

## The times they are a-changin' – news from *Acta Crystallographica Section F*

W. N. Hunter<sup>a\*</sup> and  
Manfred S. Weiss<sup>b\*</sup>

<sup>a</sup>Division of Biological Chemistry and Drug Discovery, College of Life Sciences, University of Dundee, Dundee DD1 5EH, Scotland, and

<sup>b</sup>Helmholtz-Zentrum Berlin für Materialien und Energie, Macromolecular Crystallography (HZB-MX), Albert-Einstein-Strasse 15, D-12489 Berlin, Germany

A decade ago *Acta Crystallographica Section F* was launched with the subtitle *Structural Biology and Crystallization Communications* under the excellent stewardship of Howard Einspahr and Mitchell Guss. The journal was conceived in response to developments in the field when it was recognized that our community needed a home for the rapid dissemination of structural results and a convenient way to publish crystallization reports. The founding Editors made a commitment to maintain scientific rigor and to best serve our community, the authors and readers. Since 2005 we have all strived to do just that. Of course time is relentless and the advances in biomolecular sciences, macromolecular crystallography in particular, have continued apace. Research that was considered challenging a decade ago is now routine, and is often carried out using standard reagents and protocols. However, the results generated have enriched the scientific literature, and expanded the Protein Data Bank (PDB) and other repositories. For some time now, and driven by advances in our discipline, we have been thinking about what would be considered best for the journal with respect to crystallization papers. We at first decided to change the journal's subtitle to *Structural Biology Communications* to remove the artificial segregation of crystallization from structural biology and to pave the way for *Acta Cryst. F* to become a full-fledged structural biology journal (Einspahr & Weiss, 2013). We also analyzed the papers that have focused on crystallization results (Weiss & Einspahr, 2013a; Newman *et al.*, 2013) and decided that in order to streamline their information content, a more formal structure should be put in place for these papers (Weiss & Einspahr, 2013b). This led to the development of *publBio* (<http://publbio.iucr.org>), which is now widely used to prepare and submit manuscripts for *Acta Cryst. F*.

There is still some way to go and it seems that it is now time to raise the bar even higher! We have decided that we will no longer publish articles on the routine preparation and characterization of macromolecules for which orthologues have already been published or deposited. Furthermore, for a new crystallized macromolecule we expect a degree of characterization not previously required. For example, it will become essential to demonstrate that the correct macromolecule has been crystallized. Further details are available in the new Notes for Authors, available from the *Acta Cryst. F* author services page (<http://journals.iucr.org/f/services/authorservices.html>). We are also thinking about requiring the deposition of a diffraction data set together with the submission of a manuscript that reports a successful crystallization. After all, the diffraction data set is evidence for crystallization and is typically described in the paper. Further, activity parameters will be required if an enzyme is the subject of the work and, for certain proteins or modules, information from a binding assay and the characterization of quaternary structure would be sought to provide proof of function and assignment. The decision to require more data and to publish more interesting macromolecules has been driven by two considerations. Many crystallization communications do not lead to a structural paper or to citations. This suggests that such papers are of little interest or relevance to our community. Increasingly, it is also the case that the structure of the crystallized macromolecule, the subject of the crystallization paper, can be solved and refined quickly. In such a case we would prefer to see the structure published in our journal, with details of the sample preparation and characterization as part of the publication. We believe the outcome of these changes will improve the standard of publications yet maintain support for our community in keeping up to date with the current state of structural biology.

Finally, we would like to use this editorial to thank and acknowledge everyone who has or continues to contribute to the journal as it enters its eleventh year. This extends from our founding Editors, the Editorial Board members, to the production team and of course our authors. Particular thanks however must go to those individuals who provide the carefully considered reviews on manuscripts. These are critical to what remains our charter – namely to ensure scientific rigor and to serve our community.

### References

- Einspahr, H. & Weiss, M. S. (2013). *Acta Cryst. F* **69**, 827.  
Newman, J., Burton, D. R., Caria, S., Desbois, S., Gee, C. L., Fazio, V. J., Kvensakul, M., Marshall, B., Mills, G., Richter, V., Seabrook, S. A., Wu, M. & Peat, T. S. (2013). *Acta Cryst. F* **69**, 712–718.  
Weiss, M. S. & Einspahr, H. (2013a). *Acta Cryst. F* **69**, 711.  
Weiss, M. S. & Einspahr, H. (2013b). *Acta Cryst. F* **69**, 1315.