1.	Record Nr.	UNINA9910450686303321
	Titolo	Clusters and nano-assemblies [[electronic resource]] : physical and biological systems : Richmond, Virginia, U.S.A., 10-13 November, 2003 / / editors, P. Jena, S.N. Khanna, B.K. Rao
	Pubbl/distr/stampa	Singapore ; ; New York, : World Scientific Pub., c2005
	ISBN	1-281-37280-3 9786611372804 981-270-187-7
	Descrizione fisica	1 online resource (465 p.)
	Altri autori (Persone)	JenaP KhannaS. N RaoB. K
	Disciplina	539/.6
	Soggetti	Nanostructures Microclusters 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	Preface; CONTENTS; Atomic Clusters; Organic and Molecular Clusters; Catalysis; Quantum Dots/Rings; Nano-Wires and Tubes; Magnetic Properties; Electrical and Optical Properties; Clusters on Support; Nano-Growth on Strained SurfacedNano-Assemblies; Biology at Molecular Level; Bio technology; Organization; Participants; Author Index; Subject Index
	Sommario/riassunto	While the field of clusters and nano-structures in the physical sciences has been actively pursued only over the past two decades, nature has known the benefits of the nanoscale for a very long time. The focus of the International Symposium on Clusters and Nano-Assemblies: Physical and Biological Systems was to explore ways in which an understanding of the unique properties of nano-scale biological systems such as proteins, enzyme reactions, RNA, and DNA can help us design novel materials composed of inorganic nano-scale systems, and how techniques developed in the physical sciences can lead t

2.

Record Nr.	UNINA9910141482703321
Autore	Eidhammer Ingvar
Titolo	Computational and statistical methods for protein quantification by mass spectrometry [[electronic resource] /] / Ingvar Eidhammer ... [et al.]
Pubbl/distr/stampa	Chichester, West Sussex, U.K., : John Wiley & Sons Inc., 2013
ISBN	1-118-49404-0 1-299-18826-5 1-118-49378-8 1-118-49377-X
Descrizione fisica	1 online resource (356 p.)
Altri autori (Persone)	BarsnesHarald EideGeir Egil MartensLennart
Disciplina	572.636 572/.636
Soggetti	Proteomics - Statistical methods Mass spectrometry - Data processing
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	Computational and Statistical Methods for Protein Quantification by Mass Spectrometry; Contents; Preface; Terminology; Acknowledgements; 1 Introduction; 1.1 The composition of an organism; 1.1.1 A simple model of an organism; 1.1.2 Composition of cells; 1.2 Homeostasis, physiology, and pathology; 1.3 Protein synthesis; 1.4 Site, sample, state, and environment; 1.5 Abundance and expression - protein and proteome profiles; 1.5.1 The protein dynamic range; 1.6 The importance of exact specification of sites and states; 1.6.1 Biological features; 1.6.2 Physiological and pathological features 1.6.3 Input features1.6.4 External features; 1.6.5 Activity features; 1.6.6 The cell cycle; 1.7 Relative and absolute quantification; 1.7.1 Relative quantification; 1.7.2 Absolute quantification; 1.8 In vivo and in vitro experiments; 1.9 Goals for quantitative protein experiments; 1.10 Exercises; 2 Correlations of mRNA and protein abundances; 2.1 Investigating the correlation; 2.2 Codon bias; 2.3 Main results from

	experiments; 2.4 The ideal case for mRNA-protein comparison; 2.5 Exploring correlation across genes; 2.6 Exploring correlation within one gene; 2.7 Correlation across subsets 2.8 Comparing mRNA and protein abundances across genes from two situations2.9 Exercises; 2.10 Bibliographic notes; 3 Protein level quantification; 3.1 Two-dimensional gels; 3.1.1 Comparing results from different experiments - DIGE; 3.2 Protein arrays; 3.2.1 Forward arrays; 3.2.2 Reverse arrays; 3.2.3 Detection of binding molecules; 3.2.4 Analysis of protein array readouts; 3.3 Western blotting; 3.4 ELISA - Enzyme-Linked Immunosorbent Assay; 3.5 Bibliographic notes; 4 Mass spectrometry and protein identification; 4.1 Mass spectrometry; 4.1.1 Peptide mass fingerprinting (PMF) 4.1.2 MS/MS - tandem MS4.1.3 Mass spectrometers; 4.2 Isotope composition of peptides; 4.2.1 Predicting the isotope intensity distribution; 4.2.2 Estimating the charge; 4.2.3 Revealing isotope patterns; 4.3 Presenting the intensities - the spectra; 4.4 Peak intensity calculation; 4.5 Peptide identification by MS/MS spectra; 4.5.1 Spectral comparison; 4.5.2 Sequential comparison; 4.5.3 Scoring; 4.5.4 Statistical significance; 4.6 The protein inference problem; 4.6.1 Determining maximal explanatory sets; 4.6.2 Determining minimal explanatory sets; 4.7 False discovery rate for the identifications 4.7.1 Constructing the decoy database4.7.2 Separate or composite search; 4.8 Exercises; 4.9 Bibliographic notes; 5 Protein quantification by mass spectrometry; 5.1 Situations, protein, and peptide variants; 5.1.1 Situation; 5.1.2 Protein variants - peptide variants; 5.2 Replicates; 5.3 Run - experiment - project; 5.3.1 LC-MS/MS run; 5.3.2 Quantification run; 5.3.3 Quantification experiment; 5.3.4 Quantification project; 5.3.5 Planning quantification experiments; 5.4 Comparing quantification approaches/methods; 5.4.1 Accuracy; 5.4.2 Precision; 5.4.3 Repeatability and reproducibility 5.4.4 Dynamic range and linear dynamic range
Sommario/riassunto	The definitive introduction to data analysis in quantitative proteomics This book provides all the necessary knowledge about mass spectrometry based proteomics methods and computational and statistical approaches to pursue the planning, design and analysis of quantitative proteomics experiments. The author's carefully constructed approach allows readers to easily make the transition into the field of quantitative proteomics. Through detailed descriptions of wet-lab methods, computational approaches and statistical tools, this book covers the full scope of a quantitative experim

3.	Record Nr.	UNISALENTO991002176009707536
	Autore	Finley, Moses I.
	Titolo	Ho kosmos ton Odissea = The world of Odysseus / M.I. Finley ; metaphrase Sophochle Marchianou
	Pubbl/distr/stampa	Atene : Sideris, 1966
	Descrizione fisica	1 v. ; 20 cm
	Altri autori (Persone)	Markianos, Sophokles
	Disciplina	938
	Soggetti	Civiltà omerica Omero. Odissea
	Lingua di pubblicazione	Greco Moderno
	Formato	Materiale a stampa
	Livello bibliografico	Monografia