

1. Record Nr.	UNINA9910806241903321
Titolo	Introduction to protein structure prediction : methods and algorithms / / edited by Huzefa Rangwala, George Karypis
Pubbl/distr/stampa	Hoboken, NJ, : Wiley, 2010
ISBN	1-118-09946-X 1-282-78286-X 9786612782862 0-470-88220-4 0-470-88219-0
Edizione	[1st ed.]
Descrizione fisica	1 online resource (532 p.)
Collana	Wiley series in bioinformatics ; ; 14
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Disciplina	572/.633
Soggetti	Proteins - Structure - Mathematical models Proteins - Structure - Computer simulation
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	INTRODUCTION TO PROTEIN STRUCTURE PREDICTION: Methods and Algorithms; CONTENTS; PREFACE; CONTRIBUTORS; CHAPTER 1: INTRODUCTION TO PROTEIN STRUCTURE PREDICTION; CHAPTER 2: CASP : A DRIVING FORCE IN PROTEIN STRUCTURE MODELING; CHAPTER 3: THE PROTEIN STRUCTURE INITIATIVE; CHAPTER 4: PREDICTION OF ONE - DIMENSIONAL STRUCTURAL PROPERTIES OF PROTEINS BY INTEGRATED NEURAL NETWORKS; CHAPTER 5: LOCAL STRUCTURE ALPHABETS; CHAPTER 6: SHEDDING LIGHT ON TRANSMEMBRANE TOPOLOGY; CHAPTER 7: CONTACT MAP PREDICTION BY MACHINE LEARNING CHAPTER 8: A SURVEY OF REMOTE HOMOLOGY DETECTION AND FOLD RECOGNITION METHODS CHAPTER 9: INTEGRATIVE PROTEIN FOLD RECOGNITION BY ALIGNMENTS AND MACHINE LEARNING; CHAPTER 10: TASSER - BASED PROTEIN STRUCTURE PREDICTION; CHAPTER 11: COMPOSITE APPROACHES TO PROTEIN TERTIARY STRUCTURE PREDICTION: A CASE - STUDY BY I - TASSER; CHAPTER 12: HYBRID METHODS FOR PROTEIN STRUCTURE PREDICTION; CHAPTER 13:

MODELING LOOPS IN PROTEIN STRUCTURES; CHAPTER 14: MODEL QUALITY ASSESSMENT USING A STATISTICAL PROGRAM THAT ADOPTS A SIDE CHAIN ENVIRONMENT VIEWPOINT; CHAPTER 15: MODEL QUALITY PREDICTION
CHAPTER 16: LIGAND - BINDING RESIDUE PREDICTION CHAPTER 17: MODELING AND VALIDATION OF TRANSMEMBRANE PROTEIN STRUCTURES; CHAPTER 18: STRUCTURE - BASED MACHINE LEARNING MODELS FOR COMPUTATIONAL MUTAGENESIS; CHAPTER 19: CONFORMATIONAL SEARCH FOR THE PROTEIN NATIVE STATE; CHAPTER 20: MODELING MUTATIONS IN PROTEINS USING MEDUSA AND DISCRETE MOLECULE DYNAMICS; INDEX; colour plates

Sommario/riassunto

A look at the methods and algorithms used to predict protein structure
A thorough knowledge of the function and structure of proteins is critical for the advancement of biology and the life sciences as well as the development of better drugs, higher-yield crops, and even synthetic bio-fuels. To that end, this reference sheds light on the methods used for protein structure prediction and reveals the key applications of modeled structures. This indispensable book covers the applications of modeled protein structures and unravels the relationship between pure sequence information and
