



Macromolecular Crystallography: Conventional and High Throughput Methods (The Practical Approach Series)

By Mark Sanderson, Jane V. Skelly

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Macromolecular Crystallography is the study of macromolecules (proteins and nucleic acids) using X-ray crystallographic techniques in order to determine their molecular structure. The knowledge of accurate molecular structures is a pre-requisite for rational drug design, and for structure-based function studies to aid the development of effective therapeutic agents and drugs. The successful determination of the complete genome (genetic sequence) of several species (including humans) has recently directed scientific attention towards identifying the structure and function of the complete complement of proteins that make up that species; a new and rapidly growing field of study called 'structural genomics'. There are now several important and well-funded global initiatives in operation to identify all of the proteins of key model species. One of the main requirements for these initiatives is a high-throughput crystallization facility to speed-up the protein identification process. The extent to which these technologies have advanced, calls for an updated review of current crystallographic theory and practice. This practical reference book features the latest conventional and high-throughput methods, and includes contributions from a team of internationally recognized leaders and experts. It will be of relevance and use to graduate students, research scientists and professionals currently working in the field of conventional and high-throughput macromolecular crystallography.

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Review

"It is an excellent, up-to-date review of the methods currently used by x-ray crystallography laboratories around the world." -- *The Quarterly Review of Biology*, Vol. 83

About the Author

Jane Skelly has widespread experience in the expression and crystallisation of macromolecules. Both editors lecture undergraduates in structural biology.

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