Record Nr. UNINA9910144546003321 Prediction of protein structures, functions, and interactions [[electronic **Titolo** resource] /] / 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 Proteins - Structures Soggetti Amino acid sequence Protein-protein interactions Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Description based upon print version of record. Note generali 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 Threedimensional 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 The growing flood of new experimental data generated by genome Sommario/riassunto 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