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Randy J. Read, Joel L. Sussman

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X-ray crystallography is the pre-eminent technique for visualizing the structures of macromolecules at atomic resolution. These structures are central to understanding the detailed mechanisms of biological processes, and to discovering novel therapeutics using a structure-based approach. As yet, structures are known for only a small fraction of the proteins encoded by human and pathogenic genomes. To counter the myriad modern threats of disease, there is an urgent need to determine the structures of the thousands of proteins whose structure and function remain unknown. This volume draws on the expertise of leaders in the field of macromolecular crystallography to illuminate the dramatic developments that are accelerating progress in structural biology. Their contributions span the range of techniques from crystallization through data collection, structure solution and analysis, and show how modern high-throughput methods are contributing to a deeper understanding of medical problems.

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