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Autore	Shukla Pratyoosh
Titolo	Computational Approaches in Chlamydomonas reinhardtii for Effectual Bio-hydrogen Production [[electronic resource] /] / by Pratyoosh Shukla, M.V.K. Karthik
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Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	1. Introduction -- 2. Background -- 3. Material and Methods -- 4. Results and discussions -- 5. Conclusion.
Sommario/riassunto	This book describes the feasibility of using molecular dynamics as a screening technique to identify the stability of HydA1 and PetF interactions. Structure-based computational approaches are necessary to recognize and characterize protein-protein complexes and their functions. It introduces the idea that for specific proteins, homology modeling is the most effective technique and that docking algorithms are an increasingly powerful tool for providing a detailed explanation of such interactions. This book is a useful source of information on biomass-based biofuels for researchers in the field of bio-hydrogen and bioinformatics techniques. Biofuel and bioenergy produced from unicellular microalgae Chlamydomonas reinhardtii is a clean energy

source, and providing information about functional optimization in HydA1 and PetF interactions will help researchers to adopt swift screening methods to identify key protein complexes and their functions. The book also provides an introduction to hydrogenases and associated *Chlamydomonas reinhardtii*, which is a useful model microorganism for research on biofuel production. The book focuses on the in silico methods such as phylogenetic studies, homology modeling, molecular docking, electrostatic studies and conformational analysis, which have the potential to become the most cost-effective methods for bio-fuel production. This book provides a valuable resource to senior undergraduate and graduate students, researchers, professionals and other interested individuals or groups working in the area of bioenergy with special reference to microalgal biofuel.
