BIOCHEMISTRY

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NEW INITIATIVES PERTAINING TO *BIOCHEMISTRY* IN 2008

It is with great pleasure that I convey this update to all of the readers, authors, reviewers, and members of the Editorial Advisory Board who support *Biochemistry*. In the last year several new initiatives have been implemented or considered by the journal with the underwriting by the American Chemistry Society (ACS) Publications Division. These include the introduction of a new manuscript type, *Rapid Reports*, the immediate posting of accepted manuscripts on the web, and the encouragement of authors to use uniform standards for the reporting of structural and enzymological data.

Rapid Reports. *Biochemistry* is pleased to introduce a new manuscript type this year that is designed to encourage short, timely papers on topics of unusual importance or interest. These papers will be strictly limited in length to three printed journal pages. A *Rapid Report* must include a short abstract (70−100 words maximum), a main body of text that includes (without subheadings) an introduction, a brief and general description of experimental procedures, and the results and discussion of the work accompanied by tables, schemes, structures, figures, and references. Authors are expected to submit detailed experimental procedures as Supporting Information that are sufficient for others to reproduce the reported results. *Biochemistry* will make every effort to come to an editorial decision on *Rapid Reports* within three weeks of receipt of the manuscript. A template for *Rapid Reports* will be available on the *Biochemistry* website in the second quarter of 2008. The template will help authors design their submissions to adhere to the strict three-page limit. In the meantime, authors are encouraged to submit *Rapid Reports* using the updated guidelines for authors that appear in this issue of the journal.

Acceptance to Web Accelerated. It takes four to six weeks for a normal article that is accepted by *Biochemistry* to be edited, approved by the author, and released to the web via ASAP. Other journals have a policy of immediate Web release upon editorial acceptance of a manuscript. Beginning in the third quarter of 2008, manuscripts accepted for publication in *Biochemistry* will, at the author's request, be posted as an unedited .pdf version on the web immediately after acceptance. Authors must opt in for this service. After editorial acceptance and approval by the authors, the manuscript will be openly available through the journal's website. As always, the copyright for the material is assigned to the ACS. Upon release of the edited and formatted ASAP article, the unedited manuscripts will be removed from open availability and will eventually be replaced by the final, paginated article as published by the journal's print and online editions within the scheduled issue.

I want to make an important point about this new policy. I have conducted a couple of informal surveys of younger authors as to whether they would want their unedited manuscripts posted on the web once they were accepted. I was surprised to find that only approximately half of the authors thought this was a good idea. Recognizing this divide, the post of accepted manuscripts is optional with *Biochemistry*. Authors can opt to have their accepted manuscript posted on the web. Initially four ACS journals will offer the option for posting of accepted manuscripts: *ACS Chemical Biology*, *Biochemistry*, *Journal of Proteome Research*, and *Molecular Pharmaceutics*. I applaud ACS Publications and the Governing Board of Publications for trying this. I think it is a very positive move for scientific publishing at the ACS. If you agree, vote with your submissions.

Uniform Standards for Reporting Data. As most of you are aware, there are now generally accepted (and required) standards for the submission of gene sequence data and structural data (NMR or X-ray diffraction data) to most scientific journals and public databases such as GenBank and the Protein Data Bank (PDB). For example, *Biochemistry* requires that data supporting protein or DNA structures, elucidated by either NMR spectroscopy or X-ray crystallography, must be deposited in the Protein Data Bank before publication and must be released to the public upon publication. These data include restraints and atomic coordinates for NMR-derived structures and structure factors/amplitudes, plus coordinates for X-ray-derived crystal structures. For several years, *Biochemistry* has required the submission of all of these data to the PDB before acceptance of a paper for publication. I recently received an announcement that the PDB itself now requires depositors to include both coordinates and structure factors (or NMR constraints) for PDB submission. I am glad that the journal and the PDB are now on the same page.

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I am sure that most of you know that *Biochemistry* publishes numerous papers reporting the kinetic and thermodynamic data concerning enzymes, other proteins, and nucleic acids. The following question then arises: If structural biologists and biochemists are required to report their structural data in a standard format, what about enzymologists who report kinetic data and the like for their favorite enzymes and proteins? If you read the enzymological literature as much as I do, you know that the reporting of kinetic data is far from standardized, spotty at best, and sometimes shoddy. I strongly believe that this should change, and soon.

In this regard, I would like to point out that there is a scientific organization, the Beilstein-Institut (www.beilstein-institut.de), that is taking this problem very seriously. The Beilstein-Institut formed the STRENDA (standards for reporting enzymology data) (http://www.strenda.org) commission about three years ago in an attempt to standardize the reporting of kinetic and thermodynamic characteristics of proteins and enzymes. In my view, this is a very important initiative, but an exceedingly complex one. If you reflect on the fact that the reporting of structural data (a gene sequence or even a three-dimensional structure of a molecule) can be regularized to relatively simple sets of parameters and statistics and then consider doing the same thing for kinetic and thermodynamic data obtained in a variety of ways for proteins that can have completely different functions, it is a very difficult problem. I have committed *Biochemistry* to work with the STRENDA Commission and its advocates at the Beilstein-Institut, Dr. Martin G. Hicks and Dr. Carsten Kettner, on this problem and to refine guidelines for reporting these data in future publications. Please let *Biochemistry* and the STRENDA Commission know what you think. Intelligent input from the community is the best way to move forward.

Thanks for your support.

Richard N. Armstrong
Editor-in-chief

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