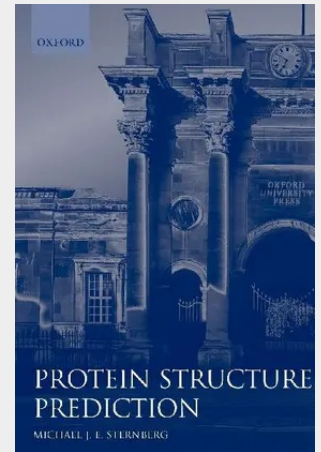


Protein Structure Prediction

A Practical Approach

The three-dimensional structure of proteins is a key factor in their biological activity. There is an increasing need to be able to predict the structure of a protein once its amino-acid sequence is known; this book presents practical methods of achieving that ambitious aim, using the latest computer modelling algorithms.

The prediction of the three-dimensional structure of a protein from its amino acid sequence is a problem faced by an increasing number of biological scientists. This book provides a practical guide to making these predictions by reviewing strategies of different computer modeling algorithms and highlighting the degree of confidence attributed to them. Also in the volume are descriptions of the following: the principles of protein folding; sequence homology and motif searches; prediction of secondary structure; homology modeling; modeling of antibody combining sites; tertiary fold recognition; modeling of transmembrane proteins; ab initio prediction; protein-ligand docking simulations; and the use of molecular mechanics and dynamics. both non-specialists who require guidance to identify and evaluate appropriate strategies and experts who require a contemporary view of the field, will find this volume a worthy addition to their research libraries.



81,60 €

81,60 € (zzgl. MwSt.)

Lieferfrist: bis zu 10 Tage

Artikelnummer: 9780199634965

Medium: Buch

ISBN: 978-0-19-963496-5

Verlag: OUP Oxford

Erscheinungstermin: 01.03.1997

Sprache(n): Englisch

Auflage: Erscheinungsjahr 1997

Produktform: Kartoniert

Gewicht: 488 g

Seiten: 318

Format (B x H): 156 x 234 mm

