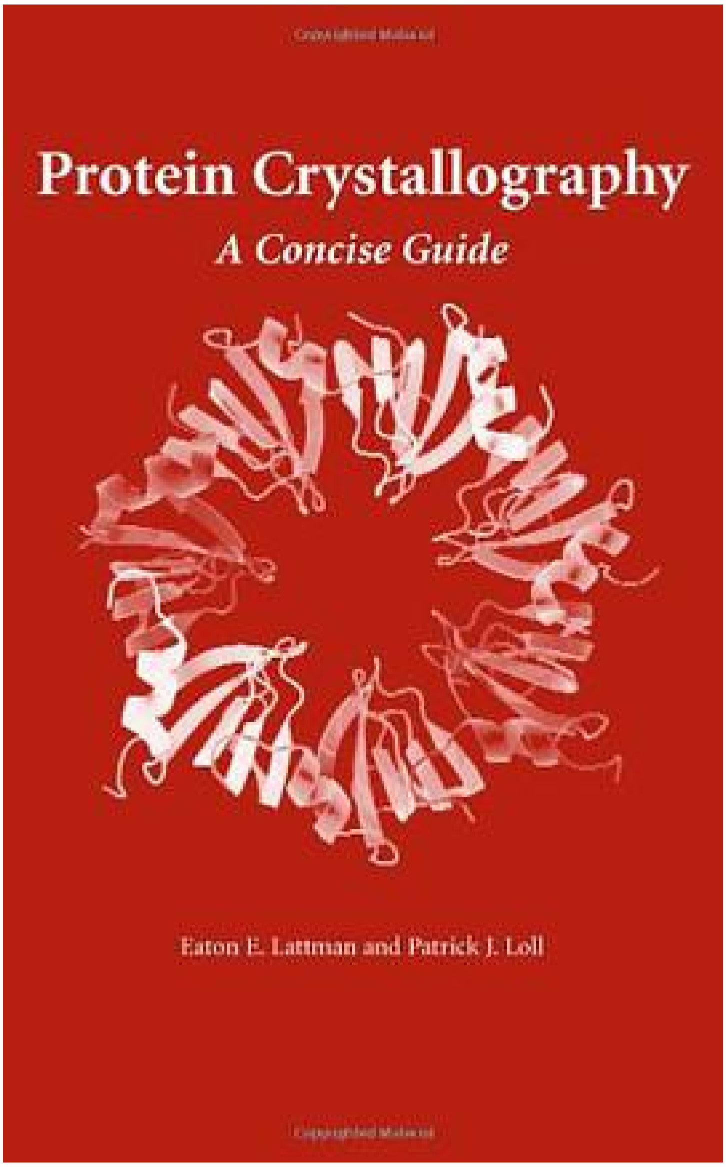
Protein Crystallography



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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.

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标签

评论

书评