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Redefining *Acta D*

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All journals evolve over time and it is a healthy sign when this is driven by growth in a field. This is a 'golden age' in biological crystallography. The field is expanding in every way, driven by the way in which structure illuminates our understanding of living systems and by its applications in medicine and biotechnology. Larger and more complex biological assemblies are being successfully tackled. Smaller protein structures are solved faster than ever before, often before the data collection is even finished at a synchrotron. And the development of innovative new methods continues apace, expanding the boundaries of what can be done, how well and how quickly.

Section D of *Acta Crystallographica* was founded in 1993, at a time when the exponential growth in the number of protein structures was just beginning; the plot of deposited structures in the Protein Data Bank (see Fig. 1) shows this quite dramatically. This also points to the reasons why journals, our own included, are changing as they respond to such growth. Traditionally *Acta D* has accepted papers dealing with all aspects of biological crystallography, with a main emphasis on new macromolecular structures and on crystallographic methods, but also covering crystallization papers and the first results from structural genomics.

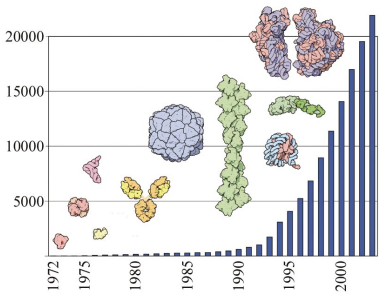

Figure 1
Structures deposited in the PDB. From the RCSB Protein Data Bank, used with permission.

In recent years, however, the rapid increase in crystallization papers has reached the point where they represent a large part of each issue. These were once published to indicate that what would be a lengthy structure analysis was under way. Now it is likely that once a crystallization paper has been published, the structure may already have been solved, and the question has been raised as to whether such papers should still be published. We believe that they should. First, they are the detailed published record of the most critical step in a crystal structure determination, without which it could not be replicated. Second, they give credit to the researchers who succeed in this important, and often underrated, step. Third, these papers also contain much of the best information on protein expression.

Last year it was decided that this growth, and the hundreds of new structures that are now emerging from structural genomics projects, justified the launch of a new partner journal for *Acta D*. This all-electronic journal, *Acta F*, will be the new home for crystallization papers and will also provide for the rapid publication of structural genomics papers.

With this issue, therefore, we welcome the arrival of *Acta F*, and herald a new step in the evolution of *Acta D*. The focus of *Acta D* will again be on new biological structures, and the light they throw on function, and on crystallographic methods, interpreted in their widest sense; this will continue to include methods development in crystallization. *Acta D* was founded to serve the biological crystallography community, and our goal is to publish your best papers, as rapidly as possible, and with the highest quality of production. We welcome your feedback and your support.