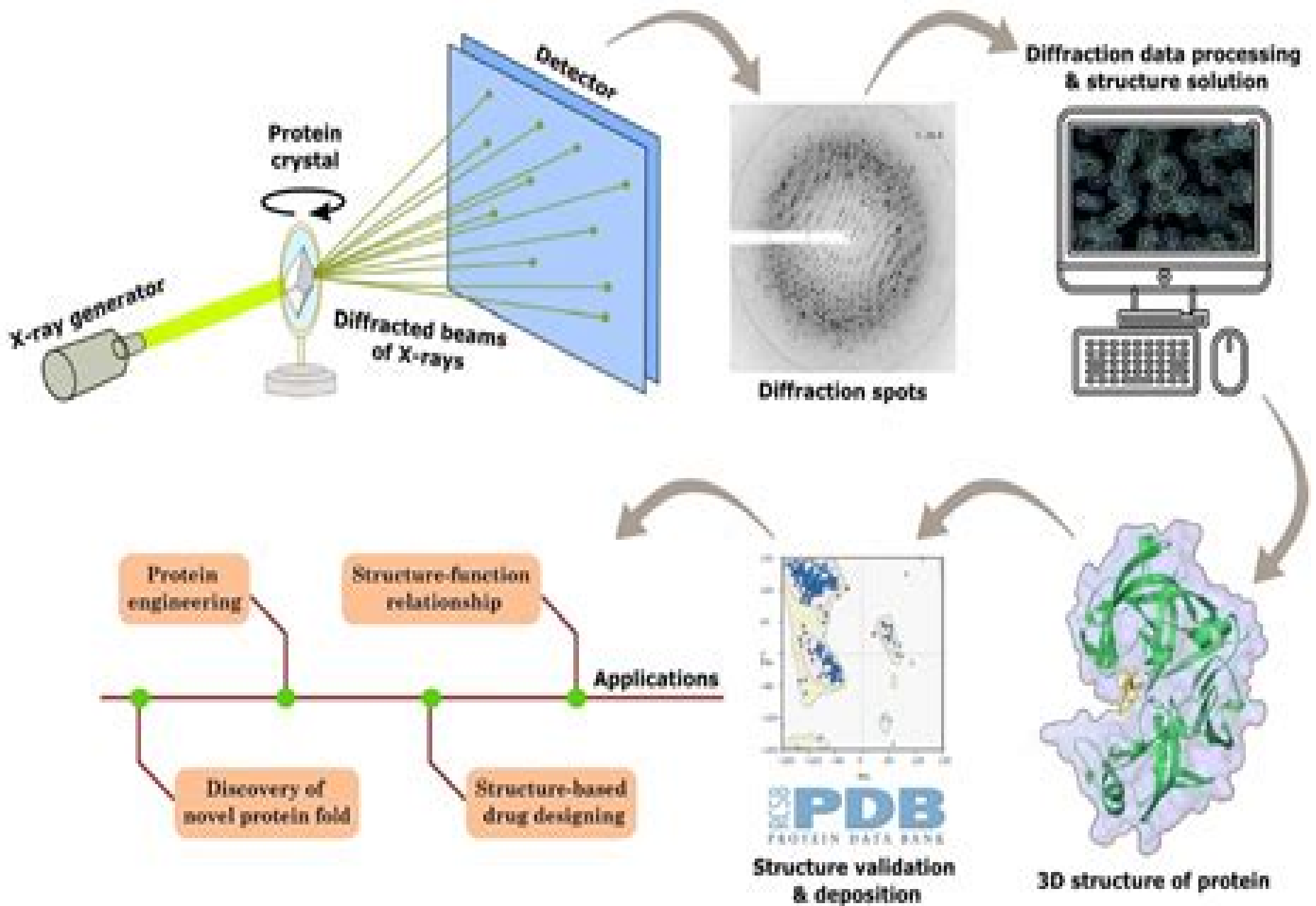




Protein Crystallography

Jan Drenth



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Protein Crystallography Eaton E. Lattman, Patrick J. Loll, 2008-03-26 The proteome remains a mysterious realm. Researchers have determined the structures of only a small fraction of the proteins encoded by the human genome. Crystallography continues to be the primary method used to determine the structures of the remaining unknown proteins. This imaging technique uses the diffraction of X rays to determine a protein's three dimensional molecular structure. Drawing on years of research and teaching experience, Eaton E. Lattman and Patrick J. Loll use clear examples and abundant illustrations to provide a concise and accessible primer on protein crystallography. Discussing the basics of diffraction, the behavior of two and three dimensional crystals, phase determination including MIR and MAD phasing, and molecular replacement, the Patterson function, and refinement, Lattman and Loll provide a complete overview of this important technique, illuminated by physical insights. The crisp writing style and simple illustrations will provide beginner crystallographers with a guide to the process of unraveling protein structure. Protein Crystallography T. L. Blundell, L. N. Johnson, 1976-01-28 Protein Crystallography Konstantinos Beis, Gwyndaf Evans, 2018-06-19 Protein crystallography has become vital to further understanding the structure and function of many complex biological systems. In recent years, structure determination has progressed tremendously; however, the quality of crystals and data sets can prevent the best results from being obtained. With contributions from world leading researchers whose software are used worldwide, this book provides a coherent approach on how to handle difficult crystallographic data and how to assess its quality. The chapters will cover all key aspects of protein crystallography from instrumentation and data processing through to model building. This book also addresses challenges that protein crystallographers will face, such as dealing with data from microcrystals and multi protein complexes. This book is ideal for both academics and researchers in industry looking for a comprehensive guide to protein crystallography. *Principles of Protein X-ray Crystallography* Jan Drenth, 2002-02-15 New textbooks at all levels of chemistry appear with great regularity. Some fields, such as basic biochemistry, organic reaction mechanisms, and chemical thermodynamics, are well represented by many excellent texts, and new or revised editions are published sufficiently often to keep up with progress in research. However, some areas of chemistry, especially many of those taught at the graduate level, suffer from a real lack of up to date textbooks. The most serious needs occur in fields that are rapidly changing. Textbooks in these subjects usually have to be written by scientists actually involved in the research that is advancing the field. It is not often easy to persuade such individuals to set time aside to help spread the knowledge they have accumulated. Our goal in this series is to pinpoint areas of chemistry where recent progress has outpaced what is covered in any available textbooks, and then seek out and persuade experts in these fields to produce relatively concise but instructive introductions to their fields. These should serve the needs of one semester or one quarter graduate courses in chemistry and biochemistry. In some cases, the availability of texts in active research areas should help stimulate the creation of new courses. Charles R. Cantor v

Preface to the Second Edition Since the publication of the previous edition in 1994 X ray crystallography of proteins has advanced by improvements in existing techniques and by addition of new techniques **Protein Crystallography** Gwyndaf Evans,Konstantinos Beis,2018-06-21 Protein crystallography has become vital to further understanding the structure and function of many complex biological systems In recent years structure determination has progressed tremendously however the quality of crystals and data sets can prevent the best results from being obtained With contributions from world leading researchers whose software are used worldwide this book provides a coherent approach on how to handle difficult crystallographic data and how to assess its quality The chapters will cover all key aspects of protein crystallography from instrumentation and data processing through to model building This book also addresses challenges that protein crystallographers will face such as dealing with data from microcrystals and multi protein complexes This book is ideal for both academics and researchers in industry looking for a comprehensive guide to protein crystallography Protein Crystallography in Drug Discovery Robert E. Babine,Sherin S. Abdel-Meguid,2008-07-15 The rational structure based approach has become standard in present day drug design As a consequence the availability of high resolution structures of target proteins is more often than not the basis for an entire drug development program Protein structures suited for rational drug design are almost exclusively derived from crystallographic studies and drug developers are relying heavily on the power of this method Here researchers from leading pharmaceutical companies present valuable first hand information much of it published for the first time They discuss strategies to derive high resolution structures for such important target protein classes as kinases or proteases as well as selected examples of successful protein crystallographic studies A special section on recent methodological developments such as for high throughput crystallography and microcrystallization is also included A valuable companion for crystallographers involved in protein structure determination as well as drug developers pursuing the structure based approach for use in their daily work Crystals, X-rays and Proteins Dennis Sherwood,Jon Cooper,2010-11-05 A complete account of the theory of the diffraction of X rays by crystals with particular reference to the processes of determining the structures of protein molecules This book is aimed primarily at structural biologists and biochemists but will also be valuable to those entering the field with a background in physical sciences or chemistry It may be used at any post school level and develops from first principles all relevant mathematics diffraction and wave theory assuming no mathematical knowledge beyond integral calculus The book covers a host of important topics in the area including The practical aspects of sample preparation and X ray data collection using both laboratory and synchrotron sources Data analysis at both theoretical and practical levels The important role played by the Patterson function in structure analysis by both molecular replacement and experimental phasing approaches Methods for improving the resulting electron density map The theoretical basis of methods used in refinement of protein crystal structures In depth explanation of the crucial task of defining the binding sites of ligands and drug molecules The complementary roles of other diffraction methods

these reveal further detail of great functional importance in a crystal structure

Principles of Protein X-Ray

Crystallography Jan Drenth, 2007-04-05 X ray crystallography is an established method for studying the structure of proteins and other macromolecules As the importance of proteins grows researchers in many fields have found that a working knowledge of X ray diffraction is an indispensable tool In this new edition of his essential work the internationally recognized researcher Dr Jan Drenth offers an up to date and technically rigorous introduction to the subject providing the theoretical background necessary to understand how the structure of proteins is determined at atomic resolution New material in the 3rd edition includes a section on twinning an additional chapter on crystal growth and a discussion of single wavelength anomalous dispersion

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