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Celebrating biological crystallography: *Acta D* twenty years on

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'It was twenty years ago today . . . ', as the Beatles told it. This year celebrates the 20th birthday of *Acta Cryst. D*, which is an appropriate time to think about how biological crystallography has developed and what the future may hold. The 20 years since *Acta D* was launched have seen extraordinary growth and development. Some of the beauty and diversity in this field is captured on the cover of this issue. We also note the spectacular increase in the number of structures held in the Protein Data Bank, from less than 2000 in 1993 to about 90 000 today, most of them solved by X-ray crystallography. This growth is paralleled by the increasing ambition in our science, in the complexity of the biological entities that are being tackled, and in their relevance to understanding and applications. Spectacular examples include the ribosome and the GPCRs, both attracting Nobel Prizes in the past few years.

The practice of biological crystallography has also changed dramatically over the past 20 years. Powerful new methods for structure determination have emerged, and have been regularly featured in this journal. Many are made possible by new developments at synchrotron sources, which continue to be crucial to the field. Increasingly, the ambition to tackle more complex and more difficult structures, in which well ordered regions co-exist with flexible parts, has led to hybrid approaches. In these cases, classical X-ray crystallography may be combined with electron microscopy or other biophysical methods, such as small-angle scattering, NMR, neutron scattering, powder diffraction and XAFS. Structural biology has become a whole lot broader!

It is our wish that all of these approaches should find a natural home in *Acta Cryst. D*. After all, the International Union of Crystallography already sponsors commissions that represent most of the structural methods mentioned above, and there are very active communities for all of them. The vigorous discussions that take place on the CCP4 Bulletin Board show that there are indeed many areas of debate in such a fast-changing science. As we enter our third decade, we will retain our focus on biological structure and structural methods, but will welcome papers over the whole range of methods that are now being applied in structural biology. We also wish to provide a forum for commentary, ideas and opinions, and thus will welcome topical reviews and other forms of commentary.