

1. Record Nr.	UNINA9910373917803321
Titolo	Actin Polymerization in Apicomplexan : A Structural, Functional and Evolutionary Analysis / / edited by Avinash Kale
Pubbl/distr/stampa	Singapore : , : Springer Nature 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	Parasitology Biomechanics Proteins Bioinformatics Protein Biochemistry
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.
