1.

Record Nr.	UNISA990005479880203316
Autore	TARALLO, Pietro
Titolo	Antiche vie del Giubileo : sette antichi itinerari italiani di arte e spiritualità / Pietro Tarallo, Gian Maria Grasselli
Pubbl/distr/stampa	Milano, : Rizzoli, 1998
ISBN	88-17-85254-6
Descrizione fisica	334 p. : ill. ; 23 cm
Altri autori (Persone)	GRASSELLI, Gian Maria
Disciplina	263.97
Soggetti	Giubilei
Collocazione	200 263.97 TAR
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

2.	Record Nr.	UNINA9911019177503321
	Titolo	Computational methods for mass spectrometry proteomics / / Ingvar Eidhammer ... [et al.]
	Pubbl/distr/stampa	Chichester, England ; ; Hoboken, NJ, : John Wiley & Sons, c2007
	ISBN	9786611321789 9781281321787 1281321788 9780470724309 0470724307 9780470724293 0470724293
	Descrizione fisica	1 online resource (298 p.)
	Altri autori (Persone)	EidhammerIngvar
	Disciplina	572/.60285
	Soggetti	Proteomics - Data processing Mass spectrometry - Data processing Bioinformatics
	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 (p. [265]-275) and index.
	Nota di contenuto	Protein, proteome, and proteomics -- Protein separation : 2D gel electrophoresis -- Protein digestion -- Peptide separation : HPLC -- Fundamentals of mass spectrometry -- Mass spectrometry : MALDI-TOF -- Protein identification and characterization by MS -- Tandem MS or MS/MS analysis -- Fragmentation models -- Identification and characterization by MS/MS -- Spectral comparisons -- Sequential comparison : de novo sequencing -- Database searching for de novo sequences -- Large-scale proteomics -- Quantitative MS-based proteomics -- Peptides to proteins -- Top-down proteomics -- Standards.
	Sommario/riassunto	Proteomics is the study of the subsets of proteins present in different parts of an organism and how they change with time and varying conditions. Mass spectrometry is the leading technology used in proteomics, and the field relies heavily on bioinformatics to process and analyze the acquired data. Since recent years have seen

tremendous developments in instrumentation and proteomics-related bioinformatics, there is clearly a need for a solid introduction to the crossroads where proteomics and bioinformatics meet. Computational Methods for Mass Spectrometry Proteomics describ