



Computational Methods for Protein Structure Prediction and Modeling: 1 (Biological and Medical Physics, Biomedical Engineering)

Ying Xu, Dong Xu, Jie Liang

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Volume one of this two volume sequence focuses on the basic characterization of known protein structures as well as structure prediction from protein sequence information. The 11 chapters provide an overview of the field, covering key topics in modeling, force fields, classification, computational methods, and structure prediction. Each chapter is a self contained review designed to cover (1) definition of the problem and an historical perspective, (2) mathematical or computational formulation of the problem, (3) computational methods and algorithms, (4) performance results, (5) existing software packages, and (6) strengths, pitfalls, challenges, and future research directions. Key Features Addresses a broad interdisciplinary audience in biophysics and biochemistry, molecular and cell biology, computational biology, and bioinformatics Provides a comprehensive overview of protein biophysics for both professionals and graduate students Presents computational methods for all major aspects of protein structure analysis Each chapter offers a self-contained review

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