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| 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 proteins
2.5 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 systems
3.4.5 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
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4.3.1 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
