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Dorothee Liebschner*

Molecular Biophysics and Integrated Bioimaging Division, Lawrence Berkeley National Laboratory (LBNL), Berkeley, CA 94720, USA. *Correspondence e-mail: dcliebschner@lbl.gov

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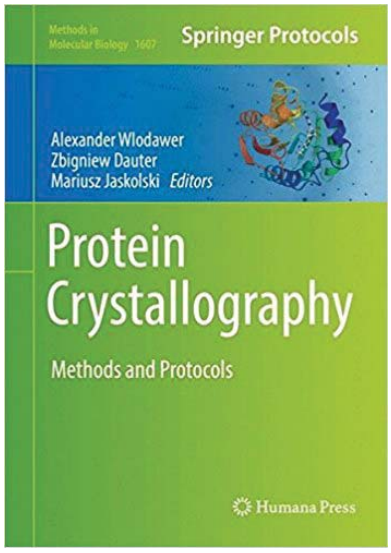
The book *Protein Crystallography – Methods and Protocols* is a new volume of Springer's *Methods in Molecular Biology* series, which aims to describe protocols and methodologies for biomedical research topics. The hardcover volume has 672 pages, divided into 27 chapters. A short preface summarizes the progress of macromolecular crystallography (MX) since the first structure determination in 1957 and highlights major achievements, underlining the importance of MX as a research discipline.

The chapters are written by specialists in their fields and intend to acquaint the reader with the newest advances in MX by describing currently available methods and tools. The order of the chapters follows the logical sequence of the protein structure determination process, starting with expression/purification and then covering topics related to protein crystallization, data collection, phasing, model building, refinement, validation and finally data deposition. Therefore, the chapters describe a wide range of methods, from wet-lab experiments to diffraction data acquisition and computer calculations.

Chapter 1 covers expression and purification of recombinant proteins and contains step-by-step protocols as well as examples for purification results. The principles and techniques of protein crystallization are discussed in chapters 2 to 5: chapter 2 gives a general overview, chapter 3 describes advanced methods, chapter 4 explains the current model of the crystallization process and chapter 5 summarizes techniques for membrane proteins. It is clear that protein crystallization is a topic deserving an entire book by itself, but the four chapters succeed in giving a concise overview and provide an extensive list of literature (637 references in total) for readers who want to delve deeper into certain techniques.

Chapters 6 to 13 are devoted to various topics related to the collection of the diffraction data. They describe more recent experimental advances that might not be familiar to every crystallographer. For example, the reader is introduced to methods for locating and visualizing crystals in diffraction experiments (chapter 6), which is of increasing importance at advanced X-ray sources. Reviews on micro-beam data collection (chapter 9), serial synchrotron X-ray crystallography (chapter 10), time-resolved MX experiments (chapter 11), X-ray free-electron laser (XFEL) structure determination (chapter 12) and XFEL data processing (chapter 13) will allow experimentalists to extend their palette of possible tools. Chapter 8 gives an overview of crystal pathologies (disorder and twinning) and several well chosen examples illustrate how they manifest themselves in diffraction images. Chapter 7 is useful as it summarizes important factors for X-ray data collection and explains appropriate strategies for various applications.

Chapters 14 to 20 are dedicated to the solution of the phase problem and some other topics that have undergone significant progress in recent years, such as long-wavelength X-ray diffraction (chapter 17), structure prediction as tool for solving molecular replacement (MR) problems (chapter 19) and radiation damage (chapter 20). The reviews will certainly be helpful to those who plan to tackle the phase problem with anomalous diffraction experiments or who are facing difficulties with MR. The next three chapters address refinement and model building, starting with an overview (chapter 21) and then presenting atomic resolution (chapter 22) and low-resolution refinement (chapter 23). Refinement constitutes an important part of the structure determination process and I feel that a greater focus on recent developments would have been useful.



Model validation and data deposition are explained in the last four chapters. Chapter 24 describes basic concepts of model validation and discusses the Protein Data Bank (PDB) validation report, which is helpful for depositors and those who want to assess the quality of a deposited model. Chapter 25 tackles the validation of protein-ligand models and provides clear guidelines on how to validate ligands and gives several examples of 'bad' ligands. The history of the PDB and its role in archiving structural models is described in chapter 26. The last chapter (27) examines the present attempts and future challenges of storing experimental data.

The emphasis of most chapters is on describing the methods and not on supplying step-by-step protocols, although a few chapters do contain lists of instructions. As stated in the preface, the aim of the book is to provide an overview of advances in the field and the chapters succeed in acquainting the reader with the current state-of-the-art in MX. It can be noted that the general approach of the chapters is not consistently the same. Some chapters contain protocols, while others provide a review of the topic and yet others may give subjective recommendations. However, this is not a disadvantage as the diverse approaches expose the reader to different viewpoints. The level of difficulty ranges from simple and intuitive to intermediate. Most topics are explained in easy-to-understand language and illustrated with appropriate pictures. There are a few typographical errors and some pictures could have been formatted a bit better, but overall, the book is well produced. In conclusion, the book contains many useful overviews to various novel aspects of protein crystallography. It is therefore an excellent complement to a regular textbook, as it focuses on recent advances and discusses topics that are often not thoroughly covered in textbooks. The book is thus a useful source of information for graduate students and more senior researchers alike.