Biofísica Magazine

May - Aug 2016
issue #5

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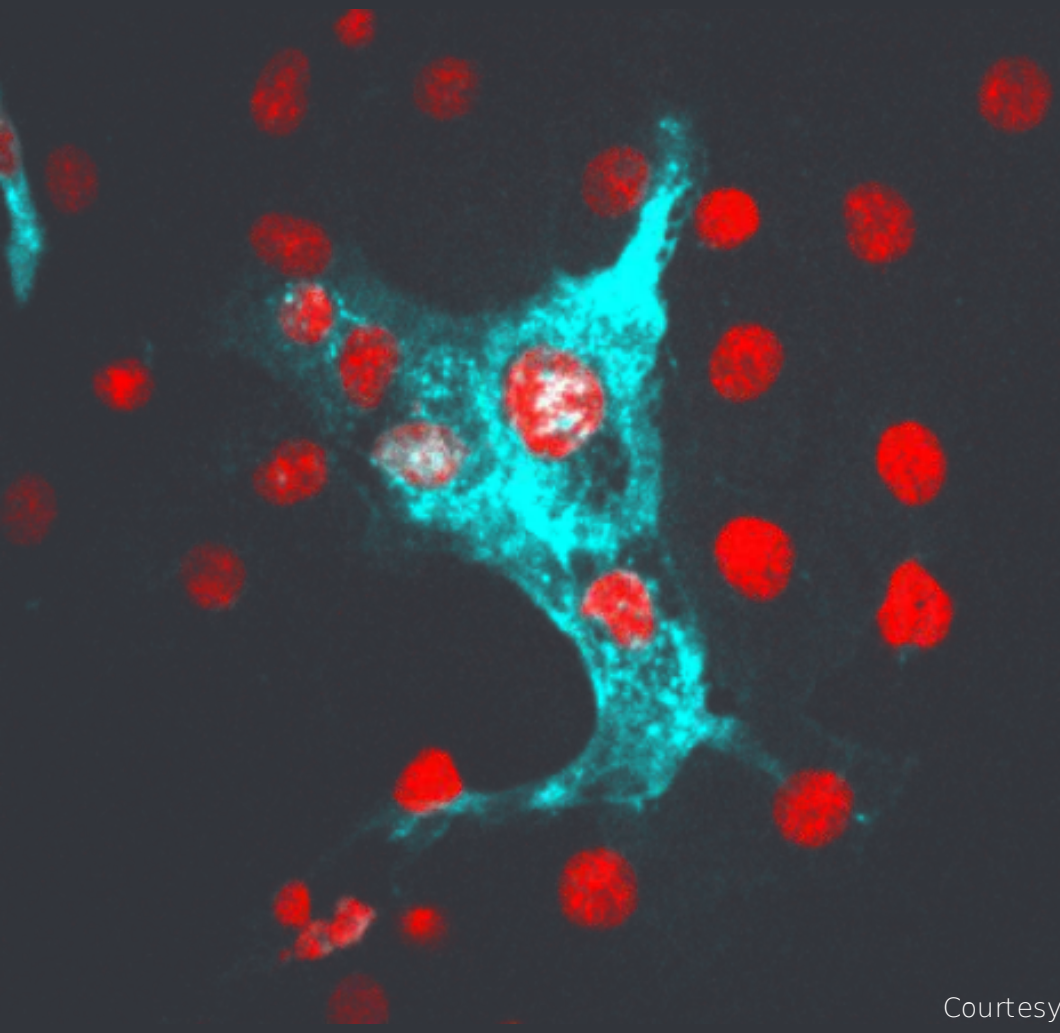

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SBE - Sociedad de Biofísica de España

ISSN 2445-4311

Biofísica
SBE Magazine

EDITORS

Jesús Salgado
Jorge Alegre-Cebollada
Xavier Daura
Teresa Giráldez

CONTACT

SBE - Sociedad de Biofísica de España
Secretaria SBE, IQFR-CSIC,
C/Serrano 119, 28006 Madrid
Email: sbe_secretaria@sbe.es
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In this issue

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EDITORIAL

Brain drain / brain gain (with a focus on Spain)

Jesús Salgado, *ICMol, Valencia (Spain)*

Science is a global activity. Hence, countries need to adopt open human-resource policies to be competitive internationally. There are many reasons to defend *transnational mobility* in science, but a simple and practical one is that the chances to attract the most talented individuals increase with the number and diversity of possible candidates, which will obviously be larger in the global pool than in regional or national pools. It is on this ground that the rate of foreign scientists and students has been for a long time identified as a key factor for innovation and economic competitiveness. A positive net transfer of human capital (*brain gain*) to a particular country has immediate consequences for the quality of its research, technology and education institutions. It has also mid-to-long term consequences for its capacity to innovate and grow, and in turn exerts a positive feedback which increases the attraction of ever more talented scientists. Not surprisingly, a recent study [1] which discusses data from the *GlobSci* survey [2,3] shows that developed countries exhibit high proportion of foreign scientists, of which the proportions of *postdocs* dominate clearly over the proportion of *professors* (**Figure 1**).

Spain is near the bottom of that group of countries, with a modest 7% of foreign scientists, clearly away from the values of main talent attractors. The weak talent attraction of Spain is much more clear when we look at the proportion of foreign professors (only 4% of total professors in the country). We can foresee that this poor performance won't be helpful for the future development of Spain; but there can be also immediate effects, like those derived from the impact of foreign talent on the ability to capture funds from very competitive international calls. A good example in the European context is ERC funding [4]. If we examine the results of recent ERC calls, we will see that a large proportion of successful grantees are foreigners in the country of their host institution. For example, in the *2105 call of ERC consolidator grants* [5], among the most

Increased opportunities and openness and flexibility in the recruitment system should favour the return of excellent national scientists as much as the attraction of excellent foreign scientists.

successful countries, 65% of the winner projects from the UK, 52% from Switzerland, 31% from Germany, 25% from France, 34% from the Netherlands and 28% from Spain correspond to foreign scientists. A rough comparison of these numbers with the shares of foreign scientists given in **Figure 1** empathizes the importance of foreign scientists for attracting resources and demonstrates the potential of open human-resource policies to self-compensate, even at short term, for the economical efforts needed to implement them.

But the game of transnational mobility involves both outgoing and incoming scientists. A positive balance in some countries may mean a negative balance (*brain drain*) for other countries, which end up loosing human resources. In fact, the brain drain consequence of open labour markets is a well known concern for underdeveloped countries and affects also Eastern and Southern European countries (Spain among them) [6]. This causes protectionism in the brain-drained countries, who then become more worried about *talent retention* (referred to their own nationals) than about *talent attraction* (of non-nationals). For example, in Spain and other southern European countries, which are currently under strong economical restrictions, people may think that the run-away and very difficult return of national scientists is a much more urgent problem than the attraction of foreign scientists. However, far from opposing each other, the attraction of non-national talent and retention (or return) of national talent share similar obstacles that must be overcome, like the lack of opportunities and incentives to work in Spain. Thus, the urge to incorporate foreign scientists, at proportions similar to our competitors, is yet another reason to solve the precarious situation of the Spanish science. Moreover, the need to increase opportunities, accompanied by openness and flexibility in the recruitment system, should favour the return of excellent national scientists as much as the attraction of excellent foreign scientists.

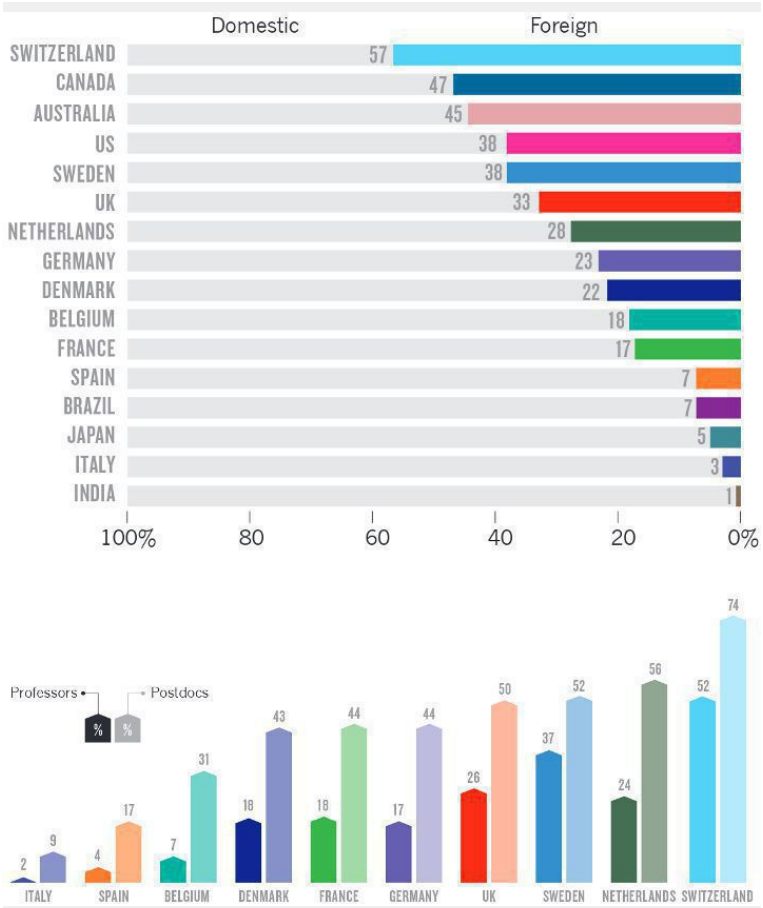

Figure 1. Proportions of foreign scientists in 16 countries according to the GlobSci survey [1–3]. *The bottom bar graph distinguishes shares of postdocs and professors in the European countries appearing in the top graph. Adapted by permission from Macmillan Publishers Ltd [1], © 2012.*

Specific data shows that in successful talent attractor countries a large proportion of foreign

scientists goes hand in hand with similar proportions of outgoing national scientists (**Figure 2**, example cases of the UK and Germany). It thus seems that the talent attraction of these countries does not cause excessive retention of their own citizen scientists. Instead, a good proportion of them look for better opportunities in other attractive countries.

This illustrates the existence of a *mobility culture* among scientists in advanced attractor countries, where the availability of a large pool of positions and sufficient resources allows reaching a state defined as *brain circulation* [7]. In contrast, the mobility numbers show disparity in weak attractor countries. Spain has low mobility numbers in either direction, while Italy has very low incoming of foreigners and large outgoing of nationals (**Figure 2**). Spain is thus positioned in a low mobility, close to equilibrium, situation, whereas Italy seems clearly in a loosing brain drain state.

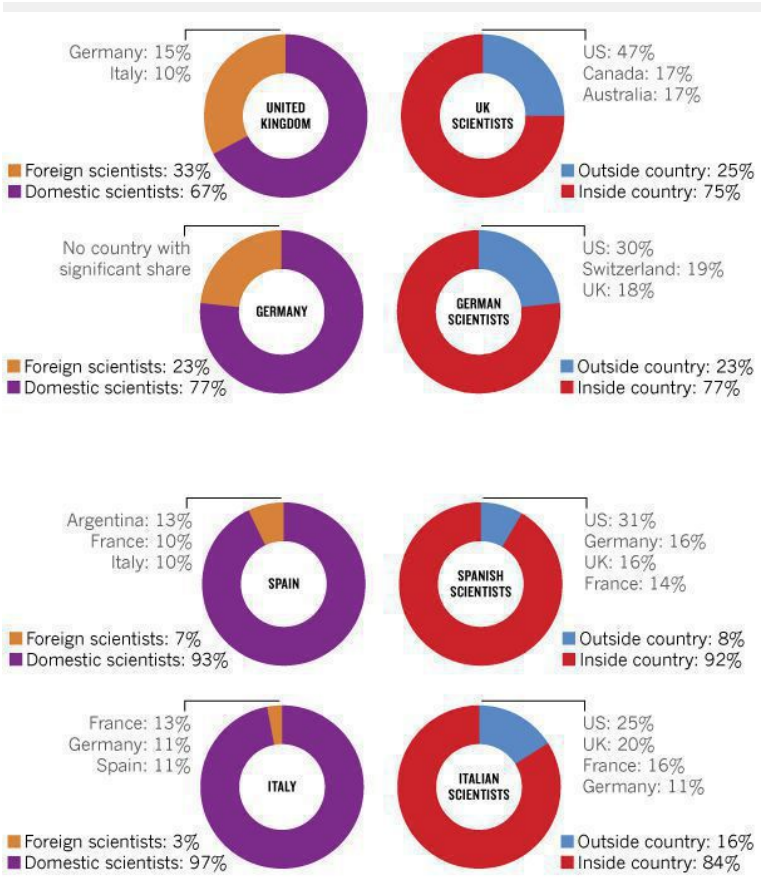

***Figure 2. Side by side comparison of incoming-foreign and outgoing-national scientists**. Proportions of incoming foreign scientists (left) and outgoing national scientists (right) for a selection of European countries. The countries of origin or destination are specified if they correspond to at least 10% of total migrating scientists. The graphs are generated using the interactive tool provided in the online version of reference 1 (Adapted by permission from Macmillan Publishers Ltd [1], © 2012), using data from the GlobSci survey [2,3].*

The main driving forces for scientists to move to another country are the search for opportunities to improve their future and the availability of outstanding colleagues [3]. In order to provide these conditions, there must be a good level of economical resources in the attractor country. Additionally, a large number of available science and technology positions and flexible, talent-based recruitment procedures, facilitate brain circulation, allowing large proportions of both, incoming foreigners and outgoing national scientists. In fact, there is a good correlation (**Figure 3**) between the talent retention capacity of a country and its economical effort in Research and Development – R&D (gross domestic expenditure on R&D – GERD, as % of the gross domestic product – GDP). Clearly, long-term talent attraction and retention have a lot to do with sustained R&D investment, like in the cases of North-West European and Scandinavian countries, exemplified by Germany and Sweden in **Figure 3**. However, there can be also other factors (social, cultural and political) influencing the capacity of a country to attract excellent scientists, as indicated

by the cases of the UK (in the attracting region, despite a moderate GERD) and France (in the loosing region despite good GERD values).

On the *loosing side*, with low R&D support , are South European countries (**Figure 3**, cases of Greece, Italy and Spain). These countries also exhibit strong vulnerability in periods of economical crisis, as seen by the very negative evolution of their brain drain values during the 2003-2013 decade. The case of Spain is peculiar. It enjoyed good talent retention at the beginning of the 21st century (2003 – 2004), despite a low GERD. However, this potential has dropped dramatically in a decade, down to the brain drain loosing area. The instability and negative evolution of the South European countries contrasts with the positive evolution during the same time period shown by the talent attracting North-West European countries, and demonstrates that in the global science market the negative balance, brain drain of some countries is quickly profited by best positioned attracting countries.

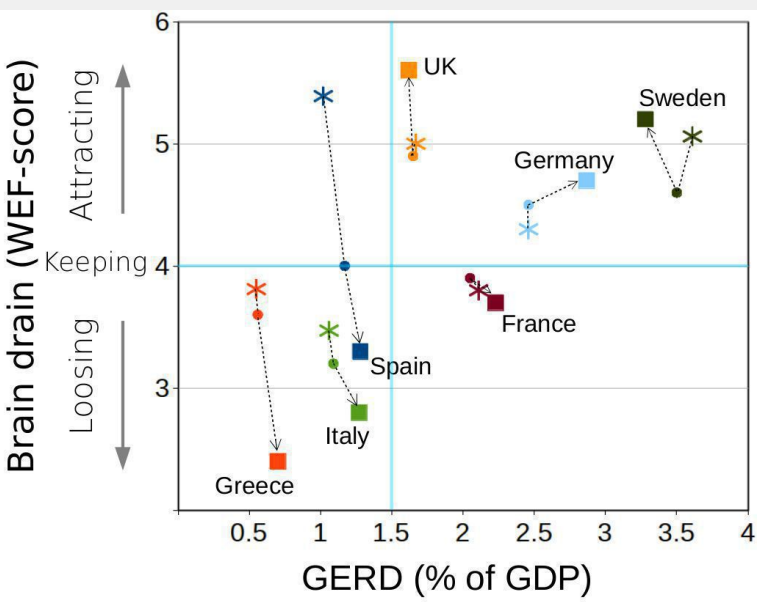

Figure 3. Brain drain parameter versus expenditure in R&D during the 2003 – 2013 decade for selected European countries. *The brain drain score values [8] are from the Global Competitiveness Reports of the World Economic Forum (WEF) [9], corresponding to years 2003 – 2004 (stars) 2006 – 2007 (dots) and 2012 – 2013 (squares). The values GERD (as % of GDP) are from eurostat [10] statistical tables. The stars, dots and squares correspond to GERD values of 2003, 2006 and 2012, respectively.*

To sum up, the mobility of scientists is critical for competitiveness and must therefore be promoted. To warrant a sound brain circulation, there is a need of sustained R&D investment and a quality-based, open human resources policy, with a flexible and fair recruitment system. This will not only attract best foreign scientists, but it will also facilitate the return of top national scientists.

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

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Biofísica Magazine

BEYOND BIOPHYSICS

Nanoscience and Biophysics

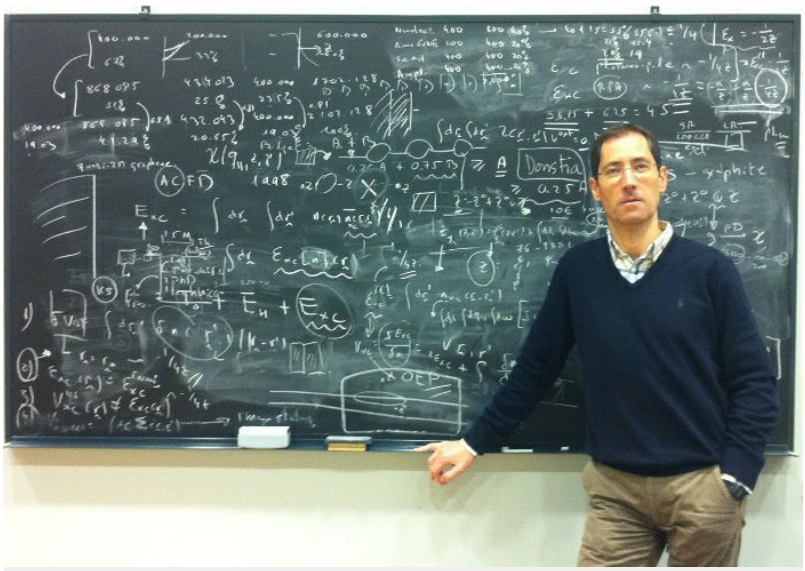
A conversation with Txema Pitarke

David de Sancho, *CIC nanoGUNE & Ikerbasque, Donostia – San Sebastián (Spain)*

Txema Pitarke (Bilbao, 1960) has since 2000 been a full Professor of condensed matter physics at the University of the Basque Country – EHU/UPV. I meet him in his office of director of CIC nanoGUNE (Donostia-San Sebastián) to discuss about the relationship between *biophysics* and *nanoscience*. In fact, his research has never come close to the realm of biophysics. Instead, Pitarke's work has focused on topics like electron dynamics, graphene, carbon nanotubes... "It's not for a lack of interest", he says, "but more due to some sort of vertigo" that he has felt when confronted with such complex systems as those in biology. "For a condensed matter physicist used to working from first principles like myself, biological systems are simply too complex". Pitarke refers to the endless number of assumptions that one has to make in order to handle the *intractable complexity of living systems*.

However, at some point just over 10 years ago, he gestated what would later become nanoGUNE, the Basque flagship for research in nanoscience and nanotechnology. Creating this research centre involved considerable work to identify strategic research areas of biology at the nanoscale. "The research centre might have well been organized around my own research interests", he says, "however I decided to make it orthogonal to them. My vision was that it should be a small centre, but at the same time *extremely interdisciplinary*, combining chemists, physicists, and biologists, all working at the nanoscale." Because "nanoscience is not about what we study, but where", as it is the nanometer scale that concerns nanoscience. "At the nanoscale everything converges, so we need people with very different backgrounds in order to make a contribution. And remember that the nanoscale is also the scale of the most primitive biological systems".

Self assembly: A common ground for Biophysics and Nanoscience



Professor Txema Pitarke.

Experimental techniques represent the most apparent common ground for biophysics and nanoscience. "These are techniques that allow for reaching and manipulating atoms and molecules at the nanoscale". Maybe the best example is a scanning probe microscopy (SPM). These probe microscopes can be used either to image the honeycomb structure of graphene layers or to stretch a protein to its unfolded conformation. But maybe we can try to establish a more interesting connection between nanoscience and biophysics than just the techniques.

Can we use the lessons learned from biophysics to generate new nanotechnologies? "That is really the core of nanoscience", Pitarke says. "We must understand the self-assembly processes found in living organisms so that we can develop new self-organized systems in a 'bottom-up' approach." Then he steps back a bit to provide a broader perspective. "Nanoscience is a combination of self-assembly, manipulation, and miniaturization". And biophysics is particularly connected to the self-assembly part. "In order to reach the dream of creating the desired nanostructure at the desired position and with the desired purpose, one needs to learn from the existing self-organization of living organisms and the rules of biology at the nanoscale".

Great expectations for new nanobiotechnologies

Nowadays there are all sorts of approaches for generating programmable self-assembled nanostructures. The most famous of them is probably *DNA origami*: the use of the building blocks of our genetic code in order to construct designed two and three dimensional materials. The applications of DNA origami range from encapsulation of compounds to the production of *nanobots* for drug delivery or circuitry for plasmonic devices. These nanotechnologies still look a bit futuristic. How far are we from making this dream come true? "Thinking that one might be able to go to the doctor, get diagnosed, and then be treated with a nanobot that delivers the required drug to the right type of cell still sounds like science fiction, but surprises are always round the corner".

How far are we from making this dream come true?... surprises are always round the corner

Pitarke is not at all naïve about the possibility that nanoscience has been hyped up and is receiving excessive attention. This translates into a seemingly unstoppable increase in research funding. "Just name the word 'nano' in your proposal and you might get more chances for being funded". As the director of a nanoscience centre, Pitarke is concerned about this hype, because it can produce false expectations. "However, we should keep moving in this direction. Now we have access to the nanoscale, which we were not able to reach before. The nanoscale is the scale of atoms and molecules, where matter behaves differently, and the nanoscale is the scale of biomolecules, the building blocks of life".

Biophysics and Nanoscience meet at Biomedicine

It is for this reason that biomedicine is moving towards nanotechnology. As of today, there are applications of *nanobiophysics* that are having an undeniable impact in real life. For example, next generation sequencing, which resides in our understanding of the physics of the pairing and replication of DNA strands, is a nanotechnology that has reduced the cost of sequencing a genome from billions to just around 1000 dollars and is currently transforming modern medicine. And researchers are now trying to make pocket DNA sequencers using nanopores for real time diagnostics. Clearly the potential for possible synergies between biophysics and nanoscience is limitless.

In order for these new technologies to emerge, researchers must share ideas and expertise. "One needs interdisciplinary research centres where experts of different disciplines meet and communicate. They will then be able to produce new ideas and move in completely unexpected directions". Pitarke is however sceptic with the training of nanoscientists as such. "I of course believe in nanoscience but I do not believe in the idea of a nanoscientist. We need very well trained people with different backgrounds and a very broad view that get together and do research at the same scale. The idea of a Renaissance individual worked well in the Renaissance but not today".

Life as an emergent property

Along our conversation, Pitarke refers to the intriguing behaviour of matter at the nanoscale. "Nanostructured matter does not behave like matter at the microscale and matter at the macroscale. At the nanoscale quantum mechanics reigns, surfaces dominate, and the physical and chemical properties of matter are size dependent, unlike at the microscale and the macroscale. One says that *nano is simply different*. And self-organization plays a key role here. Biomolecules can self-assemble in various different ways, thus building systems with new functions and new emergent properties, properties that were not present before and that were unpredictable". Hence our difficulty in predicting the folds or functions of biological macromolecules, not to mention what happens at a supramolecular scale. "Life itself could be considered to be an emergent property, cells are emergent entities that are not necessarily predictable from their constituent elements".

Cells are emergent entities that are not necessarily predictable from their constituent elements

But while evolution has made its choices using natural selection, now we have the opportunity to make completely different choices in order to produce new molecules, new materials, and new devices. “Nature has evolved in a certain given way, but for us the possibilities at hand are endless”.

Txema Pitarke

Director of CIC nanoGUNE

Tolosa Hiribidea, 76

E-20018 Donostia – San Sebastián

E-mail: nano@nanogune.eu

David de Sancho

Nanobiomechanics, CIC nanoGUNE

& Basque Foundation for Science - Ikerbasque. Tolosa Hiribidea, 76

E-20018 Donostia – San Sebastián

E-mail: d.desancho@nanogune.eu

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COOL BIOPHYSICS

Systems biophysics

Jose M. G. Vilar, *Biofisika Institute (CSIC, UPV/EHU) and Ikerbasque, Bilbao (Spain)*

Mainstream biophysics has traditionally focused on biological systems as *single entities*, such as a macromolecule, a membrane, a cell, or a tissue. The objective is typically to study physical properties of the system, such as force-extension curves of macromolecules or elastic properties of cells, or to use physical approaches to obtain information about biologically relevant properties, such as the structure of macromolecular complexes. This single-entity view of biophysics that has proved to be so prolific, however, cannot capture the origins of *emergent behavior*. Systems biophysics, in contrast, emphasizes the focus on how the system properties emerge from the relations between constituent elements (Saiz & Vilar, 2006a). These types of approaches are needed, for instance, to study how mutations affect the molecular properties of the cellular components; how the mutated components affect different signaling pathways; and how these modified pathways confer cell-growth advantages during tumor progression and metastasis (Vilar & Saiz, 2013a).

Systems biophysics is not a new field *per se*. The study of emergent behavior in terms of the properties of the components has led to historical breakthroughs. A most notable example is the work of A. L. Hodgkin and A. F. Huxley on the ionic mechanisms underlying the initiation and propagation of action potentials in the squid giant axon (Hodgkin & Huxley, 1952), for which they were awarded the **Nobel Prize in Physiology or Medicine in 1963**. After a series of experiments, Hodgkin and Huxley developed a circuit model that was able to capture how the squid axon carried an action potential in terms of the electrical properties of the cell membrane, voltage-gated conductivities for different ions, and electrochemical gradients. This model has been exceptionally successful, not just in describing but also in predicting a large number of neuronal properties, to the extent that modern investigations have confirmed many aspects of the model that were assumptions at the time.

Two main types of challenges

There have been many developments since the pioneering work of Hodgkin and Huxley. What makes systems biophysics approaches so relevant today is the need, and the opportunity, to make sense of the data obtained in two complementary fronts: new sources of high-precision data and massive amounts of data.

On the *precision-data front*, there have been tremendous advances in the cellular imaging field that can couple cellular responses and perturbations to precise measurements of the intracellular state (Wartlick, et al., 2011). Many of these advances arose from the advent of fluorescent-protein reporters, which allow us to precisely correlate molecular events on real time with behavior at the single cell level. These technologies include, among many others, quantitative time-lapse fluorescence microscopy, fluorescence/Förster resonance energy transfer (FRET), fluorescence recovery after photobleaching (FRAP), fluorescence correlation spectroscopy (FCS), and single molecule imaging. They have been used to estimate quantities such as diffusion and transport coefficients of cellular components, binding kinetics, cellular localization, lifetimes of intracellular interactions, and stochastic fluctuations in the number of components (Sung & McNally, 2011). There have also been substantial advances in structural biology and in single molecule biophysics that have provided us with an atomic level description of many of the cellular components. These types of advances have increased the quality of the data, which we now have at hand to unprecedented levels. Yet, most of these data remain disconnected from each other and it is up to systems approaches to put them together into a functional description that could indicate how the system functions as a whole.

On the *massive-data front*, there have been major breakthroughs in automated technologies for the collection of data. These range from traditional proteomics and genomics analyses to high-throughput single-cell analyses (Aghaeepour, et al., 2013), such as multichannel flow cytometry (FCM), to new genome-wide functional screens, including RNA interference and diverse types of CRISPR screens. A most prominent example of our far-reaching abilities for gathering information is single-cell genome sequencing (Gawad, Koh & Quake, 2016). These automated technologies have brought the cartoon-like representations of cellular processes to exponentially growing webs of nodes and links that seem as close to completion as ever. The complexity of the emerging picture, however, makes it clear that all this information by itself is not sufficient to truly understand complex processes. In order to piece back together the experimental information into physiologically relevant descriptions, one needs constructive methods (Vilar, Guet & Leibler, 2003). Systems biophysics approaches have emerged as a promising tool for transforming molecular detail from different sources into a more integrated form of understanding complex behavior. I discuss below two examples of these two types of challenges.

The *lac* operon: a not-so-simple paradigm of gene regulation

The *E. coli* *lac* operon is the genetic system that regulates and produces the enzymes needed to metabolize lactose, including a lactose sensor (the *repressor*), a lactose transporter (the *permease*), and an enzyme that breaks lactose into simpler sugars (the *β-galactosidase*). It has been a paradigm in genetics since F. Jacob and J. Monod used it over 50 years ago to put forward the very basic principles of gene regulation (Jacob & Monod, 1961), for which they received the **Nobel Prize in Physiology or Medicine in 1965**. They postulated the existence of molecules that bind to specific sites in nucleic acids to control the expression of genes. In the lac operon, the response to lactose is controlled by the lac repressor, which can bind to the main *operator* and prevent the RNA polymerase from transcribing the genes. When lactose is present, however, this binding is strongly reduced and transcription can take place. This leads to the production of the β-galactosidase and the permease codified in the *lacZ* and *lacY* genes (Müller-Hill, 1996). The original idea of the lac repressor preventing transcription has been refined over the years to incorporate a complex hierarchy of events that extend from specific protein-DNA interactions to the combinatorial assembly of nucleoprotein complexes (Vilar & Saiz, 2013a).

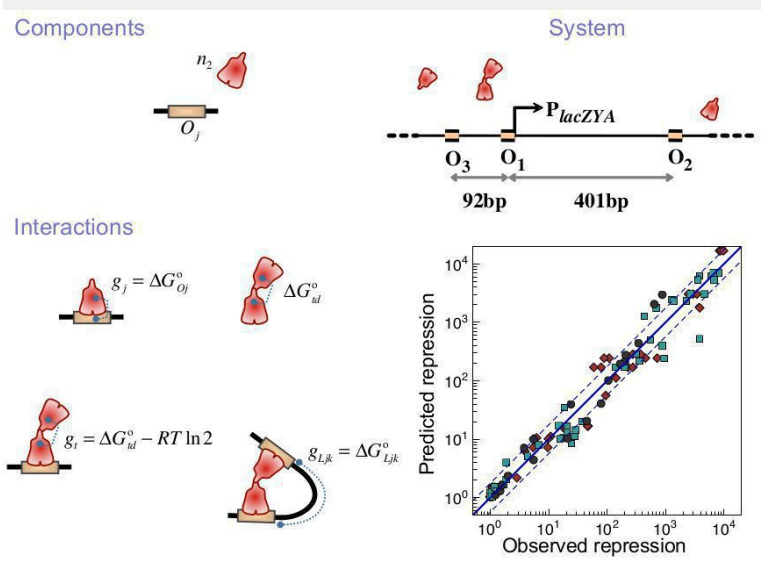

Figure 1. Modular deconstruction of the lac operon and predictive accuracy. *Components: the basic modules are the lac repressor dimers (n2) and operators (Oj). Interactions: repressor dimers interact with other dimers and with operator DNA to form tetramers in solution, to bind single DNA sites as dimers or tetramers, and to loop DNA as tetramers bound to two DNA sites. Just a few parameters are needed to characterize these interactions. System: The main, O1, and the two auxiliary, O2 and O3, operators are shown as yellow rectangles on the black line representing DNA. Binding of the lac repressor to O1 prevents transcription of the three lacZYA genes. The predicted vs. the observed repression level Vilar & Saiz, 2013b is plotted for all the available operator configurations, repressor oligomeric forms, and promoters (panel on the bottom left). The dashed lines represent a factor 1.7 higher and lower than the perfect prediction indicated by the continuous line. Adapted with permission from Vilar & Saiz, 2013b. © 2013 American Chemical Society.*

During this time, it has become evident that systems biophysics approaches are needed to tackle the complexity of the molecular interactions in the control of the response to lactose. This complexity is already present in the mode of functioning of the lac repressor, which upon binding to *O1*, the main operator, prevents the RNA polymerase from binding to the promoter (Saiz & Vilar,

2006b). There are also two distal auxiliary operators, *O2* and *O3*, where the repressor can bind specifically without preventing transcription (**Figure 1**). These two additional sites were originally considered to be remnants of evolution, because they are orders of magnitude weaker than the main site and by themselves do not affect transcription substantially. In combination with the main site, however, they were shown to increase repression of transcription by almost a factor of 100. For over 20 years after the characterization of these sites, a long-standing question was how such weak sites could help the binding to a strong one. The reason for this counterintuitive effect turned out to be that the lac repressor can also bind as a bidentate tetramer to two operators simultaneously and loop the intervening DNA. Binding while *looping DNA* is difficult to analyze with traditional biochemical methods and required new biophysical approaches to characterize it (Vilar & Leibler, 2003).

> **Despite the apparent simplicity of the lac operon, it took over 50 years to have an effective biophysical characterization of this system**

This type of behavior, involving oligomeric transcription factors that can bind simultaneously single and multiple DNA sites, is a recurrent theme in gene expression, to the extent that transcription regulation through DNA looping is nowadays considered to be the rule rather than the exception (Alberts, et al., 2014). It is present in many bacterial operons, such as *ara*, *gal*, and *deo* operons, and in bacteriophages, such as *phage λ*. DNA looping plays an important role in mediating long-range interactions because it allows proteins bound to non-adjacent DNA sites to come close to each other. This strategy is widely used in eukaryotic enhancers, as in the case of the interactions between enhancers and promoters mediated by androgen and progesterone receptors, to integrate multiple signals into the control of the transcriptional machinery. It is also present in the tumor suppressor *p53*, the nuclear factor κB (*NF-κB*), the signal transducers and activators of transcription (*STATs*), the octamer-binding proteins (*Oct*), and the retinoid nuclear hormone receptor *RXR* (Vilar & Saiz, 2011).

The lac operon is well suited to test our current understanding about these types of systems and to develop new methods. The main reason is that it embodies the core elements present across many levels of transcription regulation, it offers the possibility of considering the actual mode of binding and regulation, and it has substantial amounts of experimental data available to contrast the hypothesis and results of the model. In short, there is no room for wiggling. Currently, it is possible to predict how the effects of a single-base pair mutation in the operator DNA would propagate trough all the series of events that lead to protein production from the lac operon (Vilar & Saiz, 2013b). This task proved to be challenging in several fronts. Firstly, it requires an efficient approach to connect the parts as a system to avoid getting into a combinatorial complexity problem, in which the number of potential states of the system grows exponentially with the number of components (Vilar & Saiz, 2010). Secondly, the increase in components leads also to an increase in the number of parameters, but many of these parameters

> **This approach accurately reproduces the observed transcriptional activity of the lac operon over a 10,000-fold range**

are thermodynamically related to each other. Finally, the values of the parameters might be different under different experimental conditions.

To achieve such predictive capabilities, it was necessary to elucidate biophysical principles for integrating the prototypical complex interactions of transcription regulation into a manageable description. The key idea is to use a modular design with a decomposition of the free energy of the different states into additive contributions of the interactions (Vilar & Saiz, 2013a, Vilar & Saiz, 2013b). This approach allowed the whole system to be characterized in terms of a few parameters directly connected to the experimental data. It considers lac repressor dimers and operator sequences as elementary components. The behavior of the system is obtained starting off from the dimer assembly into tetramers, binding of dimers and tetramers to the different operators, and looping of DNA by the simultaneous binding of a bidentate tetrameric repressor to two operators (**Figure 1**). This approach accurately reproduces the observed transcriptional activity of the lac operon over a 10,000-fold range for 21 different operator setups (deletions and mutations), different repressor concentrations, and tetrameric and mutant-dimeric forms of the repressor (**Figure 1**). Incorporation of the calibrated model into more complex scenarios, taking into account stochastic transcription and translation, accurately captures the induction curves for key operator configurations and the temporal evolution of gene expression of growing cell populations (Vilar & Saiz, 2013a, Vilar & Saiz, 2013b). Despite the apparent simplicity of the lac operon, it took over 50 years to have an effective biophysical characterization of this system.

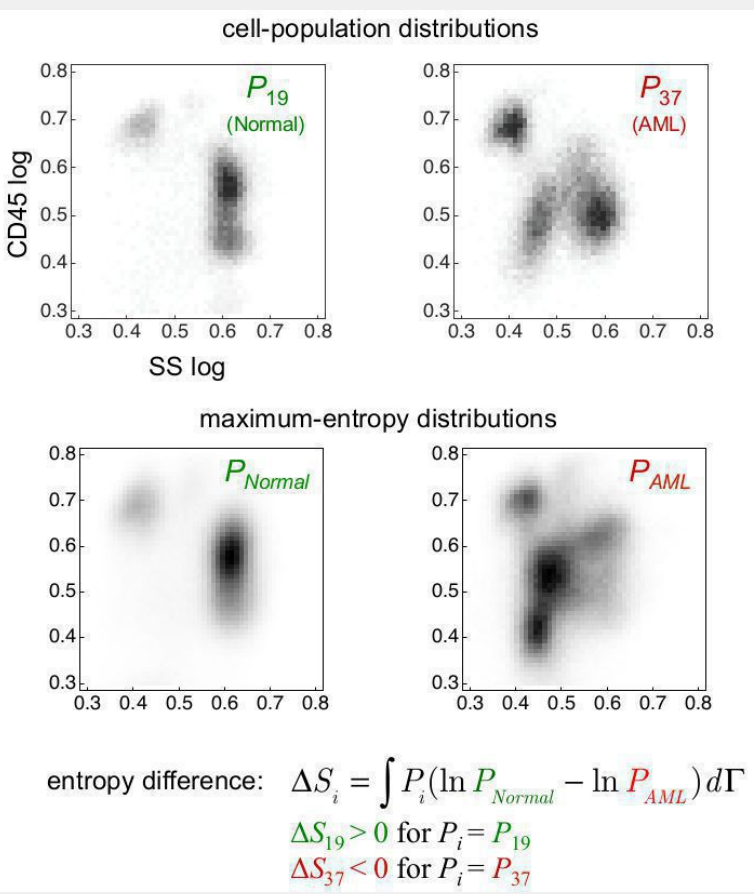

Figure 2. Diagnosing leukemia based on the entropy of distributions of cell molecular and morphological parameters. *The two-dimensional distribution of cells with given values of the logarithms of the side scatter (SS log) and the marker CD45 (CD45 log) intensities are shown for representative cell populations, with black and white representing high and zero densities, respectively (Vilar, 2014). The distributions for AML patient no. 37 (P37) and normal individual no. 19 (P19) are indicative of distributions that closely resemble the maximum-entropy distribution of their state, either AML (PAML) or normal (PNormal) states. Healthy and leukemia cell distributions are associated with positive and negative values of* ΔS_i*, respectively. The subscript i in the equation indicates the patient number and* Γ *is a two dimensional variable* Γ *= (SS log, CD45 log).*

Automated diagnosis of leukemia based on entropy

High-throughput measurement technologies, such as flow cytometry (FCM), can characterize nowadays multiple properties of a single cell at a rate of thousands of cells per second (Aghaeepour, et al., 2013). Acute myeloid leukemia (AML) epitomizes the class of highly complex diseases that these technologies aim to tackle by using large sets of single-cell-level information. Achieving such a goal, however, has proved to depend critically not only on experimental techniques but also on approaches to interpret the data. Specifically, a central aspect of all data-intensive approaches is identifying the relevant quantitative features of the disease from the massive amounts of information produced.

Several machine-learning techniques have been developed to analyze the data in order to diagnose leukemia with different degrees of success (Aghaeepour, et al., 2013). It is also possible, however, to follow more biophysically inspired approaches. Along this path, it is important to take into account that FCM data do not measure the causes of the disease but just its effects in the cellular markers, which is reflected in the statistical properties of the cell populations. From very general principles, one can show that the probability distribution that best represents the healthy or AML state is the one with the largest entropy for each state (Vilar, 2014). From this characterization one can derive, for each patient, a measure of relative entropy as the difference between the patient's distribution and the reference distributions of AML and healthy states deduced from a reference dataset (**Figure 2**). This relative entropy allows the classification of each patient as healthy or AML positive with almost perfect accuracy, which lead this approach to rank first in the DREAM6 challenge (Aghaeepour, et al., 2013). This case illustrates how using biophysical information it is possible to efficiently identify the key features that are hidden within large amounts of data.

The overarching goal

Linus Pauling noted that "life is a relationship among molecules and not a property of any molecule". The ultimate goal of systems biophysics is precisely to work out those relationships. New tools, and especially new frameworks and conceptual developments, are still needed to accurately determine the cellular behavior in terms of the physical properties of the molecular interactions. Even relatively simple systems, like the lac operon, have proved to be substantially more complex that originally speculated. Major challenges are still present on how to integrate thermodynamic and structural information with massive data in order to obtain at least information at the mesoscopic level. New approaches have to be able to describe the complex assembly dynamics of the multiple cellular components that carry out the cellular function over scales ranging from milliseconds to hours and days and they need to account for processes as diverse as protein-protein interaction, binding to DNA, transcription, translation, degradation and macromolecular

New approaches have to be able to describe the complex assembly dynamics of the multiple cellular components that carry out the cellular function

assembly of signaling complexes at membranes and scaffolds. Achieving this goal, at least partially, has important implications, as it is a prerequisite for the rational identification of therapeutic molecular targets and eventually for bridging prediction of clinical outcomes with molecular properties.

Jose M. G. Vilar

Biofisika Institute (CSIC, UPV/EHU) and Department of Biochemistry and Molecular Biology, University of the Basque Country, P.O. Box 644, 48080 Bilbao (Spain).

Basque Foundation for Science – Ikerbasque, 48011 Bilbao (Spain).

E-mail: j.vilar@ikerbasque.org

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Biofísica Magazine

NEWS / SBE PRIZES

SBE travel awards and Imagin'Action awardee, 2016

The Spanish Biophysics Society has awarded this year travel grants for a total of 14 member students to attend to the 5th International Iberian Biophysics Congress. During the congress, the winner of the First Imagin'Action contest of SBE also received her prize.

Imagin'Action Awardee

Raquel Arroyo Rodríguez (Universidad Complutense de Madrid – UCM), for her Image entitled *Doggy PC. From animals to Biophysics, going through lipids*. *Follow this link* for more information.

List of travel awardees

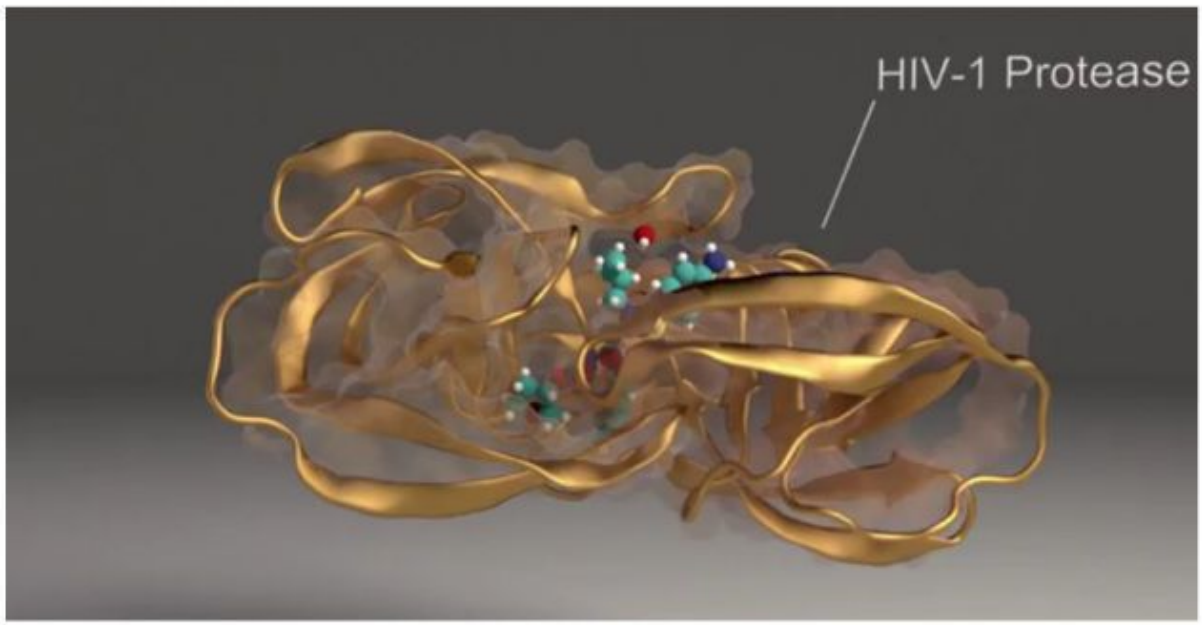
Alberto Hidalgo Román
Antonio L. Egea Jiménez
Carla Huerta López

José C. Castillo Sánchez
Chiara Pallara
Didier Barradas Bautista
Elisa Parra Ortiz
Emilio J. González Ramírez
Esperanza Rivera de Torre
Sara Hernández Mejías
Julene Madariaga Marcos
María Sebastián Valverde
Raquel Arroyo Rodríguez
Sara García Linares

Biofísica Magazine

NEWS

BSC and IrsiCaixa create a computational method to predict the effectiveness of antiretroviral drugs



The Barcelona Supercomputing Center – BSC and IrsiCaixa (the Catalan AIDS Research Institute), have developed a bioinformatics method to predict the effect of mutations on the resistance the HIV and other retroviruses to specific drugs.

See the work published in the Journal of Chemical Information and Modeling by Ali Hosseini, Andreu Alibés, Marc Noguera-Julian, Victor Gil, Roger Paredes, Robert Soliva, Modesto Orozco, and Victor Guallar.

> *In this study we demonstrate how to connect routine clinical diagnosis of HIV-1 with structural computer modelling. This is a multidisciplinary proof of concept which overcomes the limitations of current practice when deciding antiretroviral treatment and which, in addition, allows new drugs to be designed more quickly (says Marc Noguera-Julian, IrsiCaixa, co-author of the study).*

The effectiveness of antiretroviral drugs used to treat HIV (human immunodeficiency virus) is frequently affected by the virus ability to develop genetic mutations. The BSC-IrsiCaixa method predicts the effect of each mutation on the resistance of the virus to such drugs. The method combines HIV DNA sequencing, identification of genetic mutations, computational protein

modelling and the simulation of drugs binding with the proteins of the virus. The entire bioinformatics analysis can be performed in fewer than 24 hours on relatively small-scale computing equipment available to any laboratory.

One of the main features of the strategy is the use of PELE, a software developed at BSC to predict how drugs will interact with their targets, which has been shown to have competitive advantages over commercially available software. BSC has created an automatic platform, available for free via the web, on which researchers can enter a patient's HIV-1 PR protease genomic sequence and predict the effectiveness of prescribing the drugs amprenavir and darunavir. For the moment, these are the only predictions available, pending advances in research on the effect of HIV mutations on other proteins within the virus and interactions with other antiretroviral drugs.

BSC researcher Victor Guallar, PI of the study and lead developer of PELE, explains that

> *this system is one of the first tangible steps in the area of what will eventually be personalised medicine, where treatment will be decided following genetic analysis of the causes of the disease in each patient and of which drug would be most effective in each individual case.*

More information

- Original publication in the Journal of Chemical Information and Modeling.
- Victor Guallar group at BSC.

Biofísica Magazine

NEWS

Singapore Statement on Research Integrity

> *The Singapore Statement on Research Integrity is a consensus document laying out the globally-applicable principles and responsibilities related to research integrity and scientific conduct. It was agreed by the 230 participants at the 2nd World Conference on Research Integrity (WCRI), 21-24 July 2010, in Singapore.*

Preamble. The value and benefits of research are vitally dependent on the integrity of research. While there can be and are national and disciplinary differences in the way research is organized and conducted, there are also principles and professional responsibilities that are fundamental to the integrity of research wherever it is undertaken.

PRINCIPLES

Honesty in all aspects of research
Accountability in the conduct of research
Professional courtesy and fairness in working with others
Good stewardship of research on behalf of others

RESPONSIBILITIES

1. Integrity: Researchers should take responsibility for the trustworthiness of their research.
2. Adherence to Regulations: Researchers should be aware of and adhere to regulations and policies related to research.
3. Research Methods: Researchers should employ appropriate research methods, base conclusions on critical analysis of the evidence and report findings and interpretations fully and objectively.
4. Research Records: Researchers should keep clear, accurate records of all research in ways that will allow verification and replication of their work by others.
5. Research Findings: Researchers should share data and findings openly and promptly, as soon as they have had an opportunity to establish priority and ownership claims.
6. Authorship: Researchers should take responsibility for their contributions to all publications, funding applications, reports and other representations of their research. Lists of authors should include all those and only those who meet applicable authorship criteria.
7. Publication Acknowledgement: Researchers should acknowledge in publications the names and roles of those who made significant contributions to the research, including writers, funders, sponsors, and others, but do not meet authorship criteria.
8. Peer Review: Researchers should provide fair, prompt and rigorous evaluations and respect confidentiality when reviewing others' work.
9. Conflict of Interest: Researchers should disclose financial and other conflicts of interest that could compromise the trustworthiness of their work in research proposals, publications and public communications as well as in all review activities.
10. Public Communication: Researchers should limit professional comments to their recognized expertise when engaged in public discussions about the application and importance of research findings and clearly distinguish professional comments from opinions based on personal views.
11. Reporting Irresponsible Research Practices: Researchers should report to the appropriate authorities any suspected research misconduct, including fabrication, falsification or plagiarism, and other irresponsible research practices that undermine the trustworthiness of research, such as carelessness, improperly listing authors, failing to report conflicting data, or the use of misleading analytical methods.
12. Responding to Irresponsible Research Practices: Research institutions, as well as journals, professional organizations and agencies that have commitments to research, should have procedures for responding to allegations of misconduct and other irresponsible research practices and for protecting those who report such behavior in good faith. When misconduct or other irresponsible research practice is confirmed, appropriate actions should be taken promptly, including correcting the research record.

13. Research Environments: Research institutions should create and sustain environments that encourage integrity through education, clear policies, and reasonable standards for advancement, while fostering work environments that support research integrity.
14. Societal Considerations: Researchers and research institutions should recognize that they have an ethical obligation to weigh societal benefits against risks inherent in their work.

NOTE: This is not a regulatory document and does not represent the official policies of the countries and organizations that funded and/or participated in the Conference. For official policies, guidance, and regulations relating to research integrity, appropriate national bodies and organizations should be consulted. Available at: www.singaporestatement.org.

STATEMENT DRAFTING COMMITTEE:

Nicholas Steneck and Tony Mayer, Co-chairs, 2nd World Conference on Research Integrity.

Melissa Anderson, Chair, Organizing Committee, 3rd World Conference on Research Integrity.

MORE INFORMATION

- World Conferences on Research Integrity
- Printable copies in various sizes at Singapore Statement web page
- Montreal Statement on Research Integrity in Cross-Boundary Research Collaborations (PDF).
- See also: Irreproducibility in Research. What can we do about it?

Biofísica Magazine

NEWS

European research organizations call upon the European Parliament to encourage society to respect independent science advice and to condemn physical attacks on scientists

Open Letter

Brussels, 01.07.2016

TO THE PRESIDENT OF THE EUROPEAN PARLIAMENT, MR. MARTIN SCHULZ

Dear Mr. Schulz,

On 7 th June, the European Food Safety Authority (EFSA) in Parma, Italy, received a package containing explosive material addressed to a scientist providing independent scientific advice to EFSA. This incident followed a forced entry and invasion of the EFSA headquarters last year. The signatories of this letter represent major national and international science organisations. We are deeply disturbed by these attacks and direct this letter to you to express our concern. These cowardly acts are not only attacks on individual scientists performing their duties for an agency of the European Union, and thereby serving the citizens of the EU, they are also attacks on our open

and transparent society and on the scientific and intellectual process.

We feel that publicly-funded scientists are experiencing an increasing number of threats in Europe and the rest of the world. In the last few years experimental programmes have been attacked at several locations in Europe, many of them conducting EU-funded research. Similar incidents have occurred in the US, Australasia and the Philippines, and at least four life-threatening attacks have occurred on researchers and research facilities in Latin America
over the last year. Threats to publicly funded scientists are threats to a society which relies on their independent evidence. We see these attacks as resulting from a science-hostile trend that is spreading and inspiring such extremist acts. What is at stake is the independence of science and its essential role in the democratic system of decision-making.

We can no longer remain silent. These violent acts demonstrate a dangerous intolerance of openly expressed expert opinions and of democratic, social and scientific development. We believe in reason and dialogue. Through our work we aim to stimulate innovation, improve livelihoods, minimise environmental impact and provide for a better future. Furthermore, independent scientific advice is crucial to informed debate and appropriate decision-making on complex issues. We are convinced that such acts of aggression not only impede progress, but also destabilise society and undermine democracy.

As EFSA is providing the EU Institutions and Member States with independent scientific advice, there is now a need to act at the European Union level. We call upon the European Parliament to encourage society to respect independent science advice and to unanimously and unconditionally condemn the recent attacks on EFSA, reiterating its support for independent scientific research and investigation, and to propose measures to prevent attacks targeting scientists and/or research facilities. Scientific progress is of essential importance to society. We hope that you appreciate the urgency of this matter and that the European Parliament will show support for the European life sciences sector.

Yours sincerely,

Prof. Jose Pio Beltran
President European Plant Science Organisation, EPSO, www.epsoweb.org

On behalf of the undersigning science organisations, societies and academies:

- Agrobioinstitute, ABI, BG, Rossitza Batchvarova, Director; www.abi.bg
- Agroscope, CH, Michael Gysi, Head; www.agroscope.admin.ch
- Biotechnology Committee of Polish Academy of Sciences, PL, Tomasz Twardowski, President;

http://www.kbiotech.pan.pl/en

- Copenhagen Plant Science Centre, CPSC, DK, Poul Erik Jensen, Head; http://cpsc.ku.dk
- Czech National Technology Platform "Plants for the Future", CZ, Tomas Vanek, Head
- European Academies Science Advisory Council, EASAC, Europe, Jos van der Meer, President; www.easac.eu
- European Federation of Academies of Sciences and Humanities, ALLEA, Europe, Günter Stock, President; www.allea.org
- European Plant Science Organisation, EPSO, International, Jose Pio Beltran, President & Karin Metzlaff, Executive Director; www.epsoweb.org
- French Society of Plant Biologists,SFBV, FR, Anis Limami, President; http://sfbv.snv.jussieu.fr
- German Life Sciences Association, VBIO, DE, Bernd Müller-Röber, President; www.vbio.de
- Global Plant Council, GPC, International, Barry Pogson, President; http://globalplantcouncil.org
- Institute of Experimental Botany of the Academy of Sciences, CZ, Martin Vagner, President; www.ueb.cas.cz
- Instituto de Tecnologia Química e Biológica António Xavier, ITQB NOVA, PT, Cláudio M Soares, Director, Margarida Oliveira & Inês C. Pereira, vice-Directors; www.itqb.unl.pt
- Italian National Academy of Agriculture, IT, Giorgio Cantelli Forti, President
- Italian National Academy of Sciences, IT, Emilia Chiancone, President; www.accademiaxl.it/en.html
- Italian Society of Agricultural Genetics, SIGA, IT, Michele Morgante, President; www.geneticagraria.it
- Italian Society of Plant Biology, SIBV, IT, Paolo Trost, President; www.sibv.it
- Linnean Centre for Plant Biology, SE, Eva Sundberg, Chair; http://lcpu.se
- PlantLink, SE, Leif Bülow, Director; www.plantlink.se
- Polish Society of Experimental Plant Biology, PTBER, PL, Iwona Ciereszko, President; http://ptber.org.pl/default/en
- Portuguese Society of Plant Physiology, SPFV, PT, Jorge Marques da Silva, President Direction SPFV & Margarida Oliveira, President General Assembly SPFV; www.spfv.pt
- Public Research and Regulation Initiative, PRRI, International, Marc Van Montagu, Chair; www.prri.net
- Royal Danish Academy of Sciences and Letters, KDVS, DK, Michael Broberg Palmgren, Representative to EASAC; www.royalacademy.dk
- Scandinavian Plant Physiology Society, SPPS, SE, Stefan Jansson, President; www.spps.fi
- Sense about Science EU, UK, Sofie Vanthornout, Director; www.senseaboutscience.org
- Serbian Plant Physiology Society, SPPS, RS, Jovanka Miljus-Djukic, President; www.dfbs.org.rs
- Slovenian society of plant biology, SL, Spela Baebler, President;
- Society for Experimental Biology, SEB, UK, Paul Hutchinson, CEO; www.sebiology.org
- Spanish Society of Plant Physiology, SEFV, ES, Aurelio Gomez-Cadenas, President; http://sefv.net
- Swiss Society of Agronomy, SSA (SGPW), CH, Roland Kölliker, General Secretary; www.naturalsciences.ch/organisations/sgpw
- The Federation of European Societies of Plant Biology, FESPB, Europe, Stefan Jansson,

President; www.fespb.org
- The Royal Society, UK, Venki Ramakrishnan, President; https://royalsociety.org
- VTT Technical Research Centre of Finland, FI, Antti Vasara, President; www.vtt.fi
- Umeå Plant Science Centre, UPSC, SE, Ove Nilsson, Director; www.upsc.se
- Wissenschaftlerkreis Grüne Gentechnik, WGG, DE, Klaus-Dieter Jany, Chair; http://wgg-ev.jimdo.com

Contacts

Prof. Jose Pio Beltran
& Prof. Joachim Schiemann
European Plant Science Organisation
EPSO
T: +34-669638053 (JPB)
T: +49-3946-47503 (JS)
jbeltran@ibmcp.upv.es
joachim.schiemann@jki.bund.de

Prof. Stefan Jansson

Federation of European Societies of Plant Biology
FESPB
T: +46-70-677-2331

stefan.jansson@umu.se

Prof. Jos van der Meer

European Academies' Science Advisory Council
EASAC
T:+49 345 4723 9833

secretariat@easac.eu

About EPSO

EPSO, the European Plant Science Organisation, is an independent academic organisation that represents more than 220 research institutes, departments and universities from 28 European countries, Australia, Japan and New Zealand, and 3.300 individuals Personal Members, representing over 28 000 people working in plant science. EPSO's mission is to improve the impact and visibility of plant science in Europe, to provide authoritative source of independent information on plant science including science advice to policy, and to promote training of plant scientists to meet the 21st century challenges in breeding, agriculture, horticulture, forestry, plant ecology and sectors related to plant science. www.epsoweb.org

About FESPB

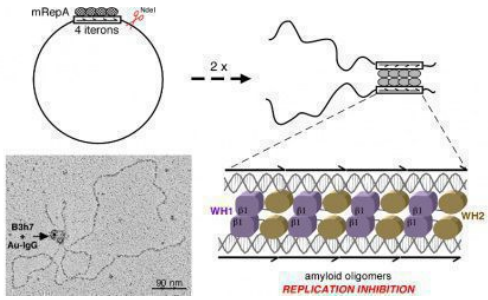
FESPB, the Federation of European Societies of Plant Biology (formerly the Federation of European Societies of Plant Physiology) was founded in 1978 and today it is one of Europe 's largest and most widely representative society of Plant Scientists. The aims of FESPB are to advance research, education, and the exchange of information amongst plant biologists within Europe and beyond, and to support the publication of the results of research through its six affiliated international journals. www.fespb.org

About EASAC

EASAC, the European Academies' Science Advisory Council, is formed by the national science academies of the EU Member States to enable them to collaborate with each other in providing independent science advice to European policy-makers. It thus provides a means for the collective voice of European science to be heard. EASAC was founded in 2001 at the Royal Swedish Academy of Sciences. National science academies recognise that the scope of their advisory functions needs to extend beyond the national to cover also the European level. Through EASAC, the academies work together to provide independent, expert, evidence-based advice about the scientific aspects of public policy to those who make or influence policy within the European institutions.
www.easac.eu

Biofísica Magazine

PAPERS OF THE MONTH BY SBE MEMBERS: MAY - AUGUST 2016

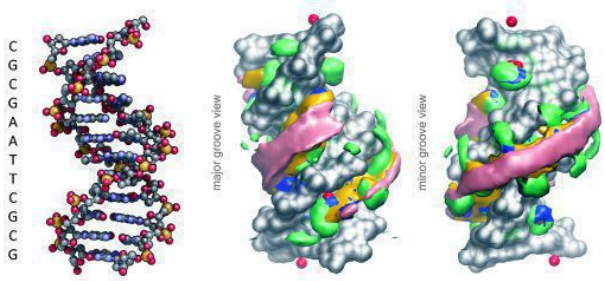


HIGHLIGHTED / MAY 2016

Functional amyloids as inhibitors of plasmid DNA replication

Molina-García L, Gasset-Rosa F, Moreno-Del Álamo M, Fernández-Tresguerres ME, Moreno-Díaz de la Espina S, Lurz R, Giraldo R.

Sci Rep 2016 May; 6: 25425.

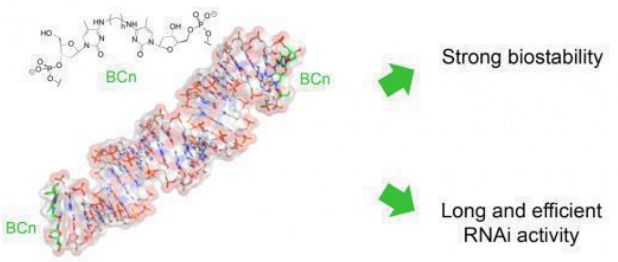


HIGHLIGHTED / MAY 2016

Long-timescale dynamics of the Drew-Dickerson dodecamer

Dans PD, Danilāne L, Ivani I, Dršata T, Lankaš F, Hospital A, Walther J, Pujagut RI, Battistini F, Gelpí JL, Lavery R, Orozco M.

Nucleic Acids Res 2016 May; 44: 4052.

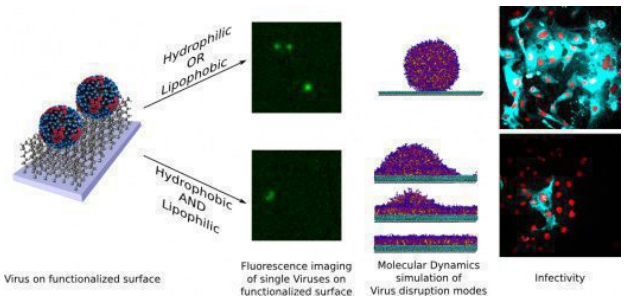


HIGHLIGHTED / MAY 2016

Rational design of novel N-alkyl-N capped biostable RNA nanostructures for efficient long-term inhibition of gene expression

Terrazas M, Ivani I, Villegas N, Paris C, Salvans C, Brun-Heath I, Orozco M.

Nucleic Acids Res 2016 May; 44: 4354.

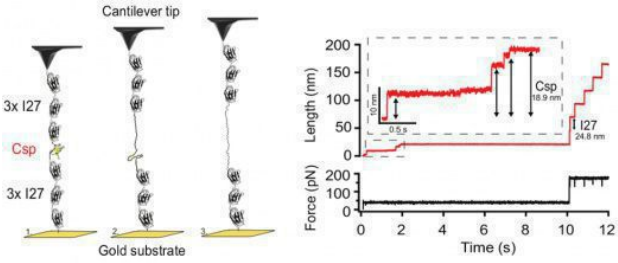


HIGHLIGHTED / JUN. 2016

Functionalized Surfaces with Tailored Wettability Determine Influenza A Infectivity

Mannelli I, Reigada R, Suárez I, Janner D, Carrilero A, Mazumder P, Sagués F, Pruneri V, Lakadamyali M.

ACS Appl Mater Interfaces 2016 Jun.; 8: 15058.

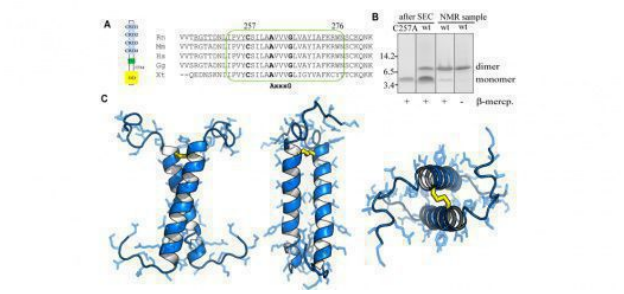


HIGHLIGHTED / JUN. 2016

A simple two-state protein unfolds mechanically via multiple heterogeneous pathways at single-molecule resolution

Schönfelder J, Perez-Jimenez R, Muñoz V.

Nat Commun 2016 Jun.; 7: 11777.

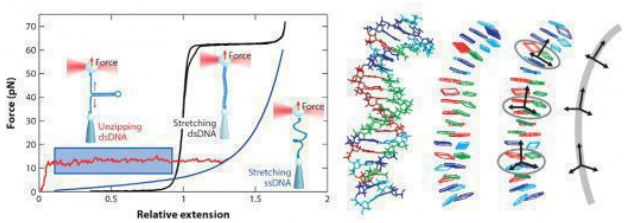


HIGHLIGHTED / JUN. 2016

Structural Basis of p75 Transmembrane Domain Dimerization

Nadezhdin KD, García-Carpio I, Goncharuk SA, Mineev KS, Arseniev AS, Vilar M.

J Biol Chem 2016 Jun.; 291: 12346.

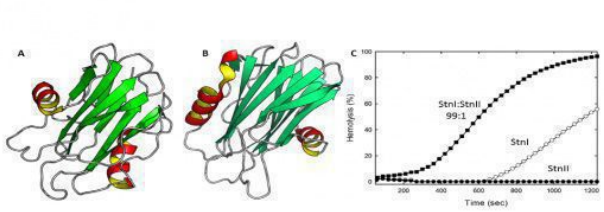


HIGHLIGHTED / JUL. 2016

Elastic Properties of Nucleic Acids by Single-Molecule Force Spectroscopy

Camunas-Soler J, Ribezzi-Crivellari M, Ritort F.

Annu Rev Biophys 2016 Jul.; 45: 65.

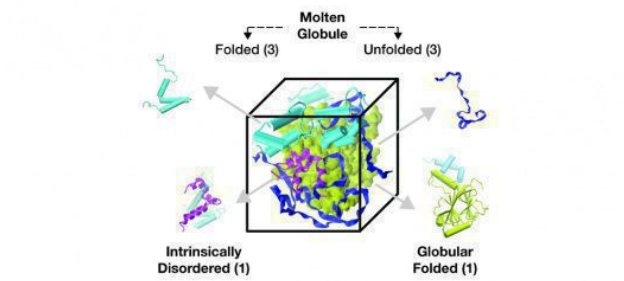


HIGHLIGHTED / JUL. 2016

Synergistic Action of Actinoporin Isoforms from the Same Sea Anemone Species Assembled into Functionally Active Heteropores

Rivera-de-Torre E, García-Linares S, Alegre-Cebollada J, Lacadena J, Gavilanes JG, Martínez-Del-Pozo Á.

J Biol Chem 2016 Jul.; 291: 14109.

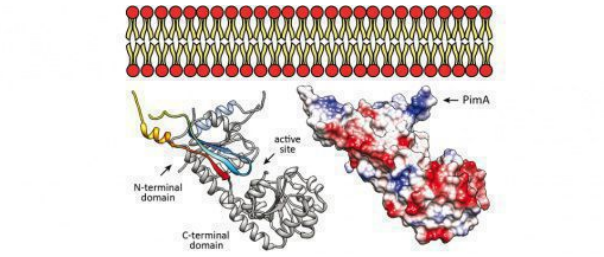


HIGHLIGHTED / JUL. 2016

The Differential Response of Proteins to Macromolecular Crowding

Candotti M, Orozco M.

PLoS Comput Biol 2016 Jul.; 12: e1005040.

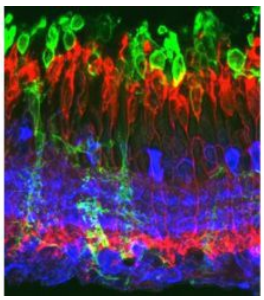


HIGHLIGHTED / JUL. 2016

Molecular Basis of Membrane Association by the Phosphatidylinositol Mannosyltransferase PimA Enzyme from Mycobacteria

Rodrigo-Unzueta A, Martínez MA, Comino N, Alzari PM, Chenal A, Guerin ME.

J Biol Chem 2016 Jul.; 291: 13955.

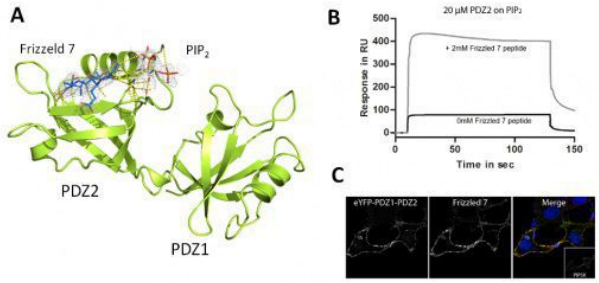


HIGHLIGHTED / JUL. 2016

Optical control of endogenous receptors and cellular excitability using targeted covalent photoswitches

Izquierdo-Serra M, Bautista-Barrufet A, Trapero A, Garrido-Charles A, Díaz-Tahoces A, Camarero N, Pittolo S, Valbuena S, Pérez-Jiménez A, Gay M, García-Moll A, Rodríguez-Escrich C, Lerma J, de la Villa P, Fernández E, Pericàs MÀ, Llebaria A, Gorostiza P.

Nat Commun 2016 July; 7: 12221.

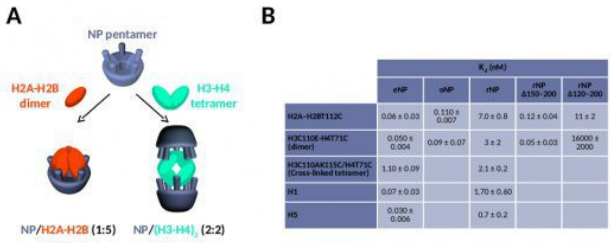


HIGHLIGHTED / JUL. 2016

Frizzled 7 and PIP2 binding by syntenin PDZ2 domain supports Frizzled 7 trafficking and signalling

Egea-Jimenez AL, Gallardo R, Garcia-Pino A, Ivarsson Y, Wawrzyniak AM, Kashyap R, Loris R, Schymkowitz J, Rousseau F, Zimmermann P.

Nat Commun 2016 July; 7: 12101.

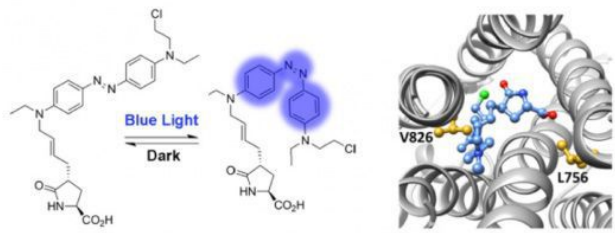


AUG. 2016 / HIGHLIGHTED

A Quantitative Characterization of Nucleoplasmin/Histone Complexes Reveals Chaperone Versatility

Fernández-Rivero N, Franco A, Velázquez-Campoy A, Alonso E, Muga A, Prado A.

Sci Rep 2016 Aug.; 6: 32114.

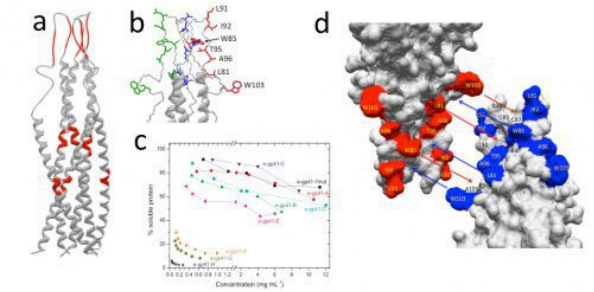


AUG. 2016 / HIGHLIGHTED

OptoGluNAM4.1, a Photoswitchable Allosteric Antagonist for Real-Time Control of mGlu4 Receptor Activity

Rovira X, Trapero A, Pittolo S, Zussy C, Faucherre A, Jopling C, Giraldo J, Pin JP, Gorostiza P, Goudet C, Llebaria A.

Cell Chem Biol 2016 Aug.; 23: 929.

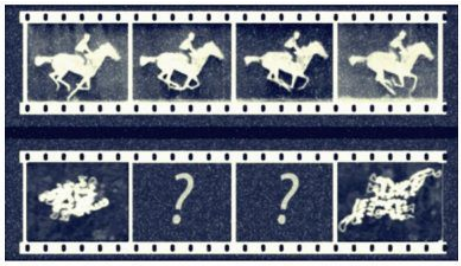


AUG. 2016 / HIGHLIGHTED

Molecular and Physicochemical Factors Governing Solubility of the HIV gp41 Ectodomain

Manssour-Triedo F, Crespillo S, Morel B, Casares S, Mateo PL, Notka F, Roger MG, Mouz N, El-Habib R, Conejero-Lara F.

Biophys J 2016 Aug.; 111: 700.



AUG. 2016 / HIGHLIGHTED

Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations

Orellana L, Yoluk O, Carrillo O, Orozco M, Lindahl E.

Nat Commun 2016 Aug.; 7: 12575.

Biofísica Magazine

FPI / JOBS / PREDOC

2016 – Predoctoral training contracts

National Programme for the Promotion of Talent and Its Employability

National Sub-Programme for Training

Deadlines: 13/09/2016 – 27/09/2016. Please note that applicants must first contact eligible research groups (see below), who may have set their own time limits.

> *The grants will include support for the funding of contracts, support for stays in other labs and support to cover the costs of enrollment in doctoral courses.*

Eligible Biophysics groups

Positions announced from this site with links to specific information:

- Membrane nanomechanics (Biophysics Unit, University of the Basque country) at Bilbao. PI: Dr. Vadim Frolov.
- *De novo* engineering and evolution of enzymes (Department of Physical Chemistry, University of Granada. PI: Dr. José Manuel Sánchez-Ruiz.

Applicant Eligibility Criteria

1. At the time of filing the application, applicants must be able to be enrolled, or accepted, into a doctoral program for the academic year 2015/2016.
2. Are not eligible for this call, students who have already started (prior to the submission of the application) a predoctoral training financed under the "State Plan of Research, Development and Technological Innovation" or any of the previous National Plans.
3. May also not be applicants, those who have enjoyed more than twelve months of a predoctoral contract before the date of the application.

Application Process

Find full instructions by following the Links below.

More Information

- Ministerio de Economía y Competitividad: National Programme for the Promotion of Talent and Its Employability 2016 (in Spanish).
- Full list of Projects eligible for contracts.

Biofísica Magazine

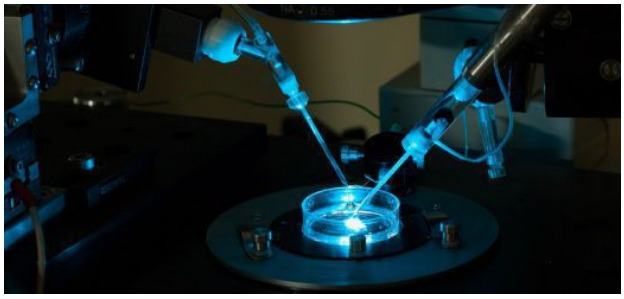
CATEGORY: JOBS

Positions in Biophysics

CALLS / JOBS 14/09/2016

Faculty Position in Bioinformatics or Systems Biology at SISSA

Expressions of interest for a Tenure Track or Associate Professor level in the group of Molecular and Statistical Biophysics, Scuola Internazionale Superiore di Studi Avanzati...



CALLS / FELLOWSHIPS / FPI / PREDOC 14/09/2016

PhD fellowship (FPI) in membrane biophysics, Bilbao

FPI fellowship 4 year PhD fellowship (FPI, funded by Spanish Ministry of Economy and Competitiveness) is available in the group of Membrane Nanomechanics (Biophysics Unit,...

CALLS / JOBS / POSTDOC 22/08/2016

Research associate positions in mechanobiology

Two postdoctoral positions are available in the group of Prof Garcia-Manyes at King's College London Position 1 Deadline: September 10th 2016. Postdoctoral Research Associate...

CALLS / JOBS 29/06/2016

Research positions in Madrid: Talent attraction program

2016 Call by "Dirección General de Universidades e Investigación de la Comunidad de Madrid" DEADLINE: July 28th 2016 The "Consejería de Educación, Juventud y Deporte"...

JOBS / POSTDOC 13/06/2016

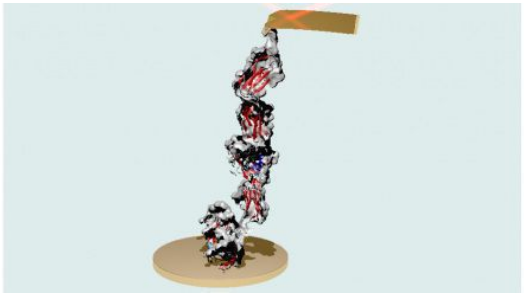
Postdoc position: Mechanics of membrane fission at single molecule level

Colaborative project between Prof V. Frolov and Dr. B. Ibarra laboratories. We are looking for a talented, hard-working postdoctoral candidate to study at the single...

CALLS / JOBS / NEWS 19/05/2016

Ikerbasque Research Professors 2016

10 permanent positions for experienced researchers, within any of the Basque Research Institutions DEADLINE: September 12th 2016, 13:00 CET Ikerbasque, the Basque Foundation for Science...



JOBS / POSTDOC 14/05/2016

Postdoctoral position in protein nanomechanics at the Cajal Institute – CSIC

The Protein Nanomechanics Lab at Institute Cajal – CSIC, Madrid We are seeking experienced researchers interested in working in nanomechanics to join the research lines...

JOBS / POSTDOC 05/05/2016

Postdoctoral position in protein engineering for functional nanostructures

Biomolecular Nanotechnology Group, CIC biomaGUNE, San Sebastián (Spain). A postdoctoral position is available in the area of computational protein engineering for functional materials and nanostructures,...

Biofísica Magazine

CATEGORY: EVENTS

Upcoming Meetings, Courses and Workshops

EVENTS / MEETINGS 14/09/2016

61st BPS Annual Meeting

61st Biophysical Society Annual Meeting. February 11 – 15, 2017, New Orleans, Louisiana (USA). Deadlines January 9, 2017. End of early bird registration October 3,...

EVENTS / MEETINGS 02/09/2016

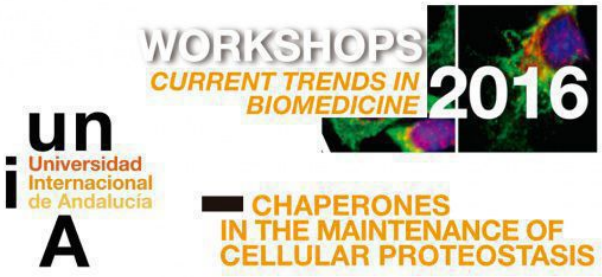
VI CNIC Conference "Mechanical Forces in Physiology and Disease"

CNIC, Madrid (Spain), November 4th – 5th 2016 . DEADLINES: pre-registration September 18th 2016. Inscription is free, and there are 3 travel bursaries available for...

COURSES / EVENTS 08/07/2016

First I2PC-FEI “hands on” course on image processing applied to the structural characterization of biological macromolecules

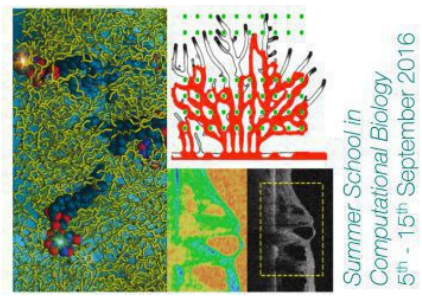
Octubre 17 – 20, 2016. Parador Nacional Alcala de Henares, Madrid, Spain Organized by The Instruct Image Processing Center at the CNB-CSIC and FEI Corporation...



EVENTS / WORKSHOPS 29/06/2016

Chaperones in the maintenance of cellular proteostasis

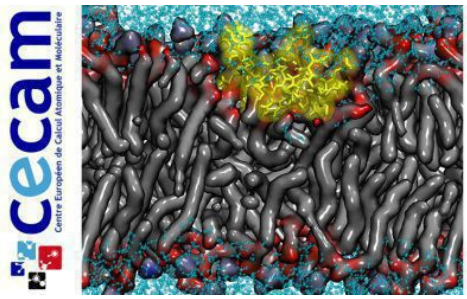
Workshops “Current Trends in Biomedicine” “Chaperones in the maintenance of cellular proteostasis” 17-19 October 2016, “Campus Antonio Machado”, (Baeza, Spain) DEADLINE: September 2nd 2016 The...



COURSES / EVENTS 20/06/2016

2nd Summer School in Computational Biology – from Molecules to Tissues

Coimbra, Portugal, 5th-15th September 2015 Website: http://www.uc.pt/en/iii/initiatives/cbuc/CBSS2 Deadline for application: 25th July, 2016 An introductory course targeted to students from M.Sc. to post-doctoral levels.....



EVENTS / WORKSHOPS 07/06/2016

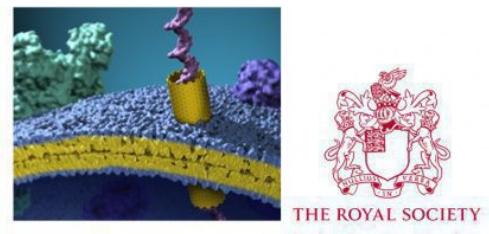
International Workshop on Biomembranes: The consequences of complexity

Sponsored by CECAM, Finnish IT Center for Science, Espoo, Finland. August 16 – 19 2016 Chemical interactions, lateral heterogeneity, and the lipid zoo. Lipidomic studies...

COURSES / EVENTS 07/06/2016

Winter School: Biology at different scales

Winter School in Les Houches, France March 13 – 25 2017 The school will focus on the interplay between physics and biology to understand biological...



EVENTS / MEETINGS 15/05/2016

Membrane pores: from structure and assembly, to medicine and technology

The Royal Society, London, June 27 – 28 2016 Biological membranes define and protect living cells. Proteins can open aqueous pores through these barriers. Such...

EVENTS / MEETINGS 15/05/2016

Physics Meets Biology

Organised by the IOP Biological Physics Group Biologically inspired Physics is an extraordinarily wide field, covering the behaviour of systems from single molecular machines to...

EVENTS / MEETINGS / NEWS 14/05/2016

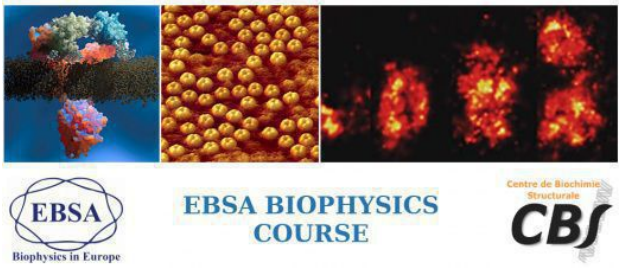
5th International Iberian Biophysics Congress

June 15th – 17th, 2016, Porto (Portugal). Congress Web Site: http://www.iberianbiophysicscongress.pt Abstracts Book Deadlines Application for grants: March 24th 2016 Abstract submission and early...

EVENTS / MEETINGS 05/05/2016

41st FEBS Congress

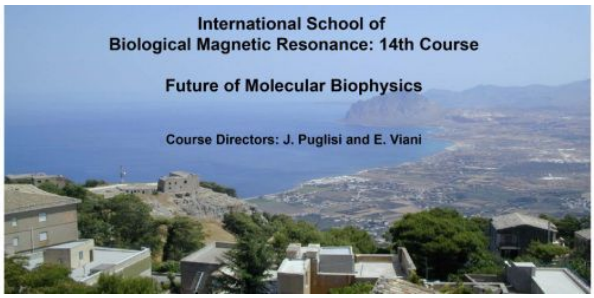
September 03 – 08, 2016, Ephesus (Turkey). The FEBS Congress aims to provide an outstanding international forum in the European area for the face to...



COURSES / EVENTS 05/05/2016

Membrane and lipid-protein interactions

EBSA Biophysics course La Grande Montte, Montpellier (France), September 11th – 16th 2016 . DEADLINE: Early registration closes 15th July 2016. Late registrations (with a...



COURSES / EVENTS 01/04/2016

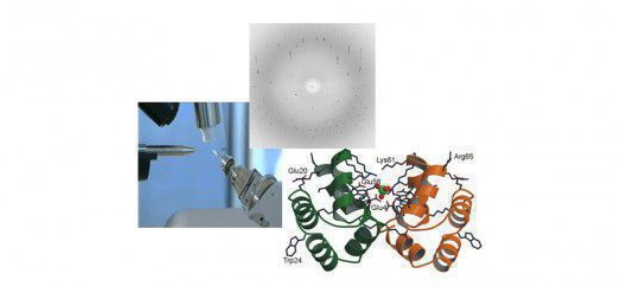
14th International School of Biological Magnetic Resonance

Future of Molecular Biophysics Ettore Majorana Centre, Erice Sicily (Italy), May 7th – 17th 2016 . This course focuses on recent advances in molecular biophysics...

EVENTS / MEETINGS 09/02/2016

13th Nanospain Conference

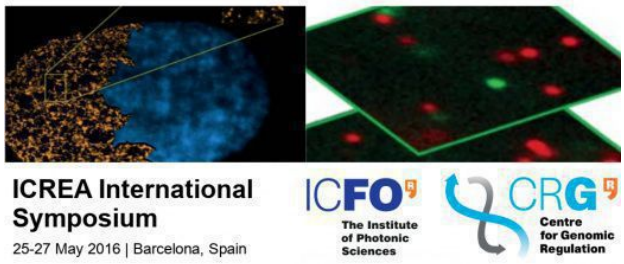
Nanoscience & Nanotechnology in Spain Rioja Forum, Logroño (Spain), March 15th – 18th 2016. DEADLINES: Abstract submission and oral request: February 15th 2016. Since 2004,...



COURSES / EVENTS 04/02/2016

7th Macromolecular Crystallography School – MCS2016

MCS2016 7th Macromolecular Crystallography School. May 25th – 29th 2016, CBE (Department of Crystallography and Structural Biology) of the Institute of Physical-Chemistry "Rocasolano", CSIC, Madrid...



EVENTS / MEETINGS 04/02/2016

BioNanoVision of cellular architecture: from the nucleus to the cell membrane

25 – 27 May 2016, ICFO – the Institute of Photonic Sciences, Barcelona, Catalonia (Spain). BioNanoVision will bring together a multidisciplinary group of world-leading scientists...

EVENTS / MEETINGS 05/05/2016

Biomembrane days – 2016

Organized by the Max Planck Institute of Colloids and Interfaces and Collaborative Research Centre 958 'Scaffolding of Membranes'. September 05 – 07, 2016, Berlin (Germany)....

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

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