

1. Record Nr.	UNINA9910456683003321
Titolo	Advances in genomic sequence analysis and pattern discovery [[electronic resource] /] / editors, Laura Elnitski, Helen Piontkivska, Lonnie R. Welch
Pubbl/distr/stampa	Hackensack, N.J., : World Scientific, 2011
ISBN	1-283-14859-5 9786613148599 981-4327-73-5
Descrizione fisica	1 online resource (236 p.)
Collana	Science, engineering, and biology informatics ; ; v. 7
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Disciplina	572.86
Soggetti	Genomes - Analysis Gene mapping - Methodology Gene mapping - Data processing Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	pt. 1. Pattern discovery methods -- pt. 2. Performance and paradigms.
Sommario/riassunto	Mapping the genomic landscapes is one of the most exciting frontiers of science. We have the opportunity to reverse engineer the blueprints and the control systems of living organisms. Computational tools are key enablers in the deciphering process. This book provides an in-depth presentation of some of the important computational biology approaches to genomic sequence analysis. The first section of the book discusses methods for discovering patterns in DNA and RNA. This is followed by the second section that reflects on methods in various ways, including performance, usage and paradigms.