

Letters to the Editor

Letters (~300 words) discuss material published in *Science* in the previous 6 months or issues of general interest. They can be submitted through the Web (www.letter2science.org) or by regular mail (1200 New York Ave., NW, Washington, DC 20005, USA). Letters are not acknowledged upon receipt, nor are authors generally consulted before publication. Whether published in full or in part, letters are subject to editing for clarity and space.

Fish in Deep-Water Coral Habitats

DAVID MALAKOFF'S ARTICLE "U.S. ASKED TO act immediately to protect deep-sea corals" (News of the Week, 2 April, p. 31), reporting on a petition to the U.S. government by the advocacy group Oceana, suggests that fish species found among deep-water corals are under threat unless this habitat is protected.

Most would agree that the destruction of habitats that are several thousands of years old is neither a sustainable or desirable activity, given likely recovery times measured in hundreds of years. Oceana's petition is reported to claim that the Federal Magnuson-Stevens Act compels U.S.

regulators to protect rare or fragile fish habitats from anything but minimal or temporary disruption. But the Act pertains only to "essential fish habitat," defined as "those waters and substrate necessary to fish for spawning, breeding, feeding or growth to maturity" (1). Of the scientific studies cited within the petition, none demonstrates a critical dependency of any fish species on the presence of deep-water corals. In the petition, much is made of two recent studies of deep-water corals off Norway (2) and in the Gulf of Alaska (3). Nevertheless, in the Norwegian study, only the abundance of redfish was significantly higher in the coral habitat compared with adjacent areas that were fished commercially. And, even for redfish, the paper recognized that it was unlikely that the coral habitat had an important role in the provision of food. Both this and the Alaskan study simply demonstrate that fish and other biota tend to aggregate around structures on the seabed. The same effect can be achieved with artificial reefs constructed of tires, concrete blocks, or even scrapped street-cars. There is as yet no scientific evidence to indi-

cate that the removal of deep-water coral reefs would have an adverse effect on wider stocks of associated species.

In an era when fisheries scientists are striving to work constructively with the fishing industry, petitions that generate confusion over the real scientific issues could divert resources away from the real problems—getting control of fishing efforts and rebuilding stocks—which are the key conservation problems facing today's marine ecosystems.

MICHEL J. KAISER

Marine Policy Center, Woods Hole Oceanographic Institute, Falmouth, MA 02543, USA.

References

1. See www.nmfs.noaa.gov/sfa/magact/mag3a.html.
2. J. H. Fossa, P. B. Mortensen, D. M. Furevik, *Hydrobiologia* **471**, 1 (2002).
3. K. J. Kreiger, B. L. Wing, *Hydrobiologia* **471**, 83 (2002).

Starting a Global Scientific Journal

DOES A COUNTRY NEED TO PUBLISH ITS OWN internationally recognized journals to be a scientific power? This question was debated recently by a group of Japanese scientists, as reported by D. Normile ("Japan ponders starting a global journal," News of the Week, 12 March, p. 1599). Following an objective analysis, they concluded that they should start publishing their own international journals.

Although our scientific production in Mexico is much lower than that of Japan or other scientific world powers, we have been posing the same question among ourselves for more than a decade. Our scientific community experiences problems similar to those discussed by the Japanese group in attempting to publish in high-ranking international journals. Furthermore, our journals have little or no visibility outside of Mexico and negligible impact in the scientific literature (1). With these problems in mind, we decided to produce a biomedical journal in English that met top-tier international standards. The local journal, *Archivos de Investigación Médica*, was transformed into *Archives of Medical Research* in a joint venture with Elsevier Science. The journal is produced entirely in Mexico and published in Philadelphia by Elsevier. The result of this enterprise has been quite gratifying. The quality of manuscripts from local scientists has increased substantially, and we now receive nearly 35% of our contributions from about 30 different countries. Approximately 70% of our reviewers are internationally recognized experts with very

strict standards, and our rejection rate has climbed to almost 60%. The visibility of our journal in the international scientific literature as measured by the ISI impact factor has increased threefold since 1989, reaching 0.606 in 2003, and our most conservative estimates forecast a figure of 0.850 for this year's impact factor (2). We have seen a striking increase of online visitors, from 9872 full-text article requests in 2001 to 53,453 in 2003 (Science Direct Online).

Our journal is subsidized by the Coordination of Health Sciences Research Center at the Mexican Institute of Social Security (IMSS), but is not by any means as expensive as the \$18-million annual subsidy estimated by the Japanese Science and Technology Agency.

Our experience with *Archives of Medical Research* is an example for other countries to follow in publishing their own international journals. We believe that our success is due to a focus on high-quality standards.

LUIS BENÍTEZ-BRIBIESCA

Editor in Chief, Archives of Medical Research, Centro Médico Nacional S-XXI, IMSS, 4o. Piso Bloque B Unidad de Congresos, Mexico, D.F. 06720. E-mail: luisbenbri@mexis.com

References

1. W. W. Gibbs, *Sci. Am.* **273**, 92 (1995).
2. L. Benítez-Bribiesca, *Arch. Med. Res.* **33**, 91 (2002).

Hog Picture Doesn't Tell Whole Story

THANK YOU FOR BRINGING US UP TO DATE on the controversy over the Bush administration's politicization of science to further its own agenda (D. Malakoff, "White House rebuts charges it has politicized science," News of the Week, 9 April, p. 184). Nevertheless, I must take issue with one of the photographs accompanying the article: the four happy hogs setting out across their barnyard from a roomy wooden barn. The hog farms that have been implicated in airborne bacteria resistant to antibiotics referred to in the article have no resemblance to this bucolic and muddy scene. Had the photo depicted the subject at hand, we would have seen hundreds or thousand of hogs crammed into metal buildings with artificial light, with high-tech waste removal and feeding systems. Suggesting a relationship between your photo and the U.S. hog industry operations is as misleading as misnaming the scientist in the other photo accompanying the article would have been.

ALICE WHITE

Hillsborough, NC, USA.



A New Beginning

SCIENCE AND TECHNOLOGY ARE THE MOST profound transforming forces in the world today. The Center for Science, Policy, and Outcomes (CSPO) is an intellectual center devoted to understanding, responding to, and shaping these forces. A Random Samples item reported on the "demise" of the Center ("Policy failure," 24 Oct., p. 563), but this report was premature; hence, my letter. CSPO has moved to Arizona State University and is evolving into a consortium that will bring together universities, philanthropic foundations, and science organizations devoted to improving the capacity of science policy decisions to link the global research agenda to social goals.

MICHAEL M. CROW

President, Arizona State University, Post Office Box 872203, Tempe, AZ 85287-2203, USA.

Predicting Protein Structures Accurately

IN THEIR RESEARCH ARTICLE "DESIGN OF A novel globular protein fold with atomic-level accuracy," B. Kuhlman *et al.* describe an extremely successful attempt to design a new protein (Top7) that folds to a predefined structure (21 Nov, p. 1364). This is the first time an artificial protein of this size has been designed and synthesized, and its predicted structure confirmed experimentally. The most intriguing aspect of this experiment is the method used. Instead of following the canonical protocol of designing a sequence, which can successfully eliminate alternative low-energy conformations during the folding process, the authors mainly attempted to stabilize the final targeted structure by carefully optimized interactions in the core of the protein. This resulted in surprising accuracy of the structure prediction and in superior stability of the synthesized protein. The innovative character of this approach is highlighted by the fact that, despite its rational design, currently available methods fail to predict the final topology of the artificial protein. In the best model, obtained with the Structure Prediction Meta Server (1), only half of the protein is within 3.5 Å of the native conformation. Fold recognition methods, which try to select the correct structure from fold libraries, can fail because they are heavily dependent on evolutionary information, which is clearly missing in this case. Even ab initio methods similar to those used by the authors (2, 3) are unable to reproduce the folding process and fail to

reliably predict the correct topology of the Top7 protein. Methods of this kind use reduced representation of proteins and coarse search strategies, which are insufficient to sample the correct fold with adequate precision to detect the fine network of highly optimized interactions. The physical folding experiment is more successful, and the strong secondary structure encoded in the sequence is sufficient to drive the chain close enough to be tightly locked in the final structure.

This novel design approach may inspire significant progress in the stagnating field of protein engineering. D. Jones is absolutely right when, in an accompanying commentary, he points to the fact that nature does not need new folds to discover new functionality ("Learning to speak the language of proteins," Perspectives, 21 Nov, p. 1347). But despite our inability to predict the folds of many proteins, the ability to design proteins opens new opportunities for using other structure assembly protocols with different building blocks.

MARCIN VON GROTHUSS,¹ LUCJAN S. WYRWICZ,² JAKUB PAS,² LESZEK RYCHLEWSKI^{1*}

¹BioInfoBank Institute, Limanowskiego 24A, 60-744 Poznan, Poland. ²Bioinformatics Unit, Faculty of Physics, Adam Mickiewicz University, Umultowska 85, 61-614 Poznan, Poland.

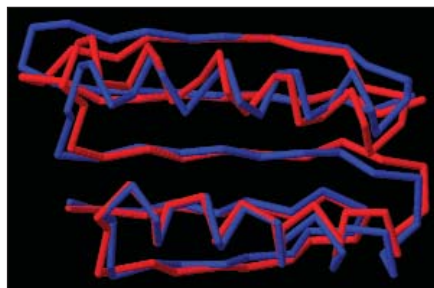
*To whom correspondence should be addressed. E-mail: leszek@bioinfo.pl

References

1. J. M. Bujnicki, A. Elofsson, D. Fischer, L. Rychlewski, *Bioinformatics* **17**, 750 (2001).
2. L. H. Hung, R. Samudrala, *Nucleic Acids Res.* **31**, 3296 (2003).
3. C. Bystroff, Y. Shao, *Bioinformatics* **18** (suppl. 1), S54 (2002).

Response

UNPUBLISHED AB INITIO STRUCTURE prediction of the Top7 structure generated by our group with the ROSETTA structure prediction methodology bear on the discussion of Top7 structure prediction in



The lowest energy decoy structure for the Top7 sequence as predicted by the ROSETTA ab initio structure prediction program (red) is very similar (1.37 Å RMSD) to the x-ray crystal structure (blue).

the Letter by von Grotthuss *et al.* Although in the most frequent topology produced by ROSETTA, the NH₂-terminal hairpin is flipped relative to the Top7 structure, the lowest energy structure is remarkably similar to Top7 (see figure). The high accuracy of this prediction contrasts sharply with the much lower accuracy of predictions for naturally occurring sequences by CASP (Critical Assessment of Techniques for Protein Structure Prediction; rarely better than 4 Å root mean standard deviation for proteins of this size). The higher accuracy of the Top7 structure prediction by ROSETTA likely reflects the optimization of the sequence for stability in the absence of functional constraints. Because of this optimization, the true free energy minimum for the sequence is so pronounced that it is found despite the inaccuracies in the potential function guiding the folding simulations. In contrast, structure prediction of naturally occurring proteins is complicated by delicate tradeoffs between optimization for stability and for function. Imperfect *de novo* structure prediction methods evidently can work on “perfect” proteins—the problem is that biological proteins are far from thermodynamic perfection.

PHIL BRADLEY,¹ BRIAN KUHLMAN,³ GAUTAM DANTAS,² DAVID BAKER^{1,2*}

¹Howard Hughes Medical Institute, ²Department of Biochemistry, University of Washington, Seattle, WA 98195, USA. ³Department of Biochemistry and Biophysics, University of North Carolina, Chapel Hill, NC 27599, USA.

*To whom correspondence should be addressed. E-mail: dabaker@u.washington.edu

Building on the IGY Anniversary

THE EDITORIAL BY M. R. ALPERT “The International Polar Year” (5 Mar., p. 1437) and the accompanying article “A year to remember at the ends of the Earth” (News Focus, R. Stone, G. Vogel, 5 Mar., p. 1458) recall the activities of previous International Polar Years (IPY) and announce a new campaign timed to coincide with the 50th anniversary of the International Geophysical Year (IGY; 1957–58). IPY 2007–08 is one of several major international geophysical research programs that will celebrate the IGY and build on that heritage to energize new global research. Another initiative is the International Year of Planet Earth (IYPE; 2005–07), a program originally proposed by the International Union of Geological Sciences and UNESCO. The major themes of IYPE include groundwater, health,

cities, natural hazards, natural resources, climate change, deep Earth, and the oceans. An outreach component will inform policy-makers and the general public of new results that impact the environment and human populations.

Other initiatives include the International Heliophysical Year 2007 (IHY) and the electronic Geophysical Year 2007–08 (eGY). The IHY will focus on fundamental global questions of the physical relationships between the Sun and Earth and will enhance an ongoing NASA program “Living with a Star” as well as a new initiative of the International Council for Science (ICSU) Scientific Committee on Solar-Terrestrial Physics entitled “Climate and Weather in the Sun-Earth System.” The eGY is a cross-cutting initiative that aims to use modern technology to revolutionize not only the dissemination of scientific data, but also the capacity to process, analyze, and visualize information in the pursuit of new knowledge.

The International Union of Geodesy and Geophysics (IUGG), one of the sponsoring and coordinating bodies of the original IGY, has established a Committee for IGY+50 to foster interactions among the various global initiatives. The IUGG General Assembly in Perugia, Italy, 2 to 13 July 2007, will provide an opportunity for new results from all of these programs to be presented to honor the 50th anniversary of the IGY.

JO ANN JOSELYN

Secretary-General, International Union of Geodesy and Geophysics, UCB 216, Boulder CO 80309–0216, USA. E-mail: secretariat@iugg.org

CORRECTIONS AND CLARIFICATIONS

Cover Caption: (30 Apr., p. 637). The cover image was incorrectly credited in the caption. The image was taken by I. Griffiths.

Table of Contents (23 Apr.): The Table of Contents for *Science Online* on page 483 lists the wrong author for an article in *Science's Next Wave*: “Bridging between research groups and direction.” The author of the article is Terry Vrijenhoek.

News of the Week: “U.S. asked to act immediately to protect deep-sea corals” by D. Malakoff (2 Apr., p. 31) The photograph accompanying the article does not illustrate deep-sea coral habitat, but rather shelf habitat (40 m) with lingcod (*Ophiodon elongatus*) and hydrocoral. Images illustrating cold water deep-sea coral habitats can be found at twww.afsc.noaa.gov/abl/MarFish/coral_gardens_video.htm.

Editors' Choice: “Splicing in diversity” (21 Nov. 2003, p. 1295). The highlighted paper by Zeytun *et al.*, “Fluorobodies combine GFP fluorescence with the binding characteristics of antibodies” has been retracted [*Nature Biotechnol.* **22**, 601 (2004)].

Predicting Protein Structures Accurately

Marcin von Grotthuss, Lucjan S. Wyrwicz, Jakub Pas and Leszek Rychlewski

Science **304** (5677), 1597-1599.
DOI: 10.1126/science.304.5677.1597b

ARTICLE TOOLS	http://science.sciencemag.org/content/304/5677/1597.2
RELATED CONTENT	http://science.sciencemag.org/content/sci/305/5680/41.full http://science.sciencemag.org/content/sci/306/5699/1135.1.full http://science.sciencemag.org/content/sci/302/5649/1364.full
REFERENCES	This article cites 2 articles, 0 of which you can access for free http://science.sciencemag.org/content/304/5677/1597.2#BIBL
PERMISSIONS	http://www.sciencemag.org/help/reprints-and-permissions

Use of this article is subject to the [Terms of Service](#)

Science (print ISSN 0036-8075; online ISSN 1095-9203) is published by the American Association for the Advancement of Science, 1200 New York Avenue NW, Washington, DC 20005. The title *Science* is a registered trademark of AAAS.

© 2004 American Association for the Advancement of Science