Acta Crystallographica Section F
Structural Biology and Crystallization Communications
ISSN 1744-3091

Editorial

Howard Einspahr[a] and Mitchell Guss[b]

[a]PO Box 6395, Lawrenceville, NJ 08648-0395,USA, and [b]School of Molecular and Microbial Biosciences, University of Sydney, NSW 2006, Australia

This issue inaugurates *Acta Crystallographica Section F: Structural Biology and Crystallization Communications*, a new all-electronic addition to the family of journals published by the International Union of Crystallography (IUCr). It is not the first IUCr journal to serve biological crystallography as its primary focus; *Acta Crystallographica Section D* recently celebrated ten years of quality service as the highly effective print journal for this area of interest. Nor is it the first all-electronic journal to be published by the IUCr; *Section E* begins its fifth year of service as the highly effective electronic complement to *Sections B* and *C*. These journals have set high standards and it is our hope that *Section F* complements *Section D* as effectively as *Section E* has done its fellow journals.

Section F has been launched to meet the increasing need for rapid publication of structural biology reports and to provide a more congenial medium for reporting crystallization results. *Section F* eagerly welcomes the very popular crystallization communications to its ‘e-pages’ where they will now be unfettered by space and media restrictions and, of special note, will no longer encounter restrictions on the use of color. These communications are evolving toward more and more experimental content, including information on initial phasing and refinement. They remain, in many cases, the sole repositories of experimental documentation of these most crucial stages of a structure determination. It is a priority of the biological crystallography community that these important communications continue to serve their role in crystallographic publication. We will therefore make every effort to assure they flourish in their spacious new quarters in *Section F*.

Few have failed to notice the explosive acceleration in depositions to the Protein Data Bank (PDB) in recent years, but unrealised by many is the number of depositions that have not been accompanied by a publication documenting the experiment and its results. Lack of publication has a number of negative consequences, not the least of which is inaccessibility to abstracting services like PubMed and hence to the wider biological audience. Add to this the accelerants of hundreds of structures generated by the international effort on structural genomics, which are required by various funding agencies to be promptly deposited and published, and the uncounted thousands of unpublished protein–ligand structures generated by drug-discovery efforts worldwide, and you begin to appreciate the challenge the community faces. This is a major reason why *Section F* has been initiated and that it is an all-electronic journal. It is fair then to judge the future success of *Section F* on how well it meets this need to accelerate the publication of structural biology reports.

The chief strategy to meet this rapid publication challenge has emerged from a collaboration between the Protein Data Bank and IUCr Journals. The goal of this collaboration is to eliminate repetition and streamline submissions by facilitating transfer of data deposited in the PDB to the journal at the point of submission. The vehicle for the transfer of information for publication is through data files with content described in the PDB Exchange Data Dictionary. Deposition tools are available at each wwPDB site to assist in the preparation of these data files. Additional tools such as PDB_EXTRACT are also available to help automate the extraction of key data items from many popular structure determination applications. It is hoped that a system combining publication and PDB deposition will reduce the overall effort required to perform both activities. As refinements are made to this evolving system they will be highlighted and described on the *Section F* website. Many other improvements and efficiencies are anticipated. Some innovations will directly assist the author in assembly of submissions while others will provide new web-based methods for speeding up the editorial process and streamlining peer review.

We are especially pleased by the strong support of the biological crystallography community as we begin *Section F*. This support is easy to appreciate from the high quality of those who have agreed to serve on its first editorial board. We thank them and salute them for their public spirit in stepping forward to help with the evolution of this new journal.

The launch of *Section F* is a major new step by IUCr Journals that continues its policy to provide the best possible service to the structural science community worldwide. Not all potential improvements and efficiencies are in place from the first issue, nor have all that are needed been identified as yet. We will depend on our authors and readers to help us in this evolution. As long as we remain true to two principles, that the journal should evolve to best serve the needs of authors and readers and that, at the same time, the journal should maintain the expected high standards of descriptive completeness and editorial review, we feel we will be assured of evolving successfully. That is what we commit to do.