1.

Record Nr.	UNINA990003043600403321
Titolo	De la bureaucratie / Léon Trotsky, Eugène Préobrajensky, Christian Rakovsky
Pubbl/distr/stampa	Paris : Francois Maspero, 1971
Descrizione fisica	132 p. ; 22 cm
Collana	Livres rouges
Disciplina	12530 19230
Locazione	SES
Collocazione	19230 TRO
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

2.

Record Nr.	UNISA990001932160203316
Autore	SCHULTE, Max
Titolo	Saggi critici : Goethe. Gotz, clavigo, Stella, egmont, Campagna in Francia, giudizi su Manzoni. Schiller. Lirica, die braut Von Messina / Massimo Schulte
Pubbl/distr/stampa	Napoli : Ed. Ist. Della Stampa, 1950
Descrizione fisica	109 p. ; 22 cm.
Collocazione	VII.2.B. 409(II T C 25)
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

3.	Record Nr.	UNINA9910782300703321
	Titolo	Genome sequencing technology and algorithms / / Sun Kim, Haixu Tang, Elaine R. Mardis, editors
	Pubbl/distr/stampa	Boston : , : Artech House, , ©2008 [Piscataqay, New Jersey] : , : IEEE Xplore, , [2007]
	ISBN	1-59693-095-0
	Descrizione fisica	1 online resource (275 p.)
	Altri autori (Persone)	KimSun <1962-> TangHaixu MardisElaine <1962->
	Disciplina	572.86
	Soggetti	Genomes - Analysis Nucleotide sequence
	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	An overview of new DNA sequencing technology -- Array-based pyrosequencing technology -- The role of resequencing arrays in revolutionizing DNA sequencing -- Polony sequencing -- Genome sequencing: a complex path to personalized medicine -- Overview of genome assembly techniques -- Fragment assembly algorithms -- Assembly for double-ended short read sequencing technologies -- Genome characterization in the post-human genome project era -- The haplotyping problem: an overview of computational models and solutions -- Analysis of genomic alterations in cancer -- High-throughput assessments of epigenomics in human disease -- Comparative sequencing, assembly, and anchoring.
	Sommario/riassunto	"From a who's who of pioneers in the field comes a unique resource covering the latest advances in next generation genome sequencing and assembly. This groundbreaking book includes non-conventional techniques that are paving the way to potential new biomedical applications. Practitioners find unparalleled access to state-of-the-art DNA sequencing technologies, new algorithmic sequence assembly techniques, and emerging methods for both resequencing and de novo genome analysis, which all together offer the most solid foundation

possible for tackling the full range of experimental and computational challenges in the genome sciences today."--Jacket.