1. Record Nr. UNINA9911019536703321

Titolo	Exploring the human plasma proteome / / edited by Gilbert S. Omenn
Pubbl/distr/stampa	Weinheim, : Wiley-VCH, c2006
ISBN	9786610722952 9781280722950 1280722959 9783527609482 3527609482 9783527609420 3527609423
Descrizione fisica	1 online resource (396 p.)
Altri autori (Persone)	OmennGilbert S
Disciplina	572.6
Soggetti	Proteomics Molecular biology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Collection of articles published previously in the journal Proteomics.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Exploring the Human Plasma Proteome; Table of Contents; Preface; List of Contributors; 1 Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database; 1.1 Introduction; 1.2 PPP reference specimens; 1.3 Bioinformatics and technology platforms; 1.3.1 Constructing a PPP database for human plasma and serum proteins; 1.3.2 Analysis of confidence of protein identifications; 1.3.3 Quantitation of protein concentrations 1.4 Comparing the specimens1.4.1 Choice of specimen and collection and handling variables; 1.4.2 Depletion of abundant proteins followed by fractionation of intact proteins; 1.4.3 Comparing technology platforms; 1.4.4 Alternative search algorithms for peptide and protein identification; 1.4.5 Independent analyses of raw spectra or peaklists; 1.4.6 Comparisons with published reports; 1.4.7 Direct MS (SELDI) analyses; 1.4.8 Annotation of the HUPO PPP core dataset(s); 1.4.9 Identification of novel peptides using whole genome ORF search

1.4.10 Identification of microbial proteins in the circulation1.5 Discussion; 1.6 References; 2 Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project; 2.1 Introduction; 2.2 Materials and methods; 2.2.1 Development of the data model; 2.2.1.1 Laboratory; 2.2.1.2 Experimental protocol; 2.2.1.3 Protein identification data set; 2.2.1.4 Peak list; 2.2.1.5 Summary of technologies and resources; 2.2.1.6 MS/MS spectra; 2.2.1.7 SELDI peak list; 2.2.2 Data submission process; 2.2.3 Design of the data repository; 2.2.4 Receipt of the data
2.3 Inference from peptide level to protein level2.4 Summary of contributed data; 2.4.1 Cross-laboratory comparison, confidence of the identifications; 2.5 False-positive identifications; 2.6 Data dissemination; 2.7 Discussion; 2.8 Concluding remarks; 2.9 Computer technologies applied; 2.10 References; 3 HUPO Plasma Proteome Project specimen collection and handling: Towards the standardization of parameters for plasma proteome samples; 3.1 Introduction; 3.2 Materials and methods; 3.2.1 HUPO reference sample collection protocol; 3.2.2 Differential peptide display
3.2.3 Stability studies and SELDI analysis3.2.4 SDS-PAGE analysis for stability studies; 3.2.5 2-DE for stability studies; 3.2.6 SELDI-TOF analysis for protease inhibitor studies; 3.2.7 2-DE for plasma protease inhibition studies; 3.2.8 Tryptic digestion and protein identification for protease inhibition studies; 3.2.9 Antibody microarray analysis using two-color rolling circle amplification; 3.3 Results; 3.3.1 Comparisons of specimen types; 3.3.1.1 Analysis of serum; 3.3.1.2 Analysis of plasma; 3.3.2 Evaluation of storage and handling conditions
3.3.3 Evaluations of the use of protease inhibitors

Sommario/riassunto

On the cutting edge of medical diagnostics, plasma proteomics promises to generate a new wave of technologies to help identify many different diseases and disease risks.Plasma and serum are the preferred non-invasive specimens to test normal individuals, at-risk groups, and patients for protein biomarkers discovered and validated to reflect physiological, pathological, and pharmacological phenotypes. These specimens present enormous challenges due to extreme complexity, huge dynamic range in protein concentrations, non-standardized methods of sample processing, and intra- and inter-individ