1. Record Nr. UNINA9910143294703321

Titolo	Plant proteomics [[electronic resource] /] / edited by Christine Finnie
Pubbl/distr/stampa	Oxford, UK ; ; Ames, Iowa, : Blackwell Pub., 2006
ISBN	1-280-74882-6 9786610748822 0-470-76427-9 0-470-98887-8 1-4051-7307-6
Descrizione fisica	1 online resource (276 p.)
Collana	Annual plant reviews ; ; v. 28
Classificazione	42.42
Altri autori (Persone)	FinnieChristine
Disciplina	572.62 572/.62 580.5
Soggetti	Plant proteins Plant proteomics 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	Plant Proteomics; Contents; Preface; Contributors; 1 Plant proteomics: challenges and resources; 1.1 Introduction; 1.2 Challenges; 1.2.1 Sample extraction; 1.2.1.1 Two-dimensional gel electrophoresis; 1.2.1.2 Direct MS analysis of samples; 1.2.2 Sample preparation and arraying; 1.2.2.1 Two-dimensional gel electrophoresis; 1.2.2.2 One-dimensional gel electrophoresis; 1.2.2.3 Blue-native gel electrophoresis; 1.2.2.4 Direct analysis of samples by MS; 1.2.3 Mass spectrometry (MALDI and ESI); 1.2.3.1 MALDI; 1.2.3.2 ESI; 1.2.4 Analysis depth; 1.2.5 Data analysis; 1.2.5.1 Peptide mass fingerprints 1.2.5.2 Peptide fragmentation data (MS/MS)1.2.5.3 Analysis options; 1.2.6 Quantitation; 1.2.6.1 Gel stains; 1.2.6.2 Chemical labelling of sample; 1.2.7 Modifications; 1.2.8 Data; 1.3 Resources; 1.3.1 Proteomic databases; 1.3.2 Online proteomic tools and resources; 1.4 Future; 2 Proteomic analysis of post-translational modifications by mass spectrometry; 2.1 Summary; 2.2 Introduction; 2.3 Considerations for

the experimental design of PTM analysis by proteomics; 2.4 Analysis of PTMs by proteomic approaches; 2.4.1 Phosphorylation; 2.4.2 Protein glycosylation; 2.4.3 GPI-AP; 2.4.4 Farnesylation
2.4.5 N-terminally modified proteins2.5 Conclusions and perspectives; 3 Strategies for the investigation of protein-protein interactions in plants; 3.1 Summary; 3.2 Introduction; 3.3 Biochemical procedures to characterize protein-protein interactions; 3.3.1 Chromatographic purifications; 3.3.2 Sucrose gradient ultrafiltration; 3.3.3 Native gel electrophoresis; 3.3.4 Immunoprecipitations; 3.4 Genetic procedures to characterize protein-protein interactions; 3.4.1 Yeast two-hybrid system; 3.4.2 Yeast three-hybrid system; 3.4.3 Yeast one-hybrid system
3.4.4 Limitations of yeast two-hybrid systems3.4.5 Split-ubiquitin system; 3.4.6 Bimolecular fluorescence complementation (BiFC); 3.4.7 Forster resonance energy transfer (FRET); 3.4.8 Tagging technologies for the purification of protein complexes; 3.5 Cytological procedures to characterize protein-protein interactions; 3.6 Outlook; 4 Proteomics of disulphide and cysteine oxidoreduction; 4.1 Introduction; 4.2 Control of cellular redox status; 4.2.1 Sequence and structural features of proteins catalysing cysteine redox modifications; 4.2.2 Catalytic mechanisms of Trxs and Grxs
4.3 Proteomics techniques for analysis of cysteine modifications4.3.1 Reagents for cysteine labelling; 4.3.2 Disulphide mapping; 4.3.3 S-glutathionylation; 4.3.4 Cysteine SOH, SO2H and SO3H; 4.3.5 Trxs and disulphide reduction; 4.3.6 S-nitrosylation; 4.4 Conclusions and perspectives; 5 Structural proteomics; 5.1 Introduction; 5.2 Project data handling: Sesame; 5.3 ORF cloning; 5.4 E. coli cell-based protein production pipeline; 5.4.1 Large-scale protein production and labeling; 5.4.2 Protein purification; 5.5 Wheat germ cell-free protein production
5.6 Mass spectrometry of purified proteins for quality assurance and analysis

Sommario/riassunto

The proteome comprises all protein species resulting from gene expression in a cell, organelle, tissue or organism. By definition, proteomics aims to identify and characterise the expression pattern, cellular location, activity, regulation, post-translational modifications, molecular interactions, three dimensional structures and functions of each protein in a biological system.In plant science, the number of proteome studies is rapidly expanding after the completion of the Arabidopsis thaliana genome sequence, and proteome analyses of other important or emerging model systems and crop