Preface to the second edition

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Ten years after the appearance of the first edition of *International Tables for Crystallography*, Volume F, *Crystallography of Biological Macromolecules*, we are pleased to present the second edition. Preparation of the second edition has reflected the continuing evolution of macromolecular crystallography. Eddy Arnold and Michael Rossmann were glad to have Daniel Himmel, an accomplished crystallographer with diverse knowledge, join this effort. The three of us brainstormed about how to update this volume most effectively, and decided to seek new articles in key areas of rapid growth and ask authors from the first edition if they wished to revise their chapters. We were delighted when so many internationally recognized experts again made generous contributions that brought the volume up to date.

In the past decade the field of macromolecular crystallography has spawned an ever-increasing array of spectacular biological structures. The amazing conquests have included the translational machinery, the ribosome, in various functional states; the transcription machinery, multisubunit cellular RNA polymerases; a multitude of membrane proteins; and many more viruses. The marriage of crystallography and cryo-electron microscopy, including electron tomography, enables a multiscale view of biological structure including macromolecular inventories of cells in three dimensions. Multiprotein complexes are more routinely studied, and small-angle X-ray scattering has grown in prominence as a complementary technique to single-crystal X-ray diffraction. Structural genomics projects have been knocking out representative structures from a wide variety of proteomes from all levels of life. Structure-based drug-design prospects and the general problem of understanding protein–ligand interactions have benefitted from the development of techniques such as fragment screening, where thousands of small-molecule fragments are systematically soaked into crystals to interrogate potential binding sites – a central tool in the emerging field of chemical genetics. Software packages continue to evolve to enable rapid and reliable structure solution, visualization and analysis. X-ray lasers are now a reality and perhaps in the future many complex structures will be solved and imaged using data sets measured from tiny microcrystals that diffract their heart out before being destroyed by the pulsed high-brilliance beams. When thinking about the next ten years, we can expect more of the unexpected.

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