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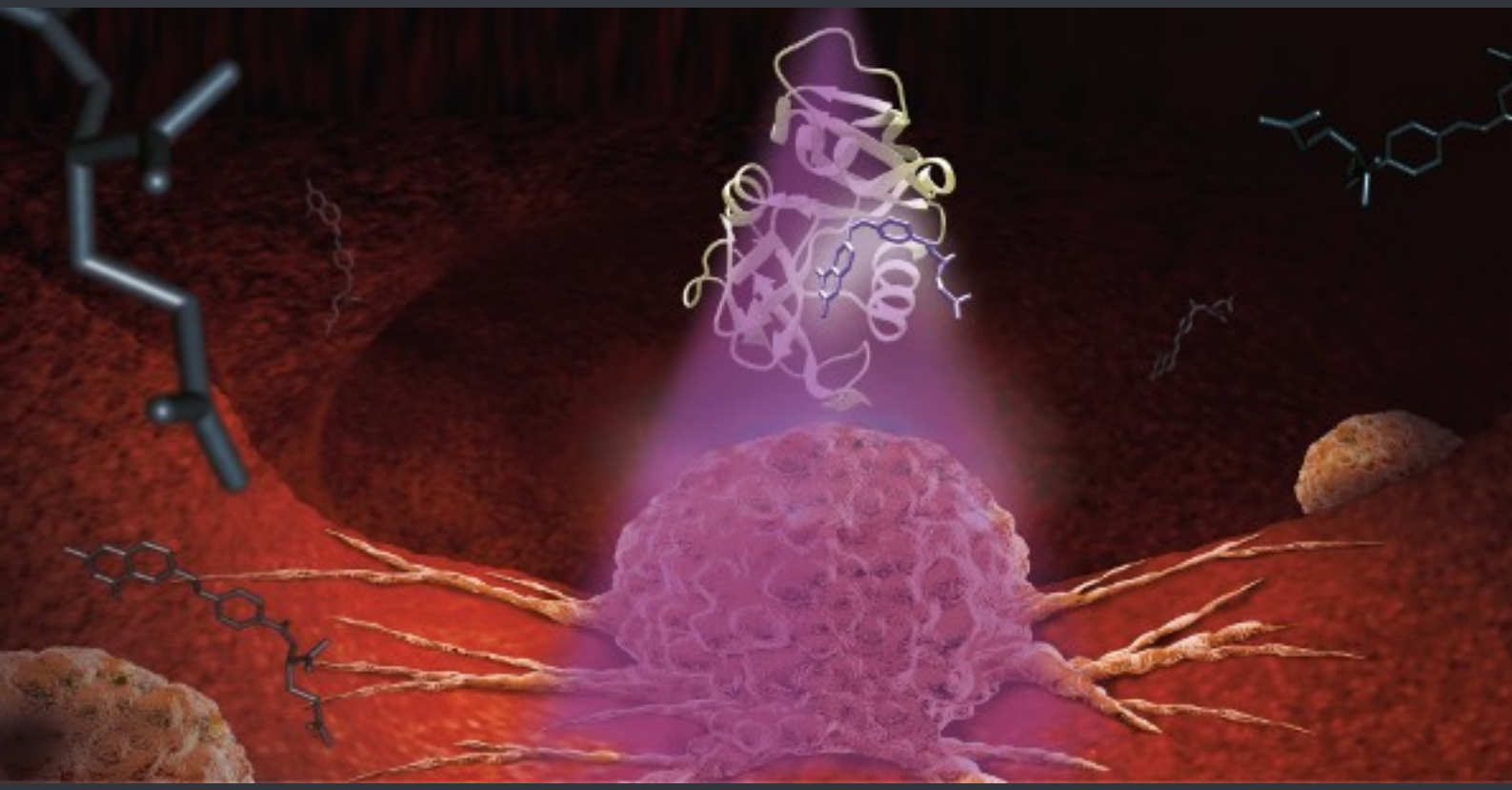

Cover image:
Courtesy of Pau Gorostiza
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About the Cover Image:

Rational structural modifications of the chemotherapy agent methotrexate enabled control of cytotoxic efficacy with light. In vitro and in vivo experiments showed that the new compound, named phototrexate, behaves as a potent antifolate in its photoactivated configuration, and that it is nearly inactive in its thermodynamically stable state. The insights provided by this work open up new possibilities for developing innovative agents for light-controlled precision chemotherapy.
Fom Matera et al., J Am Chem Soc 2018, 140: 15764. ***Image credit: Carlo Matera & Grafino.it.***

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In this issue

Biofísica Magazine

EDITORIAL / ANALYSIS

Surfing the preprint wave

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Many scientists feel trapped in a rat race these days. There is very high competition for limited resources and the time devoted to *red tape* activities is growing and growing. It is hard to get away from the feeling that scientists' top priority is to secure funding, and that this can only be achieved by publishing papers. Otherwise, you're out of business. Indeed, we tend to forget that our main goal is instead making discoveries and producing scientific and technical advances. It is certainly true that reporting on our findings, generally in the form of *peer-reviewed* papers, is a necessary step that contributes to the advancement of science. Publications allow our colleagues to judge the novelty, correctness, and impact of our scientific work, and eventually apply the new findings to the benefit of their own work. Publications also make possible that the scientific novelties can reach *the society*, which is the ultimate funder of the scientific enterprise.

However, how should scientific publishing be performed? Countless opinion articles and editorials have been devoted to that question, analyzing specific issues such as peer review [1], business model [2], evaluation of impact [3], open access [4] and the role of the new information technologies [5]. Here, we focus on preprints, a form of publication that touches on several critical issues of scientific reporting.

The core concept of preprints is very simple. Preprints are manuscripts that are made freely available, usually through dedicated web servers such as arXiv or bioRxiv, prior to or during peer review. Since peer review is considered the fundamental pillar on which the advancement of science relies, it comes as no surprise that the scientific community does not agree on whether preprints are a good idea or not [6, 7]. Proponents argue that preprinting does not substitute for peer review, but instead is a manner of improving it. Indeed, a majority of preprints end up being published in traditional, peer reviewed journals [8].

Top-notch funding agencies are embracing the preprint concept and allowing references to preprints in grant applications

For scientists, there are many potential advantages associated with preprints. A main one is that preprints disseminate results avoiding the time constraints imposed by standard peer review and editorial processes. Moreover, preprints are by nature and definition deposited in electronic format and distributed via the internet, which allows Immediate and unlimited access from anywhere in the world. In contrast, classical publishing of a paper in its final form can take months, if not years. Such slowness of scientific publication can be detrimental for scientists applying for funding or planning to move to a new job. In those cases, preprints can be also advantageous for hiring committees and evaluation panels, as they can get a better assessment of the latest research by the candidates, objectivizing references to submitted and under review statements.

Even in the absence of pending evaluations, preprints can help scientists to keep their spirits high in the long way to publish a paper. Being able to share a brand-new manuscript with the community is definitely a gratifying feeling. Top-

notch funding agencies, such as the NIH, the ERC and the Wellcome Trust, are embracing the preprint concept and allowing references to preprints in grant applications [7, 9]. In addition, open access requirements by funding agencies may be fulfilled by posting preprints.

Some editors do check on preprint servers to assess the impact of manuscripts

An interesting feature of preprint servers is that they provide direct impact measurements, such as number of abstract views and downloads. Although this novelty could also be used by any other type of publication distributed online, it has specially been embraced by preprint systems, where the free access character increases the statistical significance of text views and downloads. Jonathan Wilde, a postdoctoral scientist at MIT, tweeted recently "Another reason to love @biorxivpreprint: paper got rejected, but looking at the preprint's metrics and seeing that 1,000 people have viewed and 500 have downloaded reminded me that our work is important and interesting." Thanks to preprint servers, the assessment of impact does not depend just on the opinion of a few editors, but on metrics that report directly on the interest of the scientific community. Indeed, some editors do check on preprint servers to assess the impact of manuscripts. It is not uncommon that editors invite the authors of a preprint to submit to their journals.

Preprints are also very good to publicize results. Indeed, papers that have gone through a preprint phase gather more citations [6]. Kresten Lindorff-Larsen, a Professor at the Department of Biology of University of Copenhagen, has tweeted: "Yet another advantage of authors posting a preprint is that we can have a journal club on the paper before reviewing it". That means more students and postdocs will be exposed to the manuscript. Also, many scientists feel attracted by the feeling of novelty and immediacy brought by preprints, so they sign up for general alerts provided by preprint servers. This way, they can come across interesting findings that may have gone unnoticed otherwise.

A preprint can also be used to gather pre-submission feedback. Scientist can easily distribute preprints to colleagues in the quest for feedback – a nice strategy if we consider that those colleagues may also end up acting as reviewers for a traditional journal. Proponents argue that the preprint system can improve the overall quality of scientific production [10]. Preprint servers enable comment tools to favor discussion, although the system does not seem to be popular among scientists yet. Instead, controversial topics usually trigger publication of several preprint articles, an indication of what could be expected in the future for most fields. There is a growing interest in post-review strategies and preprints seem to be an effective way to have papers reviewed by many peers, and not just the three reviewers picked by an editor. There are even initiatives, such as Peer Community, to integrate preprinting and peer-reviewing and release formal recommendations by distinguished scientists.

Although the preprinting system has been used by the Physics community for almost 30 years now, fields such as Biology and Medicine have just started to experience it and many in these latter fields are reluctant to preprints [6, 8]. In these very competitive fields, the concerns that posting preprints can increase the risk of being scooped are common. As a matter of fact, posting a preprint is like talking about unpublished results in a conference attended by (potentially) the entire world population. The manner to handle the scoop frighten is evolving. Some journals like those published by EMBO are offering scooping protection to preprint manuscripts by accepting publication within a reasonable time since preprinting, even if another paper is published in the

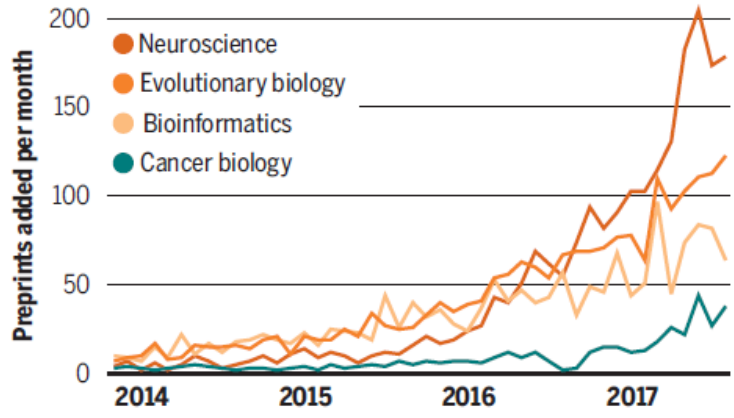

Figure 1. Per month preprints of articles from biology related fields. The number of posted preprints has increased considerably over the last few years. Data and graph by Jordan Anaya (PrePubMed). Adapted from reference [8].

interim [8]. Indeed, preprints challenge the traditional manner of claiming priority on a finding. Many would agree that reporting a finding in a preprint sets the priority on the finding.

Another major concern, especially in the medical sciences, is that fully citable preprints may decrease the quality of scientific literature [6]. Is it OK to make publicly available prior to peer review results that can impact clinical practice? Again, this is an ongoing discussion [6, 7, 10], but several leading medical journals, such as The New England Journal of Medicine, do not currently accept manuscripts that have been posted as preprints. Also, there is concern that the media can feed from preprints as if they were peer-reviewed articles, potentially providing misleading or inaccurate information to the general public [11].

Available data suggests that preprints are here to stay. The scientific community is just adjusting to this reality. Top funding agencies and philanthropists such as the Chan Zuckerberg Initiative are formally supporting the movement [8]. The last years have seen a sharp increase in the number of posted preprints and the prediction is that figures will grow even more over the next few years [8] (see accompanying Figure). In this context, it will be interesting to see whether the medical sciences find suitable preprinting strategies. As of today, many scientists feel at risk of being scooped when posting their first preprint. To them, here are some reassuring words from NIH Director Francis Collins "I've yet to see any instance where somebody was harmed by that early reveal of the work that they're doing" [8].

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Biofísica Magazine

BEYOND BIOPHYSICS

Biochemistry and Biophysics

A conversation with Félix Goñi

Vadim Frolov, *BIOFISIKA UPV/EHU, CSIC, Leioa (Spain)*.

It is natural, for a biophysicist, to reflect upon what biophysics is, here and now. These meditations occur mostly over a beer, as the subject is old, almost classical, dating back to the emergence of the term ***biophysics*** in Pearson´s musing, in 1892, where it replaced ***etiology***, emphasizing the primacy of physics laws over capricious and complex living matter. Though the word stays, its meaning keeps evolving, as each mature biophysicist nurtures his unique one. History proves that biophysics is notoriously hard to define, its true essence remaining elusive. In Wikipedia, multiple subfields are invoked in an attempt to clarify the matter, linking biophysics to almost everything, from math to myth. This is telling. Recognizing that biophysics has become a unique interdisciplinary hub does help improving our self-esteems (and funding). More importantly, it indicates that the intangible nature of biophysics could be grasped in its interactions with other scientific disciplines.

The intangible nature of biophysics could be grasped in its interactions with other scientific disciplines

This beyond-Biophysics series has already touched upon many of such interactions, successively revealing multiple facets of *biofisica*. The approach looked smart and smooth, so when the Jesús Salgado proposed biochemistry as the next subject I agreed, with some hidden enthusiasm, to quiz an exclusive expert: Félix Goñi, one of the founders of the Spanish Biophysical Society (aka SBE) and, concurrently, an extremely prolific member of the Spanish Society of Biochemistry and Molecular Biology (aka SEBBM), from which SBE branched off several decades ago. He should know firsthand how biophysics and biochemistry interact, in life and on paper.

Yet, after some reflection, I felt hesitant on what to focus. At first glance, synergistic interaction between the two disciplines is obvious. No meaningful studying of intricate transformations of living matter can be conducted without identifying key molecular players, underscoring the fundamental role of biochemical analyses. On the other hand, the intrinsic complexity of biological systems has always attracted physicists. Richard Feynman summarized this appeal decades ago:

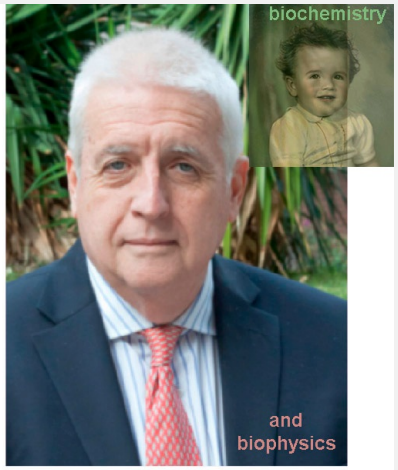
> *I am inspired by the biological phenomena in which chemical forces are used in a repetitious fashion to produce all kinds of weird effects.*

Naturally for a physicist, such ***weird effects*** are to be scrutinized by rigorous physical modeling. Yet, as Manfred Eigen noticed, while many biologists would “certainly admit that one can simulate biological phenomena by models that can be expressed in a mathematical form”, they would not accept “that biology can be given a theoretical foundation that is defined within the general framework of physics”. Well, biochemists might be different species. As I have noticed

through years, they are widely represented in various biophysical gatherings, indicating an intrinsic drive towards biophysical methods, if not thinking. I wondered whether exploring this phenomenon could help understanding biophysics *per se*.

Biochemists are widely represented in various biophysical gatherings, indicating an intrinsic drive towards biophysical methods, if not thinking

So I went up to Félix´s despacho. I must confess that established biophysicists rarely discuss their subject, it is *un peu démodé*. Jesús´ ingenious plan was to appeal to the biochemistry alter ego. However, Félix traced it even further, beyond biochemistry, back to his MD times, when he first realized that a rigorous quantitative approach might help saving a failing biological machinery. From there he goes along a lengthy, illustrious path, beginning with submersing into emerging fields of quantitative biochemistry, with the help of Gulbenkian Foundation. Next, feeling the needs of synthetic analysis, he approached Dennis Chapman to learn how physics, chemistry and biology work together yielding both structural information and mechanistic paradigms. There he became fond of lipids, that greasy substance fundamental for organization of living matter. Later on, Félix founded the Biophysics Unit, one of the first biophysics centers in Spain, with the specific focus on lipids and membrane biophysics. Sic! His favorite toys became model, synthetic membrane systems, such as supported lipid bilayers and giant blobby vesicles colored by different fluorescent markers. Those were quite in fashion back then, equally inspiring for physicists and biologists.



Prof. Félix Goñi (BIOFISIKA, CSIC and UPV/EHU), portrayed as an *incipient* biochemist (top-right) and as *mature* biophysicist (bottom).

Yet, Félix remained firmly focused, sprinkling the basic lipid toys with bioactive compounds, purified proteins and lipids, implicated in different cellular pathologies. He uses lipid templates as a tool for quantitative reconstitution of biology, albeit in a very reduced form. Though such reductionist approaches are often criticized, in vitro mechanistic analysis, one of the major achievements of biophysical chemistry, has been proved extremely useful, if not indispensable, in the functional analyses of complex intracellular processes. Here I should invoke Feynman again, with his “What I cannot create I do not understand”.

Perhaps, that is what we intuitively expect from biophysics: the knowledge enabling (re)creation of biology. With the biochemical toolkits in hands and with deep learning methodologies becoming widely available, we should be able to reconstruct increasingly more complex structures and behavior, hopefully with required caution and responsibility. But this will be the next topic: *biophysics and machine learning*.

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Biofísica Magazine

COOL BIOPHYSICS

Ancestral proteins: How and why

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Strictly speaking, ancestral proteins are proteins from extinct organisms. However, neither extinct organisms nor their proteins exist any more, which raises two questions. First, can we bring ancient proteins back? De-extinction of, for instance, the woolly mammoth or the passenger pigeon, is being discussed as a real possibility for a not too distant future [1]. A protein is certainly a much simpler system than a whole animal. But, and this is the second question, why should we want to *bring ancient proteins back to life* in any case (besides the fact that some people may think that it is a cool idea)?

Can we bring ancestral proteins back? Yes, but with some peculiarities

As to the first question (can we bring ancestral proteins back?), the answer is certainly yes, but with some peculiarities that must be noted. De-extinction of the woolly mammoth would require, first of all, finding mammoth DNA in preserved tissue remains. This is a real possibility since mammoths became extinct a few thousand years ago. However, with a few exceptions, individual proteins of this age are not expected to be of much interest by themselves because of the small sequence differences with their modern counterparts. Proteins from organisms that existed millions or even billions of years ago, on the other hand, will display substantial sequence differences with modern proteins and are a priori more interesting targets for *protein de-extinction*. However, finding useful DNA in fossils of those ages is extremely unlikely.

On the other hand, phylogenetic and bioinformatics analyses of modern protein sequences can lead to plausible approximations to the sequences of their ancestors. This process is similar to the reconstruction of words of extinct languages (**Fig. 1**) from the words in modern languages by using suitable models of language evolution [2]. Of course, once ancestral sequences are available, standard molecular biology methodologies can be used to prepare in the laboratory the proteins encoded by the reconstructed sequences. In the jargon of the field, this second step of the process is referred to as ancestral protein resurrection. At the time of writing, over 50 protein systems have been studied using sequence reconstruction followed by laboratory resurrection [3] and some of these studies have targeted phylogenetic nodes close to last common ancestor of life. Admittedly, what these studies have brought *back to life* are only plausible approximations to the proteins that existed long time ago.

As to the second question (why should we want to *resurrect* ancestral proteins?) there are actually two quite different, but also quite convincing, answers. First, research carried out in the last ~25 years has demonstrated that resurrected ancestral proteins may provide useful tools to address important problems in evolution. Secondly, more recent work has emphasized the potential biomedical and biotechnological implications of ancestral protein resurrection. Illustrative examples of these two applications are briefly described below.

Many people consume alcoholic drinks on a regular basis and some of them eventually develop serious health conditions related with alcohol consumption. One possible explanation for our *problems with alcohol* is simply that alcohol has appeared recently in our diet and that, therefore, we have not had time to adapt to it. One could argue that

the incorporation of alcohol in the diet is a consequence of the development of agriculture and the use of fermentation to process food. Agriculture originated a few thousand years ago, which is indeed a very short time in evolutionary terms. Benner and coworkers [4] recently resurrected ancestral alcohol dehydrogenases and found an increase in the ability of these enzymes to degrade alcohol at about 10 million years ago. This result supports a quite different evolutionary narrative. There is evidence that, about 10 million years ago, our ancestors left the top of the trees for the floor of the jungle and, consequently, gained access to fruit with a significant content of alcohol (i.e., fruit dropped from the trees that had undergone fermentation). It is likely, overall, that alcohol appeared in the diet of our ancestors millions of years before the development of agriculture.

In a similar study, Gaucher and coworkers [5] used ancestral protein resurrection to gain insight into the evolutionary origin of high uric acid levels in humans. The immediate cause of hyperuricemia is of course known: we, humans, do not synthesize uricase, the enzyme that degrades uric acid in most animals. This is linked to the pseudogenization of the uricase gene due, among other alterations, to a mutation that introduced a stop codon.

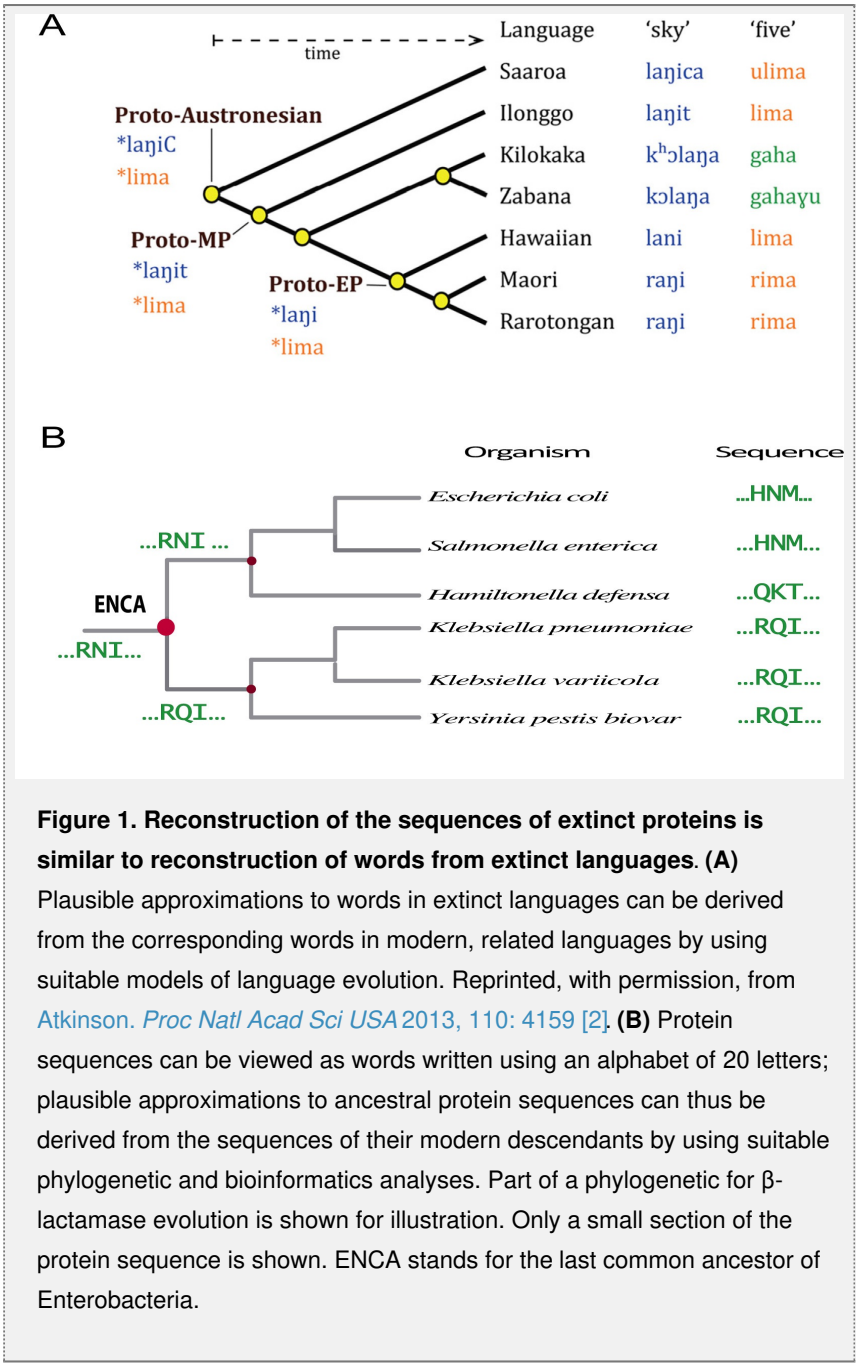

Figure 1. Reconstruction of the sequences of extinct proteins is similar to reconstruction of words from extinct languages. (A) Plausible approximations to words in extinct languages can be derived from the corresponding words in modern, related languages by using suitable models of language evolution. Reprinted, with permission, from Atkinson. *Proc Natl Acad Sci USA* 2013, 110: 4159 [2]. **(B)** Protein sequences can be viewed as words written using an alphabet of 20 letters; plausible approximations to ancestral protein sequences can thus be derived from the sequences of their modern descendants by using suitable phylogenetic and bioinformatics analyses. Part of a phylogenetic for β-lactamase evolution is shown for illustration. Only a small section of the protein sequence is shown. ENCA stands for the last common ancestor of Enterobacteria.

Resurrected ancestral proteins helps addressing problems in evolution

This seemingly simple explanation poses, however, additional questions in an evolutionary context. At the molecular level, evolution is, to some substantial extent, *purifying natural selection* that efficiently eliminates, at least in large populations, deleterious mutations. It is, therefore, puzzling that inactivating alterations of the uricase gene occurred in the line of descent that leads to humans.

One possible solution is that high levels of uric acid are actually advantageous under some circumstances. However, it is not at all clear what these advantages may be. In fact, all the consequences of high uric acid levels in humans (gout, kidney stones, etc.) appear to be harmful. To clarify these issues, Gaucher and coworkers resurrected ancestral uricases and determined their activity levels (**Fig. 2**). They found that the capability of uricase to degrade uric acid had continuously decreased before the events that led to the pseudogenization of the uricase gene. This decrease occurred at the end of the Oligocene, a period of environment cooling which made it difficult for our ancestors to find fruit, their likely staple food. However, uric acid facilitates the accumulation of fat from the metabolism of fructose by upregulating some of the enzymes involved.

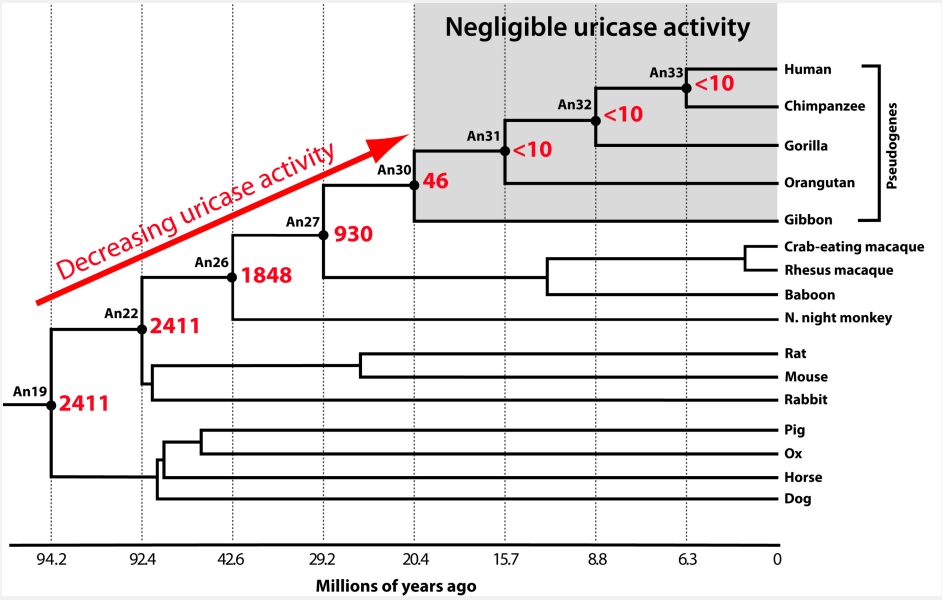

Figure 2. Evolutionary history of uricases as revealed by ancestral protein resurrection. Numbers in red are a metric of uricase activity. A gradual decrease in activity is observed before the pseudogenization events that led to the lack of uricase in humans and other primates. The decrease likely allowed our ancestors to accumulate fat from the metabolism of fructose (see text for details). This figure is modified with permission from figures originally published in Kratzer et al. *Proc Natl Acad Sci USA* 2014, 111: 3763 [5].

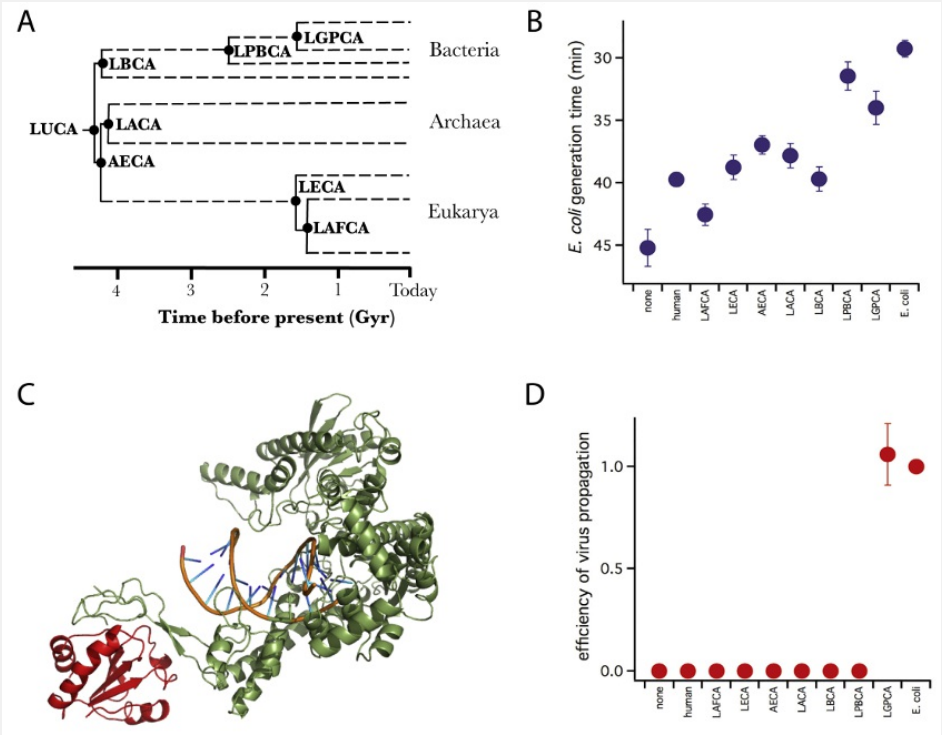

Figure 3. Ancestral enzymes in modern organisms. **(A)** Schematic phylogenetic tree used in the reconstruction of ancestral thioredoxins. **(B)** Replacement of E. coli thioredoxin with resurrected ancestral thioredoxin impairs *E. coli* fitness, as revealed by generation time determinations; a gradual dependence with evolutionary distance is, however, observed and some ancestral thioredoxins show substantial functionality within *E. coli*. **(C)** Bacteriophage T7 recruits thioredoxin (red) for its replisome, where it is involved in a strong and specific interaction with the thioredoxin binding domain of the virus polymerase gp5 (green). **(D)** Most ancestral thioredoxins cannot be recruited and block virus propagation. Figures in panels **B** and **D** are from Delgado et al. *Cell Rep* 2017, 19: 1247 [6], *Open Access* (CC BY-NC-ND 4.0 2017).

High levels of uric acid helped, therefore, our ancestors survive periods of fruit scarcity. Of course, the conditions that conferred some advantage to high uric acid levels are no longer relevant, at least in developed countries. However, there is no simple way to *unevolve* the mutational changes that led first to a decrease in uricase activity and then to the pseudogenization of the uricase gene. We are, therefore, stuck with high uric acid levels and its harmful consequences.

A given ancestral protein may preserve normal functionality and, at the same time, prevent infection by a given pathogen

Proteins often interact *in vivo* with a large number of macromolecular components. Replacing a modern protein within a modern organism with one of its resurrected ancestors will, therefore, affect many biologically relevant intermolecular interactions. There are, however, two sides to this coin. On the one hand, organismal fitness may be impaired by the replacement because the *in vivo* functionality of the replaced protein and its interacting partners will be compromised. On the other hand, the replacement might help the organism evade pathogens. The reason is that pathogens and their hosts co-evolve and a successful pathogen has evolved to efficiently recruit the proteins of its host for its own purposes. The possibility arises then that a given ancestral protein may hit the sweet spot where the normal functionality is preserved to a significant extent and, at the same time, a given pathogen is prevented from infecting the organism.

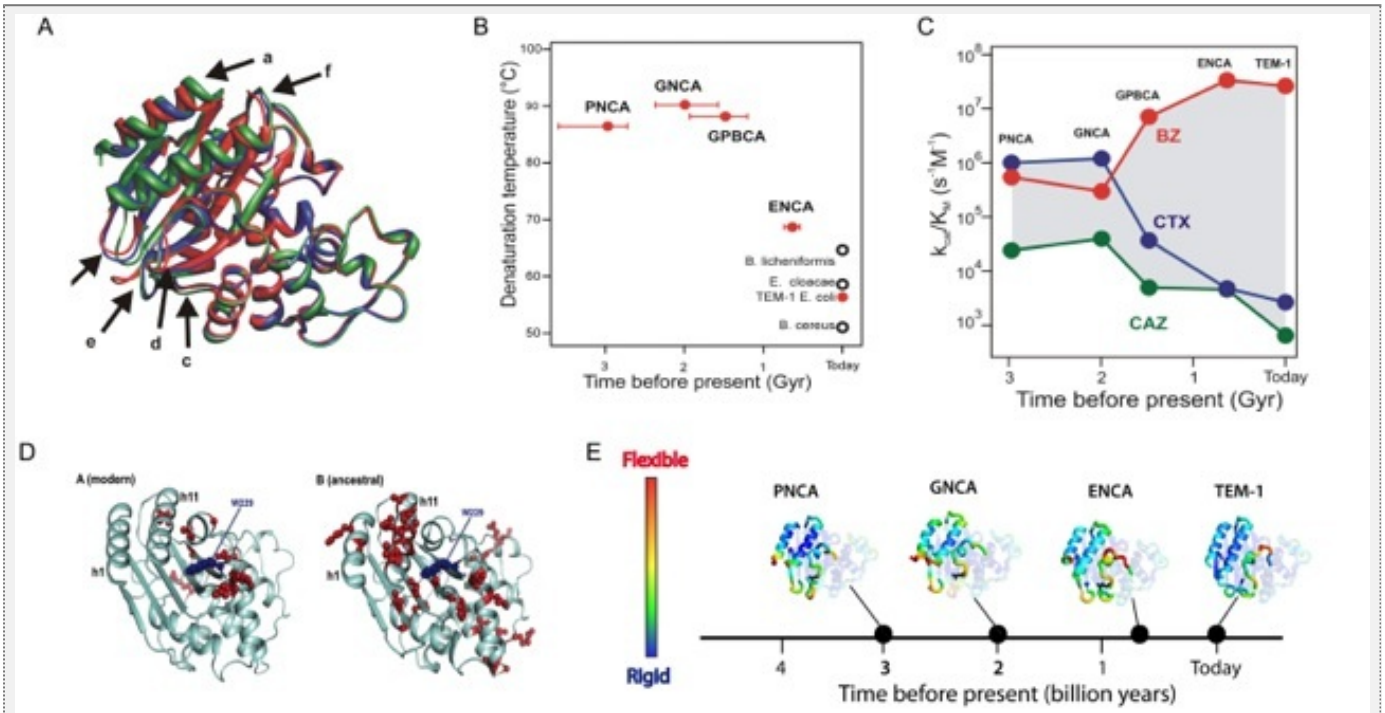

Figure 4. Enhanced stability and substrate promiscuity in resurrected ancestral lactamases (A) Ancestral and modern lactamases share the canonical lactamase fold. **(B)** Still, lactamases from 2-3 billion-year phylogenetic nodes show denaturation temperatures 30-35 degrees above the typical values for modern mesophilic lactamases. **(C)** Furthermore, the "oldest" lactamases can degrade efficiently different lactam antibiotics (BF: benzylpenicillin; CTX: cefotaxime; CAZ: ceftazidime) while the modern TEM-1 lactamase is a penicillin specialist that shows very low activity levels with third-generation antibiotics (such as CTX and CAZ). This promiscuity is linked to conformational diversity/flexibility as shown by NMR-relaxation studies **(D)**, which show a larger number of residues with dynamic contributions in the µs-ms time range (labeled in red), and by molecular dynamics simulations **(E)**. Figures in panels **A**, **B** and **C** are reproduced with permission from Risso et al. *J Am Chem Soc* 2013, 135: 2899 [7], *Copyright* 2013, American Chemical Society. Figures in panels **D** and **E** are reproduced from Risso et al. *Nat Commun* 2017, 8: 16113 [9], *Open Access* (CC BY 4.0 2017).

To explore this possibility, we recently replaced the thioredoxin within *E. coli* with several resurrected Precambrian thioredoxins [6]. Thioredoxins are general oxido-reductases in all known cells but, in addition, *E. coli* thioredoxin is a

proviral factor for the phage T7, a virus that infects *E. coli*. The phage recruits thioredoxin for its replisome where it binds strongly and specifically to the viral gp5 polymerase (**Fig. 3**), an interaction that is essential for replisome efficiency. Some resurrected ancestral thioredoxins showed acceptable levels of functionality within *E. coli* as revealed by the determination of generation times, but could not be recruited by the virus for its replisome, thus preventing virus propagation within *E. coli*. More generally, these results suggest an approach to the engineering of pathogen-resistant crops.

Instead of using modern proteins as starting point for engineering, we would use resurrected ancestral proteins

Resurrected ancestral proteins may display properties that are useful in scaffolds for protein engineering. Enhanced stability, for instance, is a common outcome of ancestral resurrection, likely linked to the thermophilic nature of primordial life. Also, resurrected ancestral enzymes are often found to be able to catalyze several more or less related reactions. This catalytic promiscuity may reflect the generalist nature of primordial enzymes or may be the result of having targeted pre-duplication nodes in the evolution of new functions. In any case, promiscuity is likely linked to conformational flexibility/diversity, i.e., to the capability to populate a diversity of conformations and it is a feature that, together with enhanced stability, should contribute to protein evolvability. That is, enhanced stability and conformational diversity contribute to the capability of a protein scaffold to generate new functionalities by allowing functionally useful but destabilizing mutations to be accepted and by promoting the efficient search of functionally competent conformations [**7**, **8**].

A few years ago [**7**], we found resurrected ancestral lactamases to combine these two features (**Fig. 4**) and, more recently [**9**], we have used a simple minimalist design to generate a *de novo* enzyme functionality in these ancestral lactamases (**Fig. 5**). Remarkably, the same minimalist approach consistently failed when we used modern lactamases as scaffolds for engineering. The engineering of new enzymes capable of catalyzing non-natural reactions is one of the most important unsolved problems in protein science. It is also a goal with enormous biotechnological implications. Our results [**9**] suggest that a molecular version of Gould's "replaying the tape of life" experiment [**10**] could provide a useful approach in this context. That is, instead of using modern proteins as starting point for engineering, we would use resurrected

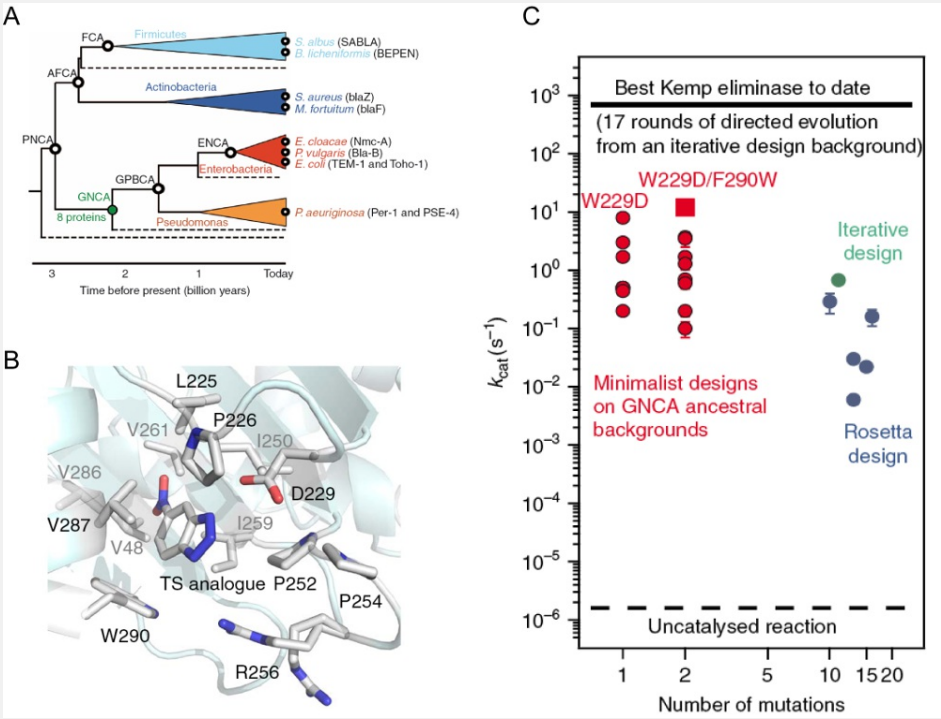

Figure 5. Using resurrected ancestral lactamases as scaffolds for the engineering of new active sites. **(A)** Schematic representation of the phylogenetic tree used for the reconstruction of ancestral lactamase sequences. **(B)** A simple minimalist design based on 1-2 mutations generates de novo catalysis for the Kemp elimination when using the ancestral lactamases as scaffolds; the figure shows the new active site generated with a bound transition-state analogue. **(C)** The levels of catalysis achieved compare well with previous rational designs and are less than two orders of magnitude from the best Kemp eliminase reported to date which was the outcome of 17 rounds of directed evolution. Reproduced from Risso et al. *Nat Commun* 2017, 8: 16113 [9], *Open Access* (CC BY 4.0 2017).

ancestral proteins. Modern
proteins are often highly specialized and it is difficult to teach an old dog new tricks. On the other hand, some resurrected ancestral proteins at least represent early stages of molecular evolution at which new functionalities were generated. Plausibly, their evolution could then be replayed in the laboratory and directed towards new functionalities of biotechnological interest. This is indeed an exciting possibility that it is being actively pursued by several groups in the field.

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EVENTS / MEETINGS

Joint 12th EBSA 10th ICBP – IUPAP Biophysics Congress

12th EBSA 10th ICBP – IUPAP Biophysics Congress
Biophysics for Life and Technology
Madrid, 20 – 24 July 2019
Important Dates
Bursaries deadline: 15 March 2019
Abstract submission deadline: 20 March 2019
Abstract notification for Oral Presentations: 4 April 2019
Presenters registration deadline to be published in Abstract book: 15 April 2019
Early registration deadline: 30 April 2019

For more information, please visit the EBSA 10th ICBP – IUPAP Biophysics Congress Website.

Biofísica Magazine

AWARDS / SBE PRIZES

SBE Prizes 2019 – Call for Nominations

The 2019 call for nominations to SBE Prizes is now open

The SBE offers yearly special awards to recognize excellence in the field of Biophysics. These prizes are given in the following three categories:

'MANUEL RICO' – BRUKER PRIZE

DEADLINE MARCH 8TH 2019

> *Recognizes an outstanding Biophysics career, performed in Spain mainly during the last 10 years.*

Sponsored by

Bruker España S.A..

Addressed to

Biophysicists working on Structure/Function of molecules who develope their main activity in Spain. **Preference** is given to members of the SBE .

Award

3000 € and a talk delivered by the awardee during a special session of the Joint 12th EBSA 10th ICBP-IUPAP Biophysics Congress (Madrid, Spain, 20th – 24th July 2019).

How to apply

E-mail a letter to José Miguel Mancheño, addressed to the President of the SBE (Dr. Jesús Pérez-Gil), attaching a *Curriculum vitae* and a summary of your most relevant scientific achievements.

More information

See *here* the Complete Bases and instructions to apply .

Past winners of this prize

2018: F. Javier Luque (Barcelona)
2017: Alicia Alonso (Bilbao) and María García-Parajo (Barcelona)
2016: F. Xavier Gomis-Rüth (Barcelona)
2015: Juan A. Hermoso (Madrid)
2014: Óscar Llorca (Madrid)
2013: José Manuel Sánchez Ruiz (Granada) and Félix Ritort (Barcelona)
2012: Antonio V. Ferrer Montiel (Elche-Alicante) and Marta Bruix (Madrid)
2011: Ignacio Fita (Barcelona)
2010: Modesto Orozco (Barcelona) and José Luis Rodríguez Arrondo (Bilbao)
2008: José García de la Torre (Murcia)
2006: Jesús Pérez Gil (Madrid)
2004: Javier Sancho (Zaragoza)
2002: José María Valpuesta (Madrid)
2000: Miquel Pons (Barcelona)
1998: Rafael Picorel (Zaragoza)

'E. PÉREZ PAYA' – SBE 40 PRIZE

DEADLINE MARCH 8TH 2019

> *Recognizes the trajectory of a Biophysicist with age limit of 40 with a special contribution to the progress of Biophysics in Spain.*

Sponsored by

BCN Peptides and Prima – Derm.

Addressed to

Biophysicists with age limit of 40 (by December 31st 2017) who develope their main activity in Spain. **Preference** is given to members of the SBE and to achievements from the last 10 years.

Award

1500 € and a talk delivered by the awardee during a special session of the Joint 12th EBSA 10th ICBP-IUPAP Biophysics Congress (Madrid, Spain, 20th – 24th July 2019).

How to apply

E-mail a letter to José Miguel Mancheño, addressed to the President of the SBE (Dr. Jesús Pérez-Gil), attaching a *Curriculum vitae* and a summary of your most relevant scientific achievements.

More information

See *here* the Complete Bases and instructions to apply .

Past winners of this prize

2018: Pere Roca-Cusachs (Barcelona)
2017: Emilio J. Cocinero (Leioa-Bizkaia) and Carlo Manzo (Vic-Barcelona)
2016: Raúl Pérez-Jiménez (San Sebastian)
2015: Irene Diaz Moreno (Sevilla)
2014: Fernando Moreno (Madrid)

Sponsored by SBE and Werfen-Izasa-Beckman-Coulter:
2013: Xavier Salvatella (Barcelona)
2012: José Manuel Gómez Vilar (Lejona-Vizcaya)
2011: Teresa Giráldez (La Laguna)
2010: Pau Bernardó (Barcelona)

ANTALGENICS – SBE 33 PRIZE

DEADLINE MARCH 8TH 2019

> *Recognizes a young Biophysicist with age limit of 33, who have contributed significantly to the developmen of Biophysics, in Spain and/or abroad.*

Sponsored by

AntalGenics.

Addressed to

Outstanding young Biophysicists with age limit of 33 (by December 31st 2017), independently of the country where their work has been done. **Preference** is given to members of the SBE.

Award

1000 € and a talk delivered by the awardee during a special session of the Joint 12th EBSA 10th ICBP-IUPAP Biophysics Congress (Madrid, Spain, 20th – 24th July 2019).

How to apply

E-mail a letter to José Miguel Mancheño, addressed to the President of the SBE (Dr. Jesús Pérez-Gil), attaching a *Curriculum vitae* and a summary of your most relevant scientific achievements.

More information

See *here* the Complete Bases and instructions to apply .

Past winners of this prize

2018: Joan Camunas-Soler (Stanford)
2017: María Queralt-Martín (Bethesda) and Álvaro Inglés (Klosterneuburg)
2016: Lorena Redondo-Morata (Marseille)
2015: Cecilia Artola (Madrid)

2014: Jorge Alegre Cebollada (Madrid)
2013: Anna Shnyrova (Bilbao)
2012: Sergi García Manyes (London)

Biofísica Magazine

SBE PRIZES

Imagin'Action image contest 2019

SBE announces the fourth "IMAGIN'ACTION" image contest!

> *Launched on February 2019 on the SBE social media and websites.*

Deadline and how to participate

Submit your images in electronic format by e-mail to community.manager@sbe.es before April 30th, 2019.

Extract of *Rules*

Download *here* the complete official rules

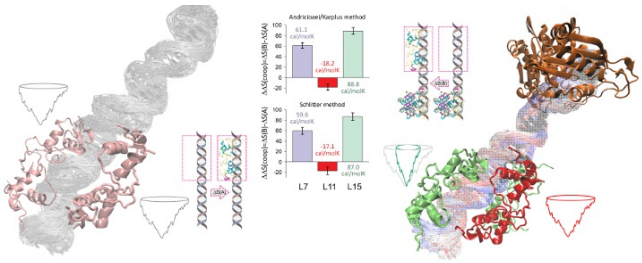
- Submissions are limited to max 3 images per contestant.
- Images may be obtained by any method, but must have a direct connection to biophysics.
- All images submitted must include a title and a short description (max. 50 words).
- The winner will be chosen among pre-selected images (max. 10) as a result of the following procedure: **a)** 50% out of Popular vote in SBE social media: / (between May 10th, 2019 and May 31st, 2019. **b)** 50% out of punctuation given by a panel of judges.
- The prize, sponsored by Hamamatsu Spain, will consist on a certificate and a contribution of € 250 to cover travel expenses to attend the 12 th EBSA – 10 th ICBP-IUPAP biophysics congress (Madrid, Spain, 20th – 24th July 2019).
- The winner and two other finalists will have their images displayed in the main hall at the location of the 12 th EBSA – 10 th ICBP-IUPAP biophysics congress (Madrid, Spain, 20th – 24th July 2019).

NOTE that the winner will be chosen 50% from public vote. Stay tunned with SBE social media: / !

Biofísica Magazine

HIGHLIGHTED PUBLICATIONS: SEPTEMBER - DECEMBER 2018

Papers of the month by SBE members



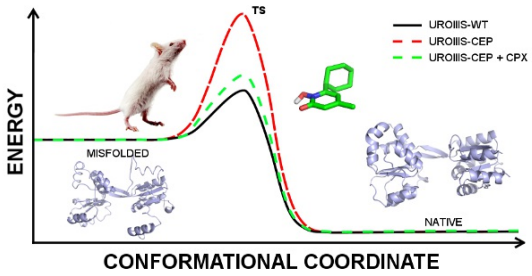
Balaceanu...Orozco {*Nucleic Acids Res* 46: 7554}

HIGHLIGHTS 2018 | SEP.

Allosterism and signal transfer in DNA

Balaceanu A, Pérez A, Dans PD, Orozco M

Nucleic Acids Res **2018** (Sep), 46: 7554



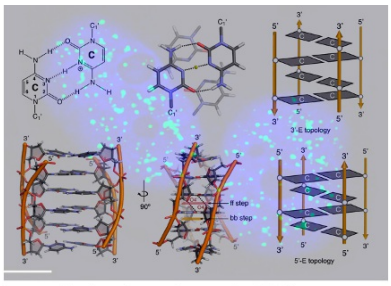
Urquiza...Millet {*Sci Transl Med* 10: eaat7467}

HIGHLIGHTS 2018 | SEP.

Repurposing ciclopirox as a pharmacological chaperone in a model of congenital erythropoietic porphyria

Urquiza P, Laín A, Sanz-Parra A, Moreno J, Bernardo-Seisdedos G, Dubus P, González E, de-Juan VG, García S, Eraña H, Juan IS, Macías I, et al

Sci Transl Med **2018** (Sep), 10: eaat7467



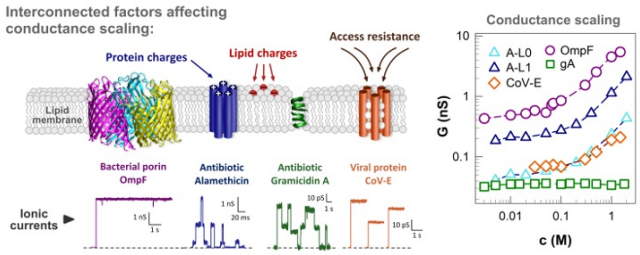
Abou Assi...Gonzalez, Damha {*Nucleic Acids Res* 46: 8038}

HIGHLIGHTS 2018 | SEP.

i-Motif DNA: structural features and significance to cell biology

Assi HA, Garavís M, González C, Damha MJ

Nucleic Acids Res **2018** (Sep), 46: 8038



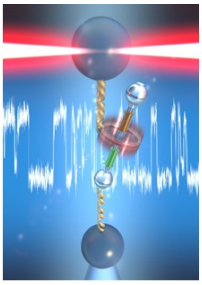
Queralt-Martin...Alcaraz {*Nano Lett* 18: 6604}

HIGHLIGHTS 2018 | OCT.

Scaling Behavior of Ionic Transport in Membrane Nanochannels

Queralt-Martín M, López ML, Aguilella-Arzo M, Aguilella VM, Alcaraz A

Nano Lett **2018** (Oct), 18: 6604



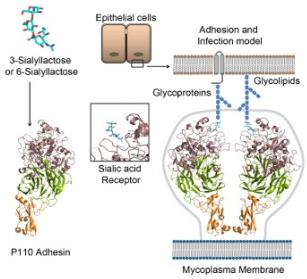
Naranjo...Ibarra {*Nat Commun* 9: 4512}

HIGHLIGHTS 2018 | OCT.

Dynamics of individual molecular shuttles under mechanical force

Naranjo T, Lemishko KM, de Lorenzo S, Somoza Á, Ritort F, Pérez EM, Ibarra B

Nat Commun **2018** (Oct), 9:



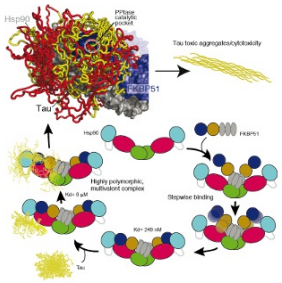
Aparicio...Fita {*Nat Commun* 9: 4471}

HIGHLIGHTS 2018 | OCT.

Mycoplasma genitalium adhesin P110 binds sialic-acid human receptors

Aparicio D, Torres-Puig S, Ratera M, Querol E, Piñol J, Pich OQ, Fita I

Nat Commun **2018** (Oct), 9:



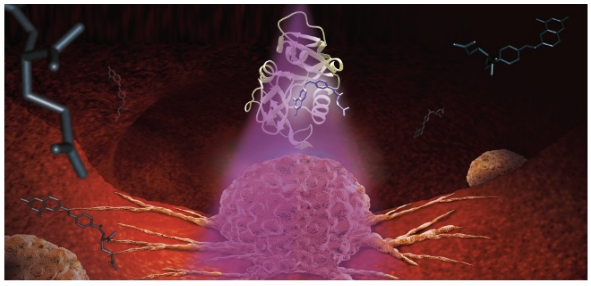
Oroz...Zweckstetter {*Nat Commun* 9: 4532}

HIGHLIGHTS 2018 | OCT.

Structure and pro-toxic mechanism of the human Hsp90/PPIase/Tau complex

Oroz J, Chang BJ, Wysoczanski P, Lee C-T, Pérez-Lara Á, Chakraborty P, Hofele RV, Baker JD, Blair LJ, Biernat J, Urlaub H, Mandelkow E, et al

Nat Commun **2018** (Oct), 9:



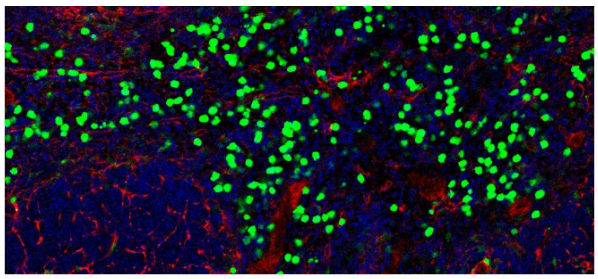
Matera...Gorostiza {*J Am Chem Soc* 140: 15764}

HIGHLIGHTS 2018 | NOV.

Photoswitchable Antimetabolite for Targeted Photoactivated Chemotherapy

Matera C, Gomila AMJ, Camarero N, Libergoli M, Soler C, Gorostiza P

J Am Chem Soc **2018** (Nov), 140: 15764



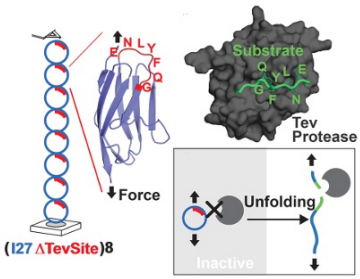
Casanova-Acebes...Hidalgo {*J Exp Med* 215: 2778}

HIGHLIGHTS 2018 | NOV.

Neutrophils instruct homeostatic and pathological states in naive tissues

Casanova-Acebes M, Nicolás-Ávila JA, Li JL, García-Silva S, Balachander A, Rubio-Ponce A, Weiss LA, Adrover JM, Burrows K, A-González N, Ballesteros I, Devi S, et al

J Exp Med **2018** (Nov), 215: 2778



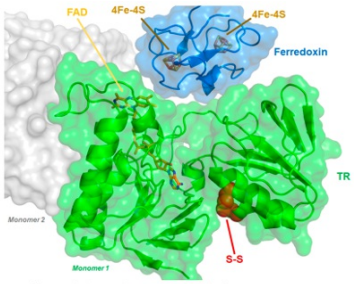
Guerin...Giganti {*Proc Natl Acad Sci USA* 115: 11525}

HIGHLIGHTS 2018 | NOV.

Conformational entropy of a single peptide controlled under force governs protease recognition and catalysis

Guerin ME, Stirnemann G, Giganti D

Proc Natl Acad Sci USA **2018** (Nov), 115: 11525



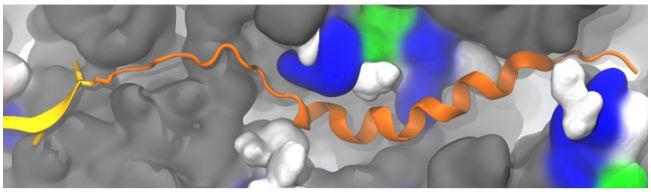
Buey...Balsera {*Proc Natl Acad Sci USA* 115: 12967}

HIGHLIGHTS 2018 | DEC.

Ferredoxin-linked flavoenzyme defines a family of pyridine nucleotide-independent thioredoxin reductases

Buey RM, Fernández-Justel D, de Pereda JM, Revuelta JL, Schürmann P, Buchanan BB, Balsera M

Proc Natl Acad Sci USA **2018** (Dec), 115: 12967



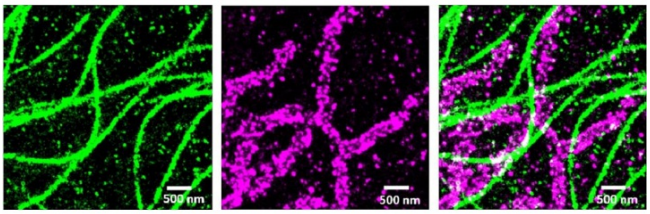
Bañó-Polo...Mingarro {*Nat Commun* 9: 5246}

HIGHLIGHTS 2018 | DEC.

Transmembrane but not soluble helices fold inside the ribosome tunnel

Bañó-Polo M, Baeza-Delgado C, Tamborero S, Hazel A, Grau B, Nilsson I, Whitley P, Gumbart JC, von Heijne G, Mingarro I

Nat Commun **2018** (Dec), 9:



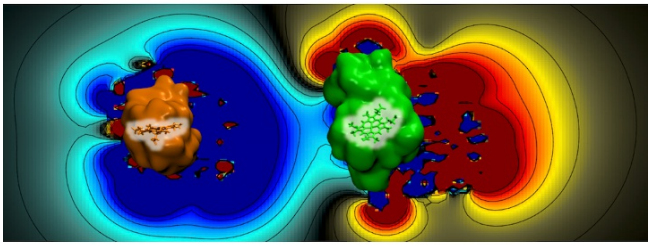
Gómez-García...García-Parajo, Lakadamyali {*Proc Natl Acad Sci USA* 115: 12991}

HIGHLIGHTS 2018 | DEC.

Excitation-multiplexed multicolor superresolution imaging with fm-STORM and fm-DNA-PAINT

Gómez-García PA, Garbacik ET, Otterstrom JJ, Garcia-Parajo MF, Lakadamyali M

Proc Natl Acad Sci USA **2018** (Dec), 115: 12991



Lagunas...Gorostiza {*Nat Commun* 9: 5157}

HIGHLIGHTS 2018 | DEC.

Long distance electron transfer through the aqueous solution between redox partner proteins

Lagunas A, Guerra-Castellano A, Nin-Hill A, Díaz-Moreno I, la Rosa MAD, Samitier J, Rovira C, Gorostiza P

Nat Commun **2018** (Dec), 9: