1.

Record Nr.	UNISA996413148103316
Autore	PARTRIDGE, Seth <1603-1686.>
Titolo	A survey of the yeer 1653, or, An alamanck for the yeare of Christ 1653 and of the worlds creation 5602 : being the first after leap-year : calculated and principally referred to the meridian and latitude of the honourable city of London and without any sensible error may serve for any part of England / composed by Seth Partridge
Pubbl/distr/stampa	London, : Printed by Jane Bell for the Company of Stationers, [1653]
Descrizione fisica	Testo elettronico (PDF) ([40] p. : ill.)
Disciplina	133.5
Soggetti	Astrologia - Almanacchi
Lingua di pubblicazione	Inglese
Formato	Risorsa elettronica
Livello bibliografico	Monografia
Note generali	Riproduzione dell'originale nella British Library.

2. Record Nr.	UNISA996466288303316
Titolo	Advances in Bioinformatics and Computational Biology [[electronic resource]] : 5th Brazilian Symposium on Bioinformatics, BSB 2010, Rio de Janeiro, Brazil, August 31--September 3, 2010, Proceedings / / edited by Carlos E. Ferreira, Satoru Miyano, Peter F. Stadler
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	3-642-15060-8
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (IX, 81 p. 18 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 6268
Disciplina	570.285
Soggetti	Life sciences Computer programming Data structures (Computer science) Artificial intelligence Computers Algorithms Life Sciences, general Programming Techniques Data Structures and Information Theory Artificial Intelligence Computation by Abstract Devices Algorithm Analysis and Problem Complexity Rio de Janeiro <2010>
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Full Papers -- Evolution of the Long Non-coding RNAs MALAT1 and MEN?/? -- Granger Causality in Systems Biology: Modeling Gene Networks in Time Series Microarray Data Using Vector Autoregressive Models -- Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data -- Bounds on the Transposition Distance for Lonely Permutations -- Insights on Haplotype Inference on Large Genotype Datasets -- Extended Abstracts -- An SVM Model Based on

Physicochemical Properties to Predict Antimicrobial Activity from Protein Sequences with Cysteine Knot Motifs -- Enabling Annotation Provenance in Bioinformatics Workflow Applications -- BAT: A New Biclustering Analysis Toolbox -- Detection of Protein Domains in Eukaryotic Genome Sequences -- Discretization of Flexible-Receptor Docking Data.