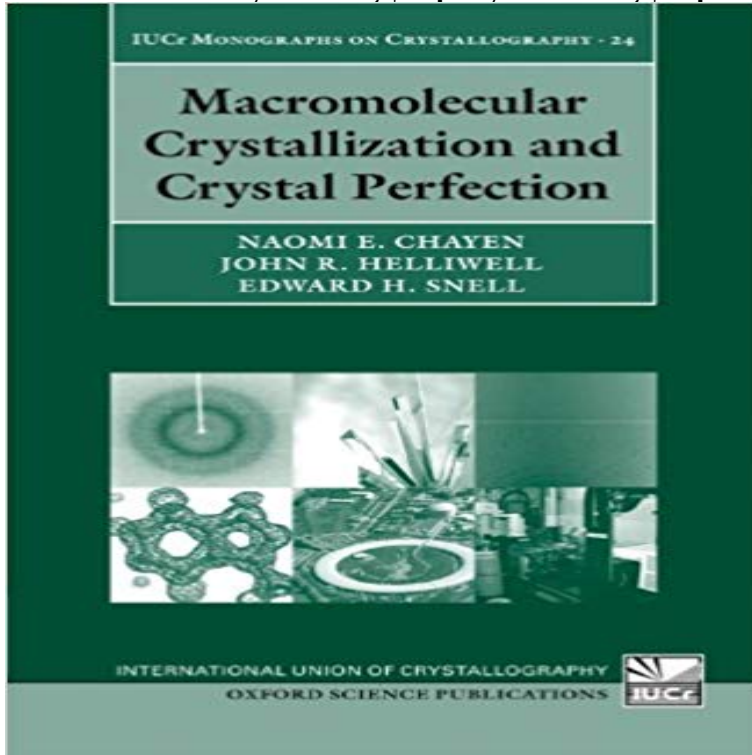


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The crystallization of proteins and nucleic acids and/or their complexes has become more highly automated but is still often a trial and error based approach. In parallel, a number of X-ray diffraction based techniques have been developed which explain the physical reasons limiting the resulting crystallographic data and thus show how that data may be improved. Crystal growth is also pivotal in neutron crystallography, which establishes the hydrogen and hydration aspects. Thus this book is aimed at addressing the science behind obtaining the best and most complete structural data possible for biological macromolecules, so that the detailed structural biology and chemistry of these important molecules emerge. Crystal imperfections such as twinning and latticedisorders, as well as multiple crystal situations, and their possible remedies, are also described. The small crystal frontier in micro-crystal crystallography, crystallites in powders and finally down to the proposed single molecule structure determination of X-ray lasers are covered. Overall this interdisciplinary book will interest crystal growers, X-ray and neutron physicists and the biological crystallographers, including graduate students.

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