Record Nr. UNINA9910299748203321 Autore Jens Marvin Titolo Dissecting Regulatory Interactions of RNA and Protein: Combining Computation and High-throughput Experiments in Systems Biology // by Marvin Jens Cham:,: Springer International Publishing:,: Imprint: Springer,, Pubbl/distr/stampa 2014 3-319-07082-7 **ISBN** Edizione [1st ed. 2014.] Descrizione fisica 1 online resource (115 p.) Collana Springer Theses, Recognizing Outstanding Ph.D. Research, , 2190-5053 Disciplina 574.873282 Soggetti Computational intelligence Systems biology Biological systems Gene expression **Biochemistry** Computational Intelligence Systems Biology Gene Expression Biochemistry, general Lingua di pubblicazione Inglese Materiale a stampa **Formato** Livello bibliografico Monografia Note generali "Doctoral Thesis accepted by Humboldt University of Berlin, Germany." Includes bibliographical references at the end of each chapters. Nota di bibliografia Nota di contenuto Introduction -- Computational analysis of PAR-CLIP data --Transcriptome-wide analysis of regulatory interactions of the RNAbinding protein HuR -- Binding site occupancy with competition interactions in equilibrium -- Circular RNAs are a large class of animal RNAs with regulatory potency -- Discussion -- Methods. Sommario/riassunto The work described in this book is an excellent example of interdisciplinary research in systems biology. It shows how concepts and approaches from the field of physics can be efficiently used to

answer biological questions, and reports on a novel methodology involving creative computer-based analyses of high-throughput biological data. Many of the findings described in the book, which are the result of collaborations between the author (a theoretical scientist)

and experimental biologists, and between different laboratories, have been published in high-quality peer-reviewed journals such as Molecular Cell and Nature. However, while those publications address different aspects of post-transcriptional gene regulation, this book provides readers with a complete, coherent and logical view of the research project as a whole. The introduction presents post-transcriptional gene regulation from a distinct angle, highlighting aspects of information theory and evolution, and laying the groundwork for the questions addressed in the subsequent chapters, which concern the regulation of the transcriptome as the primary functional carrier of active genetic information.