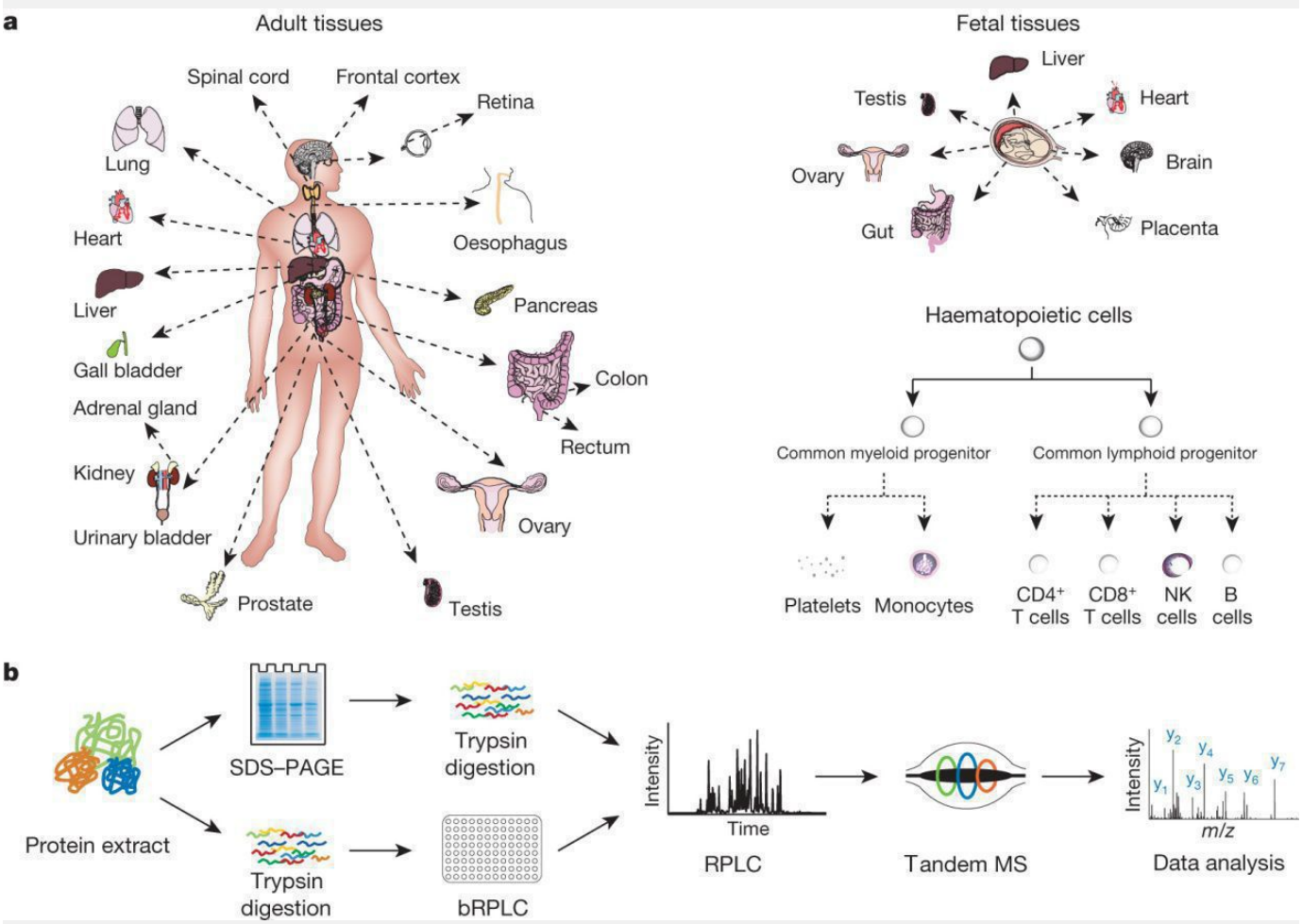
Early efforts: The proteome of specific cell lines

The first comprehensive analyses of what was at the time considered the *complete* proteome of two human cell lines (~10.000 distinct proteins) were published simultaneously in **2011** by the groups of Mann (HeLa cells, Nagaraj, et al. 2011) and Aebersold (U2OS cells, Beck, et al. 2011). This was possible by subjecting the peptidome (the result of digesting the proteins with a protease, making the products suitable to MS analysis) to considerable fractionation, and analyzing all the fractions using state-of-the art MS. Although these studies overthrew the dogma that proteins present in very few copies per cell would never be accessible to MS, subsequent experience demonstrated that surpassing the four-digit barrier was a task beyond the reach of most proteomics laboratories.

Drafts of the human proteome

The first analyses of what we could call the *human proteome* were published simultaneously in **2014** by two large laboratory consortia. One of them, led by Pandey (Kim, et al. 2014), was composed mostly of North American and Indian laboratories, while the other was composed of German groups and was directed by Kuster (Wilhelm, et al. 2014). The Pandey study used protein extracts from 30 human tissues (of normal, adult and fetal origin) and 6 hematopoietic cell lines. Each of the extracts was subjected to extensive fractionation at both the protein and peptide levels; the effort required more than 2,000 chromatography runs, which is about 20-fold more than the number

required previously to map a single human cell type, and identified ca. 17,300 gene products. In the Kuster study, 60% of the information was taken from existing MS repositories and a further 40% was new data generated by the authors. Analysis of the equivalent of 17,000 runs allowed the identification of 18,000 proteins. By that time, in a joint bioinformatics effort by two Spanish groups from the CNIO and the CNIC, in collaboration with two US groups, we were able to narrow down the number of potentially coding human genes to 19,000 (Ezkurdia, et al. 2014). The Pandey and Kuster studies were thus able to map approximately 95% of the human proteome.



Workflow and comparison of human proteome data with public repositories Used with permisson from the nature publishing group, M.S. Kim, et al. Nature 509: 575-581 (2014) doi:10.1038/nature13302. © 2014 by the nature publishing group.

These two reports provided the proteomics community with a rich source of information and their preliminary analysis yielded some interesting insights. For instance, the comparison of protein abundance profiles across all tissues and cell lines allowed the construction of the ***"housekeeping proteome"***: a list of 2,300 proteins ubiquitously and constitutively expressed in all situations, the primary function of which is the general control and maintenance of cells. Interestingly, this proteome is composed mainly of histones, ribosomal proteins, metabolic enzymes and cytoskeletal proteins, and constitutes approximately 75% of total protein mass. However, these proteins show across-tissue expression differences of up to five orders of magnitude, and the number of proteins

that are exclusively or preferentially detected in a particular organ is surprisingly small. This suggests that differences in biological function are achieved by a slightly varying set of proteins whose relative proportions are adjusted in a site-specific manner to achieve tailored biological roles. Similarly, studying the correlation of protein abundance across tissues provided important insights into the composition of complexes and the dynamic nature of protein-protein interactions. The huge amounts of protein and MS data gathered was also used for proteogenomics studies, in which, for instance, extensive analysis was conducted of the mechanisms through which protein abundance is regulated from the corresponding mRNA transcript and of the presence of isoforms, novel protein-coding regions (pseudogenes, non-coding RNAs, upstream ORFs and alike) and protein N-termini. An interesting outcome, which seems to confirm recent viewpoints, was that while mRNA abundance was a very poor predictor of protein abundance, the ratio of mRNA to protein tended to be protein-specific and was remarkably conserved across tissues, suggesting that the translation rate is characteristic of each transcript and that protein abundance in the cell is controlled predominantly at the transcriptional level.

Concerns and refinement

Very soon after the publication of these reports, criticisms were raised in the proteomics community. The first report was, again, a joint collaboration between CNIO and CNIC (Ezkurdia, et al. 2014), in which we demonstrated a lack of rigor in protein identification in the Pandey and Kuster studies. We concentrated our analysis on the olfactory receptor family, an interesting group of vertebrate-specific genes whose transcription levels are very low and which are confined to nasal tissue, not included in the earlier studies. Unexpectedly, we found 108 olfactory receptors in the Kuster report and 200 in the Pandey report. Most of the identified OR peptides shared their sequence with other proteins, and a great proportion of peptide spectra were of surprisingly low quality. Our results highlighted serious problems in the control of peptide-to-protein redundancy and the false discovery rate (FDR) of protein identification, the latter probably a consequence of the accumulation of large amounts of data and the use of very narrow precursor mass windows, as we pointed out recently (Bonzon-Kulichenko, et al. 2015).

Some proverbs say that humans are the only animals that make the same errors twice, and this story is reminiscent of past errors committed when the human genome was first published, and of the advent of high-throughput, MS-based peptide identification at the beginning of this century. The numbers of identified proteins were growing so fast that in the rush to beat records, proteomicians ignored the fact that the protein identification criteria were not extrapolatable from one situation to another. The result was that a large proportion of identifications reported at that time were incorrect. This situation was resolved by the introduction of decoy databases and the use of FDR at the peptide level, providing a robust and reproducible means of controlling identification quality that is still a must today.

Future directions

The current accumulation of proteins from large repositories and MS studies has produced what is called the *protein buildup FDR problem*, which, incidentally, was acknowledged in the Kuster report to be an *unsolved issue* (Wilhelm, et al. 2014). The conclusion is that there is an urgent need to resolve the protein FDR problem before we begin to trust the huge amounts of protein information produced in these collaborative efforts. Fortunately, the Human Proteome Organization is fully aware of the problem and is dedicating resources in this direction. This time round the Spanish proteomics community is fully implicated through the ProteoRed bioinformatics network, where we are working on the development of a novel integrative identification framework.

JESÚS VÁZQUEZ
Cardiovascular Proteomics Laboratory and Proteomics Unit
Department of Vascular Biology and Inflammation
Centro Nacional de Investigaciones Cardiovasculares – CNIC
C/ Melchor Fernández Almagro, N. 3, 28029 Madrid
E-mail: jesus.vazquez@cnic.es

References

Beck M, Schmidt A, Malmstroem J, Claassen M, Ori A, Szymborska A, Herzog F, Rinner O, Ellenberg J and Aebersold R. "The quantitative proteome of a human cell line".*Mol Syst Biol*, **2011**, 7: 549. DOI:10.1038/msb.2011.82.

Bonzon-Kulichenko E, Garcia-Marques F, Trevisan-Herraz M and Vázquez J "Revisiting Peptide Identification by High-Accuracy Mass Spectrometry: Problems Associated with the Use of Narrow Mass Precursor Windows". *J Proteome Res*, **2015**, 14: 700. DOI:10.1021/pr5007284.

Ezkurdia I, Juan D, Rodriguez JM, Frankish A, Diekhans M, Harrow J, Vázquez J, Valencia A and Tress ML"Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes". *Hum Mol Genet*, **2014**, 23: 5866. DOI:10.1093/hmg/ddu309.

Ezkurdia I, Vázquez J, Valencia A and Tress M "Analyzing the First Drafts of the Human Proteome".*J Proteome Res*, **2014**, 13: 3854. DOI:10.1021/pr500572z.

Kim MS, Pinto SM, Getnet D, Nirujogi RS, Manda SS ... and Pandey GA"A draft map of the human proteome". *Nature*, **2014**, 509: 575. DOI:10.1038/nature13302.

Nagaraj N, Wisniewski JR, Geiger T, Cox J, Kircher M, Kelso J, Pääbo S and Mann M"Deep proteome and transcriptome mapping of a human cancer cell line". *Mol Syst Biol*, **2011**, 7: 548. DOI:10.1038/msb.2011.81.

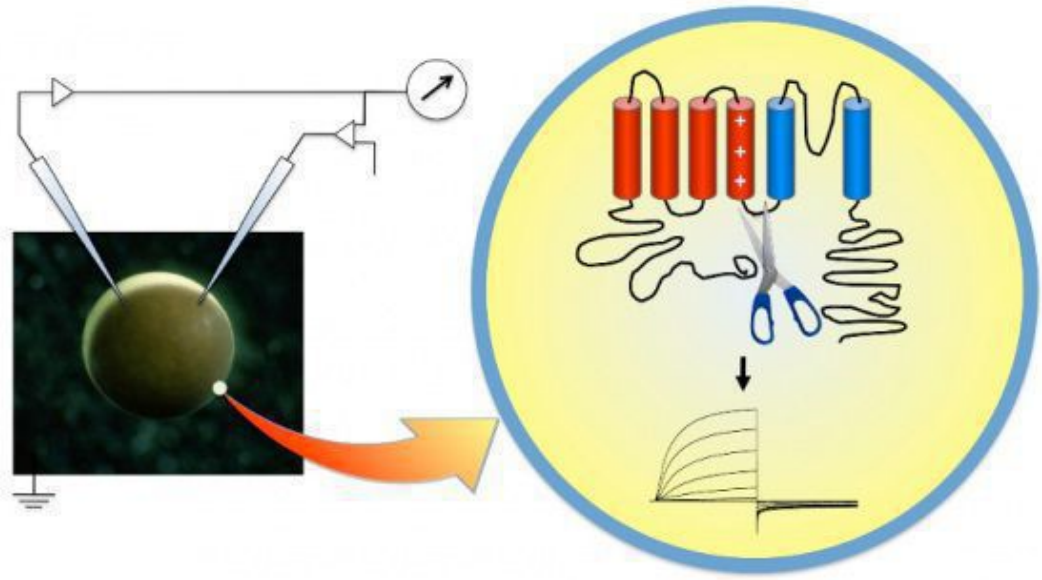
Wilhelm M, Schlegl J, Hahne H, Gholami AM, Lieberenz M ... and Kuster B"Mass-spectrometry-based draft of the human proteome". *Nature*, **2014**, 509: 582. DOI:10.1038/nature13319.

Biofísica Magazine

COMMENTARIES

Allosterism versus mechanical coupling: Truncated KCNH channels defy the classical mechanism of voltage-dependent gating

09/06/2015



Commentary to *Voltage-dependent gating of KCNH potassium channels lacking a covalent link between voltage-sensing and pore domains* (Nat Commun, 6: 6672).

Francisco Barros and Pilar de la Peña, *Universidad de Oviedo (Oviedo, Spain)*.

Voltage-gated potassium (**Kv**) channels are crucial regulators of cell excitability by mediating selective K+ flow across the plasma membrane. These proteins switch on and off with changes in membrane voltage and have three crucial functional elements: an ion conduction pore, a gate that controls the ionic flow, and a voltage sensor that triggers opening and closing of the gate. It is well established that these elements correspond to a modular structure of the protein, with a permeation module (transmembrane helices S5 and S6 and their intervening loop), surrounded by a voltage-sensing module (transmembrane S1-S4). However, the mechanism responsible for converting the changes occurring in the voltage sensing module into an opening of the gate of the permeation module are not entirely understood. It is generally assumed that the intracellular S4–S5 linker translates a conformational change from the voltage sensor into gating of the channel, via

direct mechanical coupling of the two regions. This well accepted model, has been questioned in a recent investigation by the Hormone Receptors and Ion Channels Group from the University of Oviedo and the Oncophysiology and Molecular Biology of Neuronal Signals Groups of the Max Planck Institute of Experimental Medicine in Göttingen.

The work published now challenges the classical view and demonstrates that physical continuity between modules is not necessary for voltage-dependent gating

The work addresses the voltage-dependent gating of two members of the **KCNH** family of Kv channels (Kv10.1 and Kv11.1). In humans, KCNH channels participate in nerve impulse transmission, hormone secretion and tumour cell proliferation. The Kv11.1 channel (also named hERG, that centres the work of the Oviedo University Group), has been also recognized as a key determinant of cardiac rhythm. Indeed, functional alterations in hERG are one of the most frequent causes of arrhythmia, linked to cardiac sudden death. As in other Kv channels the S4-S5 linker of KCNH channles would provide physical continuity for so called electromechanical coupling, by forming a rigid connection between the voltage-sensing and permeation modules, which acting as a mechanical lever, exerts force on the bottom of the channel to open the gate. However, the work published now challenges this classical view by interrupting the loop which links covalently the two modules, and demonstrates that physical continuity between them is not necessary for voltage-dependent gating. Indeed, the expressed split channels are still able to respond to changes in voltage and close and open in a near normal way. This new evidence points to an alternative mechanism based on non-covalent/allosteric interactions, as the molecular basis for coupling between voltage sensing and channel gating (de la Peña and Barros, unpublished results).

The conclusions of this research can be extrapolated to other channels of the Kv family and should also motivate revision of the general mechanical coupling model of voltage-gated channels. Apart from the important physiopathological implications of a better knowledge of these relevant proteins, the reported results open new exciting questions: They suggest the possibility that this sophisticated molecular machineries may arise from two independent modules, fused at any period along the molecular evolution of ion channels. How possible ancient cells could have indeed used both modules, synthesized as independent molecules, but able to interact and make a fully functional channel, remains to be established.

More Information

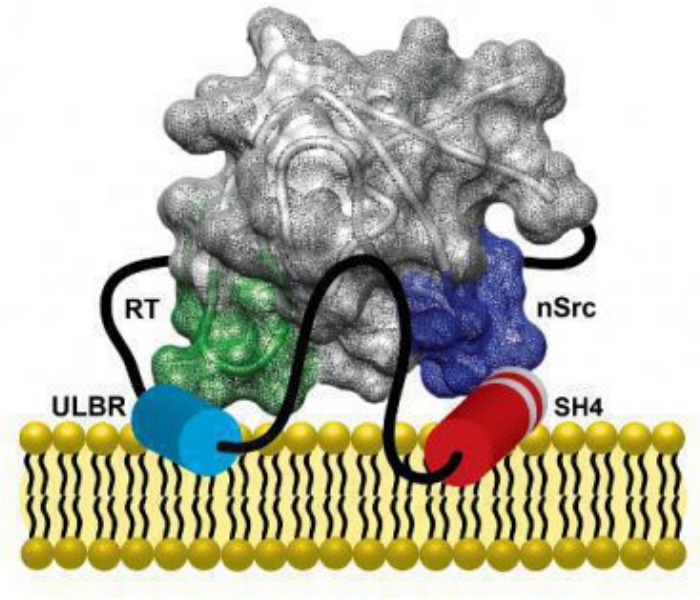
- Publication in *Nat Common*: Voltage-dependent gating of KCNH potassium channels lacking a covalent link between voltage-sensing and pore domains.
- Hormone Receptors and Ion Channels Group at the University of Oviedo.
- Oncophysiology Group, at the Max Planck Institute of Experimental Medicine in Göttingen.
- Molecular Biology of Neuronal Signals Group, at the Max Planck Institute of Experimental Medicine in Göttingen.

Biofísica Magazine

COMMENTARIES

STRUCTURING DISORDER: The case of the Unique domain of the oncoprotein c-Src

05/06/2015



Commentary to *The SH3 Domain Acts as a Scaffold for the N-Terminal Intrinsically Disordered Regions of c-Src* (Structure, 23: 1).

Tiago N. Cordeiro, *CBS (Montpellier, France).*

Proteins have different "flavours" of structural order/disorder, and the interplay between structured and disordered regions is key for their function. The continuum of protein structural sates spans from fully and intrinsically disordered entities to well folded and structured ones. It is becoming increasingly evident that most eukaryotic proteins have both types of regions.

Mariano Maffei, Miquel Pons and colleagues, at the University of Barcelona, have shed light on the synergy between the structured SH3 domain and the contiguous intrinsically disordered N-terminus of c-Src protein. The latter was the first proto-oncogene to be discovered and it plays a crucial role in cell signalling transduction pathways, all of which contribute to its oncogenic potential. c-Src contains a 85-residues intrinsically disordered region located at the N-terminus (SH4 and Unique domain) whose biological function has been recently clarified. However, the connection with the classical c-Src regulatory mechanisms involving the SH3 and SH2 domains is still missing.

The binding of a poly-proline peptide allosterically modulates most of the observed interactions, both in absence and presence of lipid bicelles

Through the application of state-of-the-art NMR techniques, the authors showed that the SH3 domain acts as a scaffold for the intrinsically disordered Unique domain. The work, which has been highlighted with the cover of the Structure journal, describes the interaction between the SH3 and the SH4 domains, that forms a long-loop including the entire Unique domain. The conformational freedom of this disordered region is further restricted through direct contacts between the RT-loop of the SH3 domain and, primarily, residues located within the recently discovered Unique lipid binding region (ULBR).

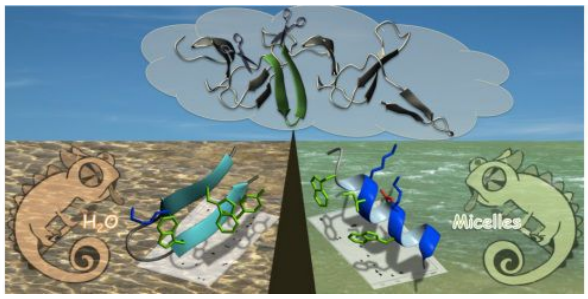
In this elegant work, Maffei *et al.* have also discovered that the binding of a poly-proline peptide allosterically modulates most of the observed interactions, both in absence and presence of lipid bicelles. These results demonstrate a direct connection between classical c-Src regulation involving the SH3 domain and the new regulation mechanisms involving the intrinsically disordered regions and provide new evidence of the functional importance and the underlying mechanism behind regulation of signalling pathways by intrinsically disordered domains.

More Information

- Publication in *Structure*: The SH3 Domain Acts as a Scaffold for the N-Terminal Intrinsically Disordered Regions of c-Src.
- May issue of *Structure* (Cover).
- Interview with Dr. Maffei and Prof. Miquel Pons.

Biofísica Magazine

PAPERS OF THE MONTH BY SBE MEMBERS: MAY - AUGUST 2015

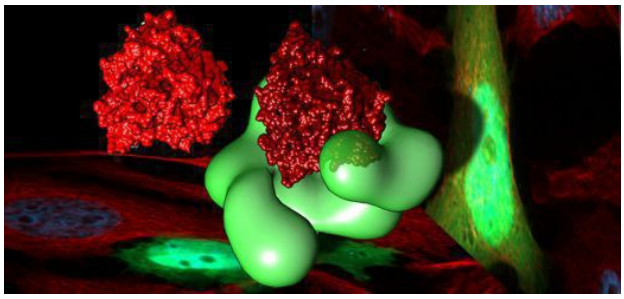


HIGHLIGHTED / MAY 2015

Micelle-Triggered β-Hairpin to α-Helix Transition in a 14-Residue Peptide from a Choline-Binding Repeat of the Pneumococcal Autolysin LytA

Zamora-Carreras H, Maestro B, Strandberg E, Ulrich AS, Sanz JM, Jiménez MÁ.

Chemistry. 2015 May; 21: 8076.

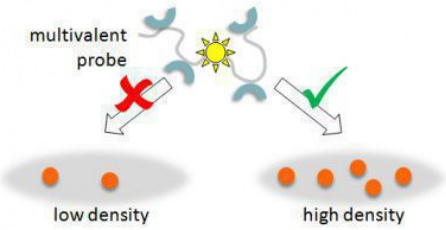


HIGHLIGHTED / MAY 2015

The structure of the complex between α-tubulin, TBCE and TBCB reveals a tubulin dimer dissociation mechanism

Serna M, Carranza G, Martín-Benito J, Janowski R, Canals A, Coll M, Zabala JC, Valpuesta JM.

J Cell Sci. 2015 May; 128: 1824.

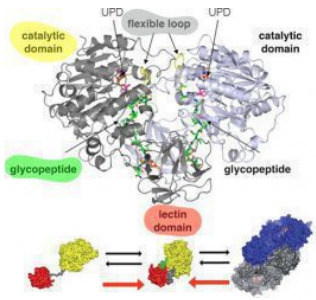


HIGHLIGHTED / MAY 2015

Designing multivalent probes for tunable superselective targeting

Dubacheva GV, Curk T, Auzély-Velty R, Frenkel D, Richter RP.

Proc Natl Acad Sci USA. 2015 May; 112: 5579.

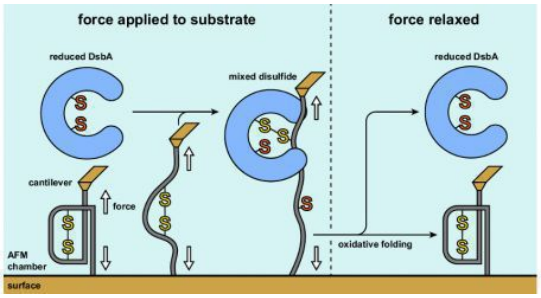


HIGHLIGHTED / MAY 2015

Dynamic interplay between catalytic and lectin domains of GalNAc-transferases modulates protein O-glycosylation

Lira-Navarrete E, de Las Rivas M, Compañón I, Pallarés MC, Kong Y, Iglesias-Fernández J, Bernardes GJ, Peregrina JM, Rovira C, Bernadó P, Bruscolini P, Clausen H, Lostao A, Corzana F, Hurtado-Guerrero R.

Nat Commun. 2015 May; 6:6937.

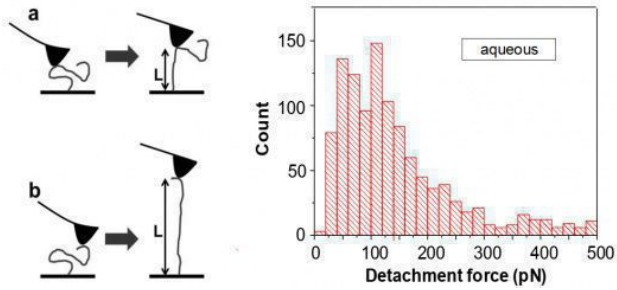


HIGHLIGHTED / JUN. 2015

Monitoring Oxidative Folding of a Single Protein Catalyzed by the Disulfide Oxidoreductase DsbA

Kahn TB, Fernández JM, Perez-Jimenez R.

J Biol Chem. 2015 Jun; 290: 14518.

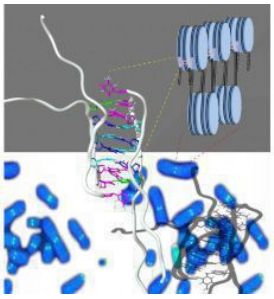


HIGHLIGHTED / JUN. 2015

Chain Length and Grafting Density Dependent Enhancement in the Hydrolysis of Ester-Linked Polymer Brushes

Melzak KA, Yu K, Bo D, Kizhakkedathu JN, Toca-Herrera JL.

Langmuir 2015 Jun; 31: 6463

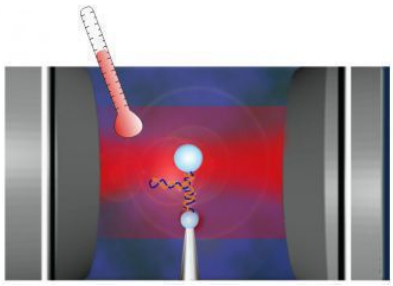


HIGHLIGHTED / JUN. 2015

Centromeric Alpha-Satellite DNA Adopts Dimeric i-Motif Structures Capped by AT Hoogsteen Base Pairs

Garavís M, Escaja N, Gabelica V, Villasante A, González C.

Chemistry 2015 Jun; 21: 9816.

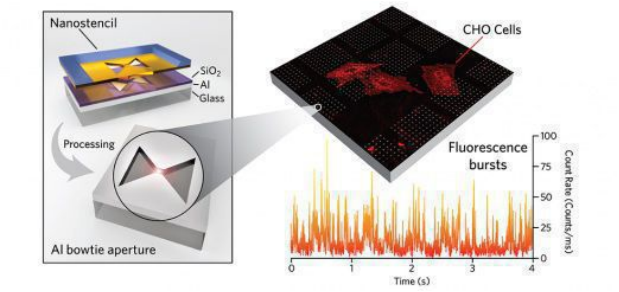


HIGHLIGHTED / JUN. 2015

A Temperature-Jump Optical Trap for Single-Molecule Manipulation

de Lorenzo S, Ribezzi-Crivellari M, Arias-Gonzalez JR, Smith SB, Ritort F.

Biophys J. 2015 Jun; 108: 2854.

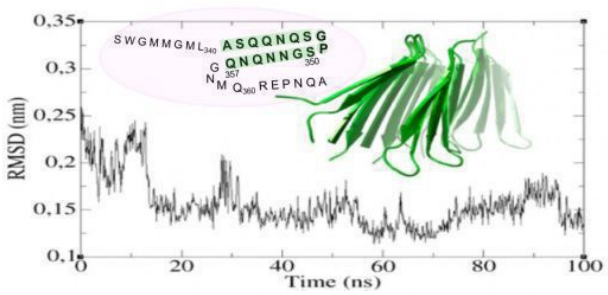


HIGHLIGHTED / JUN. 2015

Large-Scale Arrays of Bowtie Nanoaperture Antennas for Nanoscale Dynamics in Living Cell Membranes

Flauraud V, van Zanten TS, Mivelle M, Manzo C, Garcia Parajo MF, Brugger J.

Nano Lett. 2015 Jun; 10: 4176.

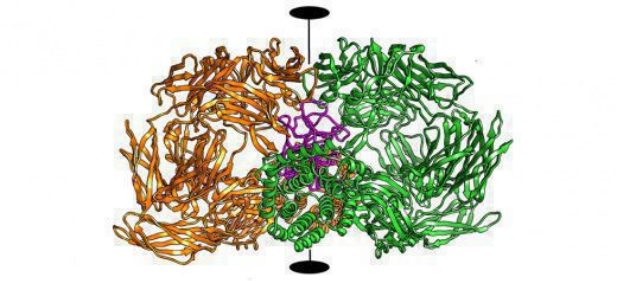


HIGHLIGHTED / JUL. 2015

Structural Evidence of Amyloid Fibril Formation in the Putative Aggregation Domain of TDP-43

Mompeán M, Hervás R, Xu Y, Tran TH, Guarnaccia C, Buratti E, Baralle F, Tong L, Carrión-Vázquez M, McDermott AE, Laurents DV.

J Phys Chem Lett. 2015 Jul; 6: 2608.

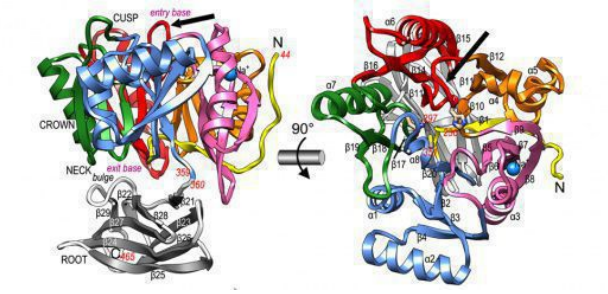


HIGHLIGHTED / JUL. 2015

Structural and functional insights into Escherichia coli α2-macroglobulin endopeptidase snap-trap inhibition

Garcia-Ferrer I, Arêde P, Gómez-Blanco J, Luque D, Duquerroy S, Castón JR, Goulas T, Gomis-Rüth FX.

Proc Natl Acad Sci U S A. 2015 Jul; 112: 8290.

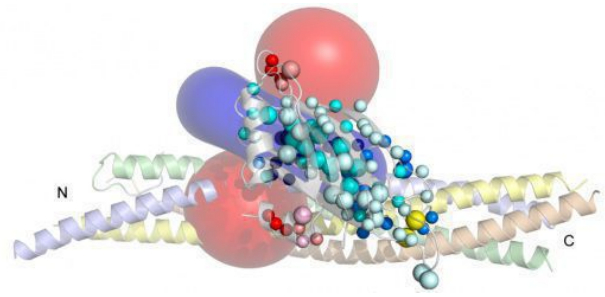


HIGHLIGHTED / JUL. 2015

Structure and mechanism of a bacterial host-protein citrullinating virulence factor, Porphyromonas gingivalis peptidylarginine deiminase

Goulas T, Mizgalska D, Garcia-Ferrer I, Kantyka T, Guevara T, Szmigielski B, Sroka A, Millán C, Usón I, Veillard F, Potempa B, Mydel P, Solà M, Potempa J, Gomis-Rüth FX.

Sci Rep. 2015 Jul; 5: 11969.

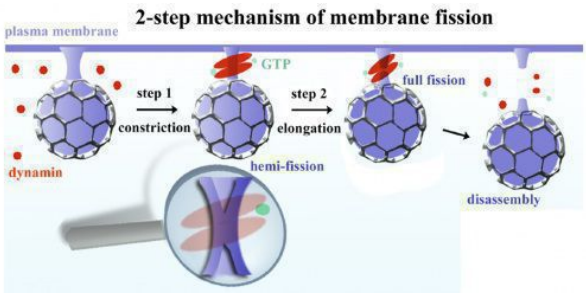


HIGHLIGHTED / JUL. 2015

Dynamic binding mode of a Synaptotagmin-1-SNARE complex in solution

Brewer KD, Bacaj T, Cavalli A, Camilloni C, Swarbrick JD, Liu J, Zhou A, Zhou P, Barlow N, Xu J, Seven AB, Prinslow EA, Voleti R, Häussinger D, Bonvin AM, Tomchick DR, Vendruscolo M, Graham B, Südhof TC, Rizo J.

Nat Struct Mol Biol. 2015 Jul; 22: 555

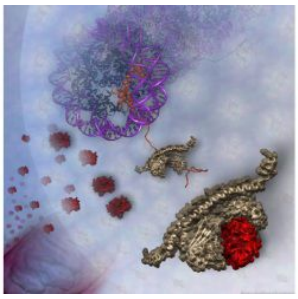


AUG. 2015 / HIGHLIGHTED

A hemi-fission intermediate links two mechanistically distinct stages of membrane fission

Mattila JP, Shnyrova AV, Sundborger AC, Hortelano ER, Fuhrmans M, Neumann S, Müller M, Hinshaw JE, Schmid SL, Frolov VA.

Nature. 2015 Aug; 524: 109.

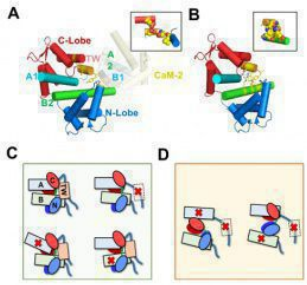


AUG. 2015 / HIGHLIGHTED

Structural basis for inhibition of the histone chaperone activity of SET/TAF-Iβ by cytochrome c

González-Arzola K, Díaz-Moreno I, Cano-González A, Díaz-Quintana A, Velázquez-Campoy A, Moreno-Beltrán B, López-Rivas A, De la Rosa MA.

Proc Natl Acad Sci USA. 2015 Aug; 112: 9908.

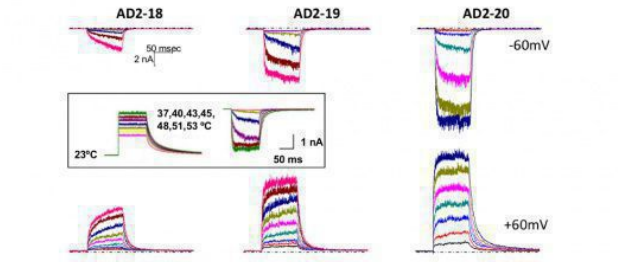


AUG. 2015 / HIGHLIGHTED

An unconventional calmodulin-anchoring site within the AB module of Kv7.2 channels

Gomis-Perez C, Alaimo A, Fernandez-Orth J, Alberdi A, Aivar-Mateo P, Bernardo-Seisdedos G, Malo C, Areso P, Felipe A, Villarroel A.

J Cell Sci. 2015 Aug; 128: 3155.

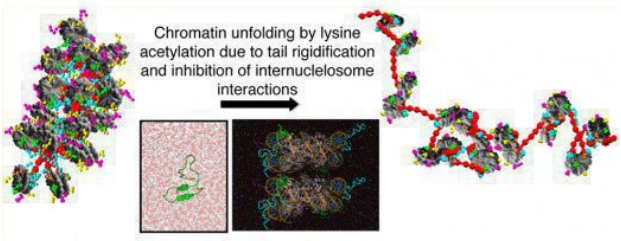


AUG. 2015 / HIGHLIGHTED

The Integrity of the TRP Domain Is Pivotal for Correct TRPV1 Channel Gating

Gregorio-Teruel L, Valente P, Liu B, Fernández-Ballester G, Qin F, Ferrer-Montiel A.

Biophys J. 2015 Aug; 109: 529.

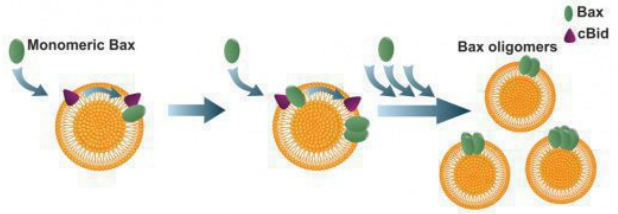


AUG. 2015 / HIGHLIGHTED

Chromatin Unfolding by Epigenetic Modifications Explained by Dramatic Impairment of Internucleosome Interactions: A Multiscale Computational Study

Collepardo-Guevara R, Portella G, Vendruscolo M, Frenkel D, Schlick T, Orozco M.

J Am Chem Soc. 2015 Aug; 137: 10205.

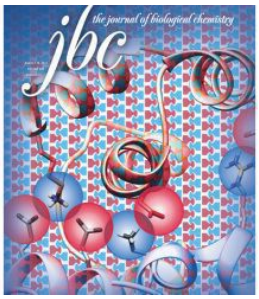


AUG. 2015 / HIGHLIGHTED

Bax monomers form dimer units in the membrane that further self-assemble into multiple oligomeric species

Subburaj Y, Cosentino K, Axmann M, Pedrueza-Villalmanzo E, Hermann E, Bleicken S, Spatz J, García-Sáez AJ.

Nat Commun. 2015 Aug; 6: 8042.

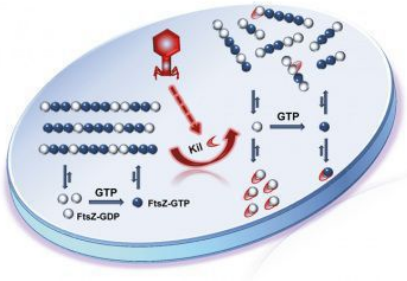


AUG. 2015 / HIGHLIGHTED

A Three-protein Charge Zipper Stabilizes a Complex Modulating Bacterial Gene Silencing

Cordeiro TN, García J, Bernadó P, Millet O, Pons M.

J Biol Chem. 2015 Aug; 290: 21200. 2015 Aug; 290: 21200.



AUG. 2015 / HIGHLIGHTED

Evidence That Bacteriophage λ Kil Peptide Inhibits Bacterial Cell Division by Disrupting FtsZ Protofilaments and Sequestering Protein Subunits

Hernández-Rocamora VM, Alfonso C, Margolin W, Zorrilla S, Rivas G.

J Biol Chem. 2015 Aug; 290: 20325.

Biofísica Magazine

NEWS

Announcing the 5th International Iberian Biophysics Congress

June 15th – 17th, 2016, Porto (Portugal).

Congress Web Site: Stay informed visiting Biofisica.info.

> *The Spanish and Portuguese Biophysical Societies have agreed to reestablish Biannual meetings under the name of International Iberian Congress. They will keep the typical structure of International SBE Congresses. In particular, the two societies have agreed to maintain low registration fees and travel bursaries for young scientists, include awards of SBE prizes within the program of the Congress and keep the usual "structure" of symposia as well as the recently established workshop New and Notable in Biophysics.*

Grants

Travel bursaries will be available for young (PhD students and postdocs) attendees who are members of SBE.

Deadlines

- Applications for bursaries: Expected, begining of March 2016
- Abstract submission: Expected, begining of May 2016

More information

Get updated information in Biofisica.info and in the Web Sites of the Spanish Biophysical Society – SBE and the Portuguese Biophysical Society – SPBf.

Biofísica Magazine

NEWS

López-Barneo's Group, Winner of an ERC Advanced Grant

José López-Barneo, from the Institute of Biomedicine of Seville (Instituto de Biomedicina de Sevilla – IBiS), Seville (Spain), prominent Spanish Biophysicist and member of SBE, has been awarded a 2014 ERC Advanced Grant.

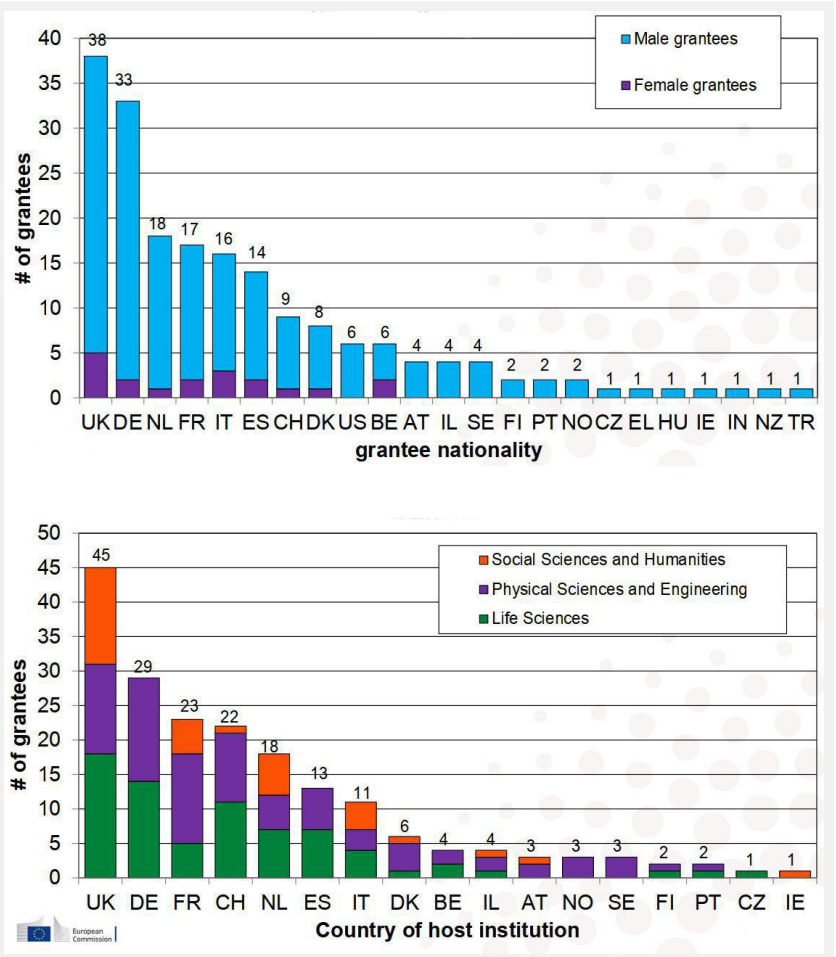
The results of the latest ERC Advanced Grant competition (2014 call) were recently announced. This prestigious program will fund €445 million from the EU to 190 senior research leaders, under the 'excellent science' pillar of **Horizon 2020**, launched in 2014.

ERC grants are awarded to researchers of any nationality based in, or willing to move to, Europe. In this competition ERC has awarded grants to researchers of 23 different nationalities, being British (38), German (33) and Dutch (18) scientists the most successful. Spanish scientists were sixth, with 14 grants.

The research group lead by prof. López-Barneo investigates the cellular mechanisms for rapid-response sensing of O2 changes and has made seminal contributions to unveiling the cellular bases of arterial chemoreception.

Their **winner proposal** deals with the study of the molecular mechanisms underlying acute O2 sensing by cells. It will be focused mainly on arterial chemoreceptors: carotid body (CB) and adrenal medulla. Additionally, the studies will be extended to other organs (e.g. pulmonary and systemic arteries) of the homeostatic acute O2- sensing system, and to the role of mitochondrial complex I

(MCI) in acute O2 sensing. Previous data from the group have demonstrated that rotenone, a MCI blocker, selectively occludes responsiveness to hypoxia in CB cells. In addition, they have shown that the adult CB is a plastic organ that contains a population of multipotent neural stem cells. Hence, another objective of the project is to study the role of these stem cells in CB modulation, which may participate in the pathogenesis of diseases. The discovery of stem cells in the CB and the generation of new genetically modified mouse models, puts López-Barneo's Team in a leading position to elucidate the molecular bases of acute O2 sensing and their biomedical implications.



ERC Advanced Grant 2014 Call. Grantees by nationality and by country of host institution. Source: ERC Advanced Grants 2014 Outcome: Indicative statistics (European Research Council)

More information

- José López-Barnero Group at IBiS, Seville, Spain.
- ERC Advanced Grants: Results from 2014 call.
- ERC Funding.

Biofísica Magazine

CALLS / GRANTS / NEWS

ERC Annual Work Programme 2016

On 28 July 2015 the European Commission published the Annual Work Programme for 2016, funded by the European Union's Horizon 2020 Framework Programme for Research and Innovation

Three ERC frontier research grants will be available under Work Programme 2016: Starting; Consolidator; and Advanced Grants.

> *The ERC operates according to an "investigator-driven" (or "bottom-up") approach, allowing researchers to identify new opportunities in any field of research, without thematic priorities. Under the first pillar ("Excellent science") of the new EU Programme for Research and Innovation (2014-2020), Horizon 2020, the ERC has had a budget of approximately €1.6 billion for each of the years 2014, 2015 and 2016.*

Summary of main calls

- Starting Grants. The call **opens** on 29 July 2015 and the **deadline** is 17 November 2015
- Consolidator Grants. The call **opens** on 15 October 2015 and the **deadline** is 2 February 2016
- Advanced Grants. The call **opens** on 24 May 2016 and the **deadline** is 1 September 2016

Principal Investigators whose proposal was evaluated as category B at step 2 in the Starting, Consolidator or Advanced Grant calls for proposals under Work Programme 2015 will not be subject to restrictions in calls for proposals made under Work Programme 2016.

ERC Principal Investigators will also continue to be able to apply for Proof of Concept Grants.

More Information

- The programme package can be downloaded *from here*.
- Information for Applicants: Starting and Consolidator Grant calls 2016.
- Applications will need to be made through the Participants Portal.
- ERC website.
- The EU Framework Programme for research and Innovation Horizon 2020.

Biofísica Magazine

CALLS / NOMINATIONS / NEWS

21 Premio Carmen y Severo Ochoa 2015

FUNDACIÓN
CARMEN Y SEVERO OCHOA

BASES

1. Se convoca el Premio "Carmen y Severo Ochoa", en su vigésimo primera edición, al objeto de ofrecer este reconocimiento a una persona de nacionalidad española que investigue en el campo de la Biología Molecular.
2. La cuantía es de doce mil euros, que se entregarán con un diploma.
3. El premio se otorgará a un investigador por el trabajo realizado principalmente en España, en los últimos cinco años. Para su asignación el jurado tendrá en cuenta el valor científico de dicho trabajo en el contexto de los avances actuales, así como el conjunto de la labor investigadora de la persona premiada.
4. Los candidatos podrán presentarse personalmente o ser presentados por alguna de las instituciones de relevancia en el campo de la Biología Molecular, universidades, facultades, departamentos universitarios, institutos de investigación, sociedades, reales academias, así como por otros científicos.
5. Las propuestas incluyendo las publicaciones representativas de la labor del candidato y su curriculum vitae deben remitirse a la dirección de correo icosano@ucm.es, hasta el 15 de octubre de 2015.

Biofísica Magazine

NEWS

EditorSelect: A selection of News from External Sources

Brought to you by the Editors. News are picked up from **RSS-feeds** of Science Daily, EurekAlert, Nature and Science. Here is just the *head end* of our news lists. To see all selected news please visit the online version of EditorSlect. To access the complete original text of particular News, just *follow its associated link*.

BIOPHYSICS RELATED NEWS

- [Cryo-EM] The revolution will not be crystallized: a new method sweeps through structural biology: 09/09/15
- [DNA] Using DNA origami to build nanodevices of the future: 31/08/15
- [Fluid Dynamics] Energetic bacteria form frictionless superfluids: 10/07/15
- [Cell Biophysics] Magnetic levitation of single cells: 01/07/15
- [Emerging Techniques] Ultra-stable JILA microscopy technique tracks tiny objects for hours: 01/07/15
- [Emerging Techniques] X-rays and electrons join forces to map catalytic reactions in real-time: 29/06/15
- ['Clock' protein] Earth's daily rotation period encoded in an atomic-level protein structure: 25/06/15
- [Protein Design] Designing proteins to self-assemble: 19/06/15
- [cyo-EM]:
  - Pushing the limits of electron microscopy: 05/06/15
  - Near-atomic resolution of protein

GENERAL SCIENCE NEWS

- [Interdisciplinary] *Trends...*
  - Interdisciplinary research by the numbers: 16/09/15.
  - Grant giving: Global funders to focus on interdisciplinarity: 16/09/15.
- [Teaching of science] Why we are teaching science wrong, and how to make it right: 15/07/15.
- [Big Data] *Trends...*
  - European labs set sights on continent-wide computing cloud: 08/07/15.
  - Opposition to storing vast scientific data sets on cloud-computing platforms is weakening: 08/07/15.
- [Funding] A call to fund people not proposals triggers strong reactions online: 25/06/15.
- [Science Quality] *Debate*:
  - Irreproducible biology research costs put at $28 billion per year: 09/06/15.
  - Potential flaws in genomics paper scrutinized on Twitter: 20/05/15.

Biofísica Magazine

JOBS: POSITIONS IN BIOPHYSICS

CALLS / JOBS 17 SEP, 2015

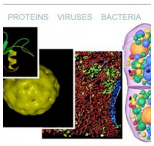
Platform coordinator position, long-term contract

The Institut Curie seeks an experienced coordinator The Institut Curie is a private non-profit organization which combines a leading European cancer research center with currently...

JOBS / POSTDOC 17 SEP, 2015

Postdoc Positions at López-Barneo's Lab

Announcement of recruitment of research personnel Three jobs are available at the laboratory of José López-Barneo at the Institute of Biomedicine of Seville, Seville, Spain....



JOBS 13 SEP, 2015

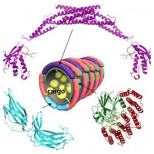
Software Developer at INSTRUCT

Position open at the INSTRUCT Image Processing Center in Microscopy, CNB-CSIC, Madrid (Spain). We are looking for a technically oriented candidate (engineer, physicist, mathematician, computer...

CALLS / JOBS / NEWS 26 JUN, 2015

Ikerbasque Research Professors 2015

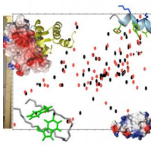
10 positions for experienced researchers, within any of the Basque Research Institutions DEADLINE: September 10th 2015, 13:00 CET Ikerbasque, the Basque Foundation for Science launches...



FELLOWSHIPS / FPI / PREDOC 17 JUN, 2015

PhD Fellowship (FPI-MINECO) at CIC bioGUNE – Crystallography Group

4 years PhD position to join the Structural Biology Unit, group of Aitor Hierro, at the Center for Cooperative Research in Biosciences – CIC bioGUNE,...



FELLOWSHIPS / FPI / PREDOC 17 JUN, 2015

PhD Fellowship (FPI-MINECO) at IQFR – NMR Proteins

4 years PhD position to join the "Protein structure, dinamics and interactions by NMR" Group led by Marta Bruix and Ángeles Jiménez at the Rocasolano...

CALLS / FELLOWSHIPS / GRANTS / JOBS / NEWS / PREDOC 16 JUN, 2015

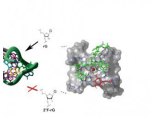
Grants for predoctoral training contracts (former FPI)

National Programme for the Promotion of Talent and Its Employability National Sub-Programme for Training The grants will include support for the funding of contracts, support...

FELLOWSHIPS / FPI / PREDOC 16 JUN, 2015

PhD Fellowship (FPI-MINECO) at IBGM – Valladolid

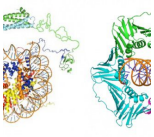
4 years PhD contract to join the group of Subcellular Ca2+ homeostasis in the Institute of Biology and Molecular Genetics – IBGM from the University...



FELLOWSHIPS / FPI / PREDOC 16 JUN, 2015

PhD Fellowship (FPI-MINECO) at IQFR – NMR Nucleic Acids

4 years PhD position to join the Nucleic Acids NMR group led by Carlos González at the Rocasolano Institute of Physical Chemistry, CSIC, Madrid (Spain)....



FELLOWSHIPS / FPI / PREDOC 16 JUN, 2015

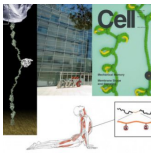
PhD Fellowship (FPI-MINECO) at CIC bioGUNE – NMR Group

4 years PhD position to join the Structural Biology Unit, group of Francisco J. Blanco at the Center for Cooperative Research in Biosciences – CIC...

FELLOWSHIPS / FPI / PREDOC 16 JUN, 2015

4 PhD Positions at IBMB-CSIC Unit of Excellence 'María de Maeztu'

4 pre-doctoral contacts to join the Structural Biology (SB) 'María de Maeztu' Unit of Excellence, IBMB-CSIC, Barcelona (Spain). The Maria de Maeztu Structural Biology Unit...



FELLOWSHIPS / FPI / PREDOC 15 JUN, 2015

PhD Fellowship (FPI-MINECO) at CNIC

4 years PhD position to join the Single-Molecule Mechanobiochemistry Laboratory led by Jorge Alegre-Cebollada at the National Institute of Cardiovascular Research (CNIC), Madrid (Spain). We...

JOBS 15 JUN, 2015

Max Planck Tandem Research Group positions – MPTRG

2 Max Planck Tandem Research Group positions (MPTRG) in the area of Neurosciences and Computational Neuroscience open by the Centro Interdisciplinario de Neurociencia de Valparaíso...

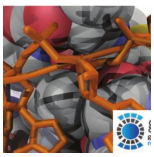
JOBS / POSTDOC 15 JUN, 2015

Postdoc: Optoelectrical Dynamics of Ion Channel Activation in Nanodomains

5 years Postdoctoral positions open at the Center for Biomedical Research of the Canary Islands – CIBICAN and the University of La Laguna, Ion channels:...

Biofísica Magazine

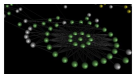
EVENTS: UPCOMING MEETINGS, COURSES AND WORKSHOPS



EVENTS / WORKSHOPS 17 SEP, 2015

Workshop on Molecular Recognition by NMR

October 30, 2015, Instituto de Química Física Rocasolano, CSIC Madrid (Spain). geRMN | Grupo Especializado de RMN de la RSEQ Topics Self assembly Carbohydrate-protein interactions...



COURSES / EVENTS 30 JUL, 2015

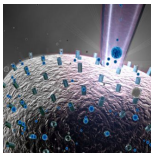
Computational analysis of protein-protein interactions: From sequences to networks

28 September – 4 October 2015, Norwich (UK). EMBO | Practical Course: . Course Web Site: Follow this Link Recent growth in protein-protein interaction (PPI)...

EVENTS / MEETINGS 23 JUL, 2015

44th European Muscle Conference

September 21st – 25th, 2015, Warsaw (Poland). Congress Web Site: Follow this Link Topics Acto-Myosin Interactions Excitation-Contraction Coupling Heart and Heart Failure Molecular Motors Muscle...



EVENTS / MEETINGS 22 JUL, 2015

RECI V – 5th Spanish Ion Channel Network Meeting

October 4 – 6, 2015, Barcelona (Spain). Deadline: 31st May 2015. Congress Web Site: Follow this Link More than 30 excellent talks in three days...

EVENTS / MEETINGS 22 JUL, 2015

Seeing is Believing – Imaging the Processes of Life

October 6 -10, 2015, EMBL Heidelberg (Germany). EMBO | EMBL Symposium

Symposium Web Site: Follow this Link The processes of life are naturally dynamic in...

EVENTS / MEETINGS 22 JUL, 2015

New Approaches and Concepts in Microbiology

October 11 -14, 2015, EMBL Heidelberg (Germany). EMBO | EMBL Symposium Symposium Web Site: Follow this Link This meeting aims to bridge the gap between...

EVENTS / MEETINGS 21 JUL, 2015

Biophysics of Proteins at Surfaces

October 13 – 15, 2015, Madrid, Complutense University (Spain). BPS Thematic Meeting | Biophysics of Proteins at Surfaces: Assembly, Activation, Signaling. Meeting Web Site: Follow...

EVENTS / WORKSHOPS 1 JUL, 2015

Stem cell mechanobiology in development and disease

18 – 21 October 2015, Capri (Italy). EMBO | Workshop: Workshop Web Site: Follow this Link This EMBO Workshop aims at providing a cutting-edge view...

EVENTS / MEETINGS 26 JUN, 2015

Emerging Biotechnologies – EMBO Event

November 5th – 6th, 2015, Heidelberg | EMBL (Germany). Congress Web Site: Follow this Link. The conference will focus on the impacts of life sciences...

EVENTS / MEETINGS 24 JUN, 2015

IX Meeting of the Structure and Function of Proteins Network

November 11 – 13, 2015, Sevilla, cicCartuja (Spain). Congress Web Site: Follow this Link This year meeting will be held in memoriam of Prof. Manuel...

EVENTS / MEETINGS 23 JUN, 2015

Biological Oscillators: Design, Mechanism, Function

November 12 -14, 2015, EMBL Heidelberg (Germany). EMBO | EMBL Symposium Symposium Web Site: Follow this Link Oscillations are abundant – from hormonal oscillations with...

EVENTS / WORKSHOPS 17 JUN, 2015

5th SFICT Workshop Lisbon 2015

5th Workshop Structure and Function of Ion Channels and Transporters November 12th – 14th, 2015, Faculty of Pharmacy of the University of Lisbon, Lisbon (Portugal)....

EVENTS / MEETINGS / NEWS 16 JUN, 2015

5th International Iberian Biophysics Congress

June 15th – 17th, 2016, Porto (Portugal). Congress Web Site: Stay informed visiting this page. The Spanish and Portuguese Biophysical Societies have agreed to reestablish...

EVENTS / MEETINGS 15 JUN, 2015

The 3rd International Conference on Physiological Computing Systems – PhyCS 2016

July 27th – 28th, 2016, Lisbon (Portugal). Congress Web Site: Follow this link. Physiological data in its different dimensions, either bioelectrical, biomechanical, biochemical or biophysical,...

CALLS / EVENTS / MEETINGS 26 MAY, 2015

Call for 2017 BPS – Thematic Meeting Proposals

The Biophysical Society sponsors each year small focused-topic Thematic Meetings that are organized by Society members. Submission deadline for proposals for 2017 meetings is July...

EVENTS / MEETINGS 22 MAY, 2015

XXXVIII SEBBM Congress

XXXVIII Congress of the Spanish Society of Biochemistry and Molecular Biology – SEBBM. September 7th – 10th, 2015, Valencia (Spain). Congress Web Site: Follow this...

EVENTS / MEETINGS 5 MAY, 2015

6th EMBO Meeting 2015

September 5st – 8th, 2015, Birmingham (UK). Congress Web Site: Follow this Link Grants EMBO travel grants are available for PhD students and postdocs Deadlines...

CONTACT

SBE - Sociedad de Biofísica de España

Secretaria SBE, IQFR-CSIC,

C/Serrano 119, 28006 Madrid

Email: sbe_secretaria@sbe.es

WEB: http://www.sbe.es

SPONSORS