

1. Record Nr.	UNINA9910373917803321
Titolo	Actin Polymerization in Apicomplexan : A Structural, Functional and Evolutionary Analysis // edited by Avinash Kale
Pubbl/distr/stampa	Singapore : , : Springer Singapore : , : Imprint : Springer, , 2019
ISBN	981-13-7450-3
Edizione	[1st ed. 2019.]
Descrizione fisica	1 online resource (XI, 101 p. 11 illus. in color.)
Disciplina	616.96
Soggetti	Enginyeria de proteïnes Parasitology Biomechanics Proteins Bioinformatics Protein Science Protein Structure Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Chapter 1. Synthesis and Characterization of nano Apicomplexan motility: A cellular perspective particles -- Chapter 2. Introduction: Gliding Motility- The model and the mechanism -- Chapter 3. Actin: The central ubiquitous player in the phenomenon -- Chapter 4. Formin: The multidomain elongator of polymer -- Chapter 5. Profilin: The associates of Formin -- Chapter 6. ADF (Actin Depolymerizing Factor): The breaker of the polymer in homeostasis -- Chapter 7. Cyclase associated protein (CAP): The silent worker -- Chapter 8. Capping Protein (CP): The formin competitor -- Chapter 9. Coronin: An Overview -- Chapter 10. Mathematical Model: A revelation of synergistic cross talks between the actin regulators -- Chapter 11. Evolution: The hallmarks of Gliding motility in apicomplexan.
Sommario/riassunto	This book discusses in detail the structural, evolutionary and functional role of actin and its regulatory proteins in gliding motility in apicomplexan organisms, a unique phenomenon found in actin-myosin cytoskeletal elements. The book also explores the potential of different

actin regulators, namely formin, profilin, actin depolymerization factor (ADF), capping proteins (CP and CP), cyclase-associated protein (CAP) and coronin 13–24 as potential drug targets against malaria. As the chief components of the gliding motor, the actin-regulator proteins are characterized by unique features that make them promising targets for structure-based drug design. Lastly, the book proposes a mathematical model, based on kinetic data mining, to help understand the most vital regulators for actin polymerization dynamics.
