1. Record Nr. UNINA9910877567303321

Titolo	Computational methods for protein folding / / edited by Richard A. Friesner
Pubbl/distr/stampa	New York, : Wiley, 2002
ISBN	1-280-36766-0 9786610367665 0-470-34930-1 0-471-46523-2 0-471-22442-1
Descrizione fisica	1 online resource (546 p.)
Collana	Advances in chemical physics ; ; v. 120
Altri autori (Persone)	FriesnerRichard A
Disciplina	541.305 541/.08 547.75
Soggetti	Protein folding - Mathematical models Proteins - Conformation - Mathematical models
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di contenuto	COMPUTATIONAL METHODS FOR PROTEIN FOLDING A SPECIAL VOLUME OF ADVANCES IN CHEMICAL PHYSICS VOLUME 120; CONTRIBUTORS TO VOLUME 120; INTRODUCTION; PREFACE; CONTENTS; STATISTICAL ANALYSIS OF PROTEIN FOLDING KINETICS; INSIGHTS INTO SPECIFIC PROBLEMS IN PROTEIN FOLDING USING SIMPLE CONCEPTS; PROTEIN RECOGNITION BY SEQUENCE-TO-STRUCTURE FITNESS: BRIDGING EFFICIENCY AND CAPACITY OF THREADING MODELS; A UNIFIED APPROACH TO THE PREDICTION OF PROTEIN STRUCTURE AND FUNCTION; KNOWLEDGE-BASED PREDICTION OF PROTEIN TERTIARY STRUCTURE AB INITIO PROTEIN STRUCTURE PREDICTION USING A SIZE-DEPENDENT TERTIARY FOLDING POTENTIALDETERMINISTIC GLOBAL OPTIMIZATION AND AB INITIO APPROACHES FOR THE STRUCTURE PREDICTION OF POLYPEPTIDES, DYNAMICS OF PROTEIN FOLDING, AND PROTEIN-PROTEIN INTERACTIONS; DETECTING NATIVE PROTEIN FOLDS AMONG LARGE DECOY SITES WITH THE OPLS ALL-ATOM POTENTIAL AND THE

	SURFACE GENERALIZED BORN SOLVENT MODEL; AUTHOR INDEX; SUBJECT INDEX
Sommario/riassunto	Since the first attempts to model proteins on a computer began almost thirty years ago, our understanding of protein structure and dynamics has dramatically increased. Spectroscopic measurement techniques continue to improve in resolution and sensitivity, allowing a wealth of information to be obtained with regard to the kinetics of protein folding and unfolding, and complementing the detailed structural picture of the folded state. Concurrently, algorithms, software, and computational hardware have progressed to the point where both structural and kinetic problems may be studied with a fair d