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Editorial

This is the tenth year in which *Acta Crystallographica D* has been published and my term as Editor is now over. It has been a wonderful time and I send my best wishes to Zbigniew Dauter and Ted Baker who will now be the new joint Editors. During these ten years the science of macromolecular crystallography has advanced extensively. A greater number of structures are being reported at high (now atomic) resolution. In addition, larger structures, including many-component macromolecular complexes, are being determined. Protocols for the crystallization of macromolecules are now more sophisticated. Many improvements have been made in methods for solving the phase problem for macromolecular structures. The informational crystallographic databases, particularly the Protein Data Bank and Nucleic Acid Database, are expanding rapidly with the fine data from structural papers in *Acta Cryst. D*. New initiatives, particularly high-throughput crystallography and electronic presentation of results, as well as problems of archiving data, are now editorial concerns. *Crystallization Papers*, along with *Structural Genomics Papers*, may eventually be published in an electronic-only form. We welcome Mitchell Guss as a Co-editor helping us with this.

The journal was originally published every two months but, by 1999, became a monthly journal. Also all articles published since 1993 became available online via **Crystallography Journals Online**. *Research Papers*, *Topical Reviews*, *Short Communications*, *Crystallization Papers*, and *Book Reviews* are published, and the annual content has remained rather constant at 170 *Research Papers* (including *Short Communications*) together with about 200 *Crystallization Papers*. A strong and welcome component was the addition of the Proceedings of CCP4 Study Weekends that are now published in *Acta Cryst. D* each year. A joint issue on databases has also been published in collaboration with *Acta Cryst. B*. The dissemination of crystallization data is still of importance to the international scientific community that we serve. The three Crystallization Co-editors – Naomi Chayen, Adriana Zagari and Marc Pusey – handle most of these articles.

During my term as Editor I was helped by many and I especially want to thank all of the authors and reviewers. Without them there would be no journal. The hard-working Co-editors oversee the publication fate of a large proportion of the submitted manuscripts. The Chester staff assisted greatly in the launching and maintaining of this journal. They do a wonderful job and their input is essential in ensuring the high standards of the journal. Louise Jones has been of particular help, shepherding accepted articles to the publishers, and assisting in the design of the monthly cover. My thanks also to Charlie Bugg, John Helliwell, Peter Strickland and Simon Glynn. Finally I want to thank Eileen Pytko, Amy Katz and Carol Afshar here in Philadelphia for their efficient handling of queries from authors and the processing of manuscripts sent to my office.

I view the future of this journal as bright, and note that its many colored pictures of molecules will eventually grace our biological and biochemical textbooks. There are several roles for *Acta Cryst. D*, all concentrated on biologically relevant molecules. They include reports on advancements in crystallization methods, structure determinations and methods for achieving them, and information that will help in an understanding of the functions of these biological systems. The impact of each of these on the current genome initiatives will continue to be significant.