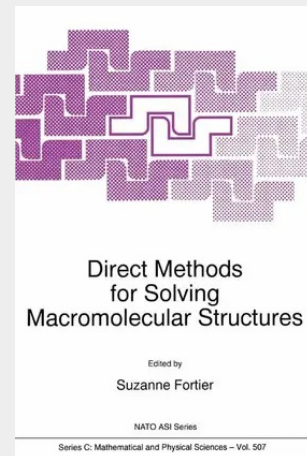


Direct Methods for Solving Macromolecular Structures

This book of the proceedings of the 1997 NATO Advanced Study Institute (ASI) on Direct Methods for Solving Macromolecular Structures was assembled from the lecturers' contributions and represents a comprehensive and in-depth overview of crystallographic structure determination methods for macromolecules. While having a focus based on the direct methods, the Institute adopted an inclusive and broad perspective. Thus, both direct and experimental phasing techniques are presented in this book, highlighting their complementarities and synergies. As well, methodologies spanning the full crystallographic image reconstruction process - from low resolution envelope definition to high resolution atomic refinement- are discussed. The first part of the book introduces the array of tools currently used in structure determination, whether originating from a mathematical, computational or experimental framework. This section of the book displays the variety and ingenuity of old and new phasing approaches developed to solve increasingly complex structures. Some of the contributions focus on recent developments and/or implementations that have given older approaches a new life. A case in point is the re-implementation of Buerger's superposition approach, which is now solving protein structures. Another beautiful example is found in the introduction to the traditional multiple isomorphous replacement approach where new techniques, such as site-directed mutagenesis and the use of inert gases in the preparation of heavy atom derivatives, are described. Equally impressive are the presentations of newer approaches, which take advantage of advances on the experimental front (e. g.

This book of the proceedings of the 1997 NATO Advanced Study Institute (ASI) on Direct Methods for Solving Macromolecular Structures was assembled from the lecturers' contributions and represents a comprehensive and in-depth overview of crystallographic structure determination methods for macromolecules. While having a focus based on the direct methods, the Institute adopted an inclusive and broad perspective. Thus, both direct and experimental phasing techniques are presented in this book, highlighting their complementarities and synergies. As well, methodologies spanning the full crystallographic image reconstruction process - from low resolution envelope definition to high resolution atomic refinement- are discussed. The first part of the book introduces the array of tools currently used in structure determination, whether originating from a mathematical, computational or experimental framework. This section of the book displays the variety and ingenuity of old and new phasing approaches developed to solve increasingly complex structures. Some of the contributions focus on recent developments and/or implementations that have given older approaches a new life. A case in point is the re-implementation of Buerger's superposition approach, which is now solving protein structures. Another beautiful example is found in the introduction to the traditional multiple isomorphous replacement approach where new techniques, such as site-directed mutagenesis and the use of inert gases in the preparation of heavy atom derivatives, are described. Equally impressive are the presentations of newer approaches, which take advantage of advances on the experimental front (e. g.



213,99 €

199,99 € (zzgl. MwSt.)

Lieferfrist: bis zu 10 Tage

Artikelnummer: 9780792349495

Medium: Buch

ISBN: 978-0-7923-4949-5

Verlag: Springer

Erscheinungstermin: 28.02.1998

Sprache(n): Englisch

Auflage: 1998

Serie: Nato Science Series C:

Produktform: Gebunden

Gewicht: 969 g

Seiten: 526

Format (B x H): 160 x 241 mm

