

1. Record Nr.	UNINA9910298412703321
Autore	Kadkhodaei
Titolo	Cis/Transgene Optimization : Systematic Discovery of Novel Gene Expression Elements Using Bioinformatics and Computational Biology Approaches // by Saeid Kadkhodaei, Farahnaz Sadat Golestan Hashemi, Morvarid Akhavan Rezaei, Sahar Abbasiliasi, Joo Shun Tan, Hamid Rajabi Memari, Faruku Bande, Ali Baradaran, Mahdi Moradpour, Arbakariya B, Ariff
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2018
ISBN	3-319-90391-8
Edizione	[1. 2018.]
Descrizione fisica	1 online resource (XVII, 120 p. 24 illus.)
Collana	SpringerBriefs in Systems Biology, , 2193-4746
Altri autori (Persone)	Saeid
Disciplina	615.32
Soggetti	Bioinformatics Computational biology Systems biology Proteomics Computer Appl. in Life Sciences Systems Biology Computational Biology/Bioinformatics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	1. Introduction -- 2. Systematic Strategies -- 3. Outcomes Assessment -- 4. Conceptual Models.
Sommario/riassunto	This book is a practical review which focuses on computational analysis and on in silico approaches towards the systematic discovery of various key functional gene expression elements in microalgae as a model. So far, in this regard very little information is available. Efficient stepwise procedures for analysing the matrix attachment regions (MARs) are outlined, as well as for translation initiation sites (TIS), signal peptide (SP) sequences, gene optimization and transformation systems. These outlines can be efficiently deployed as practical models for the systematic discovery of key expression elements and for the optimization of cis/transgenes in other micro/organisms. The first

chapter is an introduction on the key gene expression elements analysed in this book, including scaffold/matrix attachment regions, translation initiation sites, signal peptides as well as gene optimization. Chapter 2 focuses on systematic strategies and computational approaches toward in silico analysis of each factor. The analyses outcomes is assessed individually in chapter 3 followed by developing the specific conceptual models for each element in Chapter 4. The concluding remarks are discussed in Chapter 5. This work is of interest to computational and experimental biologists interested in transcriptional regulation analysis as well as to researchers and scientists who wish to consider the use of bioinformatics and computational biology in design, analysis, or regulatory reviews of key gene expression elements for the production of recombinant proteins experiments.
