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Changing of the guard

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This section of *Acta Crystallographica*, with its subtitle of Biological Crystallography, was introduced ten years ago, in response to the rapid growth in macromolecular crystallography. Jenny Glusker served as founding Editor of *Acta D* and has steered the journal superbly through a period of almost unbelievable change and growth in the field. We are enormously indebted to her for her wisdom and dedication.

Now, as new Editors take over (two this time, though not clones!) it is a good time to reflect on the field we serve and contribute to. Crystallography provides a uniquely powerful window into biology. It is possible to see several distinct strands emerging today. One is the 'big science' of amazing macromolecular complexes and machines; the ribosome, ATP synthase, integral membrane complexes and viruses are some examples. Many more of these will be unveiled as we learn how to stabilize and crystallize such complexes. Another strand is represented by structural genomics, with its aims of discovering function through structure, and of developing new high throughput technologies. One way or another, we are going to see a lot of new structures! A third strand arises from this. Biological structural information is becoming firmly integrated into all of biology, whether the structures are used to model related proteins; to direct functional studies; to help develop drugs; or simply to explain biological processes. For this reason we firmly believe in the requirement that both the structures and the experimental data should be deposited in the Protein Data Bank, for all to use.

Those who have attended crystallographic meetings in recent years will have noticed the intense interest in sessions dealing with methods. This aspect is a cornerstone of *Acta D*; we seek to publish the latest methodological developments in biological crystallography, from all parts of the field. We seek also to be at the forefront of pushing and applying these methods. As a vivid illustration, this issue of the journal contains no fewer than four structures determined at better than 1.1 Å resolution, demonstrating the sort of atomic detail that can nail down biological mechanisms. It also contains one of our first structural genomics reports, in which the crystal structure of a 'hypothetical protein' is found to have a cofactor bound, as an intriguing indicator of function. We hope to feature many more of these, together with the 'big' structures and the methods used to produce them.

Above all, we seek to stand for quality. Many new researchers will use crystallography as a tool, or use crystallographic results, in the coming years. Many will not have rigorous crystallographic training. In this environment, it is critical that the journal should not only ensure the quality of the structures it publishes, but also be at the forefront of efforts to make the quality of structural data more intelligible to users.

Biological crystallography has never been more vibrant, and it is a pleasure to work for a journal that is at the heart of this field.