1.	Record Nr.	UNINA9910877633003321
	Titolo	Prediction of protein structures, functions, and interactions / / edited by Janusz M. Bujnicki
	Pubbl/distr/stampa	Chichester, U.K., : Wiley, 2009
	ISBN	1-282-03426-X
		9786612034268
		0-470-74189-9
		0-470-74190-2
	Descrizione fisica	1 online resource (306 p.)
	Altri autori (Persone)	BujnickiJanusz M
	Disciplina	572.633
		572/.633
	Soggetti	Proteins - Structures
		Amino acid sequence
		Protein-protein interactions
	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	Prediction of Protein Structures, Functions, and Interactions; Contents; List of Contributors; Preface; 1 The Basics of Protein Sequence Analysis; 2 First Steps of Protein Structure Prediction; 3 Automated Prediction of Protein Function from Sequence; 4 Template Based Prediction of Three-dimensional Protein Structures: Fold Recognition and Comparative Modeling; 5 Template-free Predictions of Three-dimensional Protein Structures: From First Principles to Knowledge-based Potentials; 6 Quality Assessment of Protein Models
		7 Prediction of Molecular Interactions from 3D-structures: From Small Ligands to Large Protein Complexes8 Structure-based Prediction of Enzymes and Their Active Sites; 9 The Prediction of Macromolecular Complexes by Docking; 10 Protein Function Prediction via Analysis of Interactomes; 11 Integrating Prediction of Structure, Function, and Interactions; Index; Color Plate
	Sommario/riassunto	The growing flood of new experimental data generated by genome sequencing has provided an impetus for the development of automated methods for predicting the functions of proteins that have been

deduced by sequence analysis and lack experimental characterization. Prediction of Protein Structures, Functions and Interactions presents a comprehensive overview of methods for prediction of protein structure or function, with the emphasis on their availability and possibilities for their combined use. Methods of modeling of individual proteins, prediction of their interactions, and docking of comp