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	ISBN	1-281-32178-8 9786611321789 0-470-72430-7 0-470-72429-3
	Descrizione fisica	1 online resource (298 p.)
	Altri autori (Persone)	EidhammerIngvar
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	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