Record Nr.	UNINA9910830092103321
Titolo	Redox proteomics [[electronic resource] ] : from protein modifications to cellular dysfunction and diseases / / edited by Isabella Dalle-Donne, Andrea Scaloni, and D. Allan Butterfield
Pubbl/distr/stampa	Hoboken, N.J., : Wiley-Interscience, c2006
ISBN	1-280-45036-3 9786610450367 0-470-32490-2 0-471-97312-2 0-471-97311-4
Descrizione fisica	1 online resource (978 p.)
Collana	Wiley-interscience series in mass spectrometry
Altri autori (Persone)	Dalle-Donnelsabella <1964-> ScaloniAndrea ButterfieldD. Allan
Disciplina	572.6 612.3/98
Soggetti	Proteomics Oxidation-reduction reaction Pathology, Cellular Proteins Genomics
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	REDOX PROTEOMICS; CONTENTS; Preface; Contributors; PART I OXIDATIVELY MODIFIED PROTEINS AND PROTEOMIC TECHNOLOGIES; 1 Chemical Modification of Proteins by Reactive Oxygen Species; 1.1 Introduction; 1.2 Peptide Bond Cleavage; 1.3 b-Scission; 1.4 Oxidation of Amino Acid Residue Side Chains; 1.4.1 Oxidation of Aromatic and Heterocyclic Amino Acid Residues; 1.4.2 Methionine Oxidation; 1.4.3 Protein Carbonylation; 1.4.4 Protein-Protein Cross-Linkage; 1.4.5 Protein Modification by Reactive Nitrogen Species; 1.4.6 Chlorination Reactions; 1.4.7 Accumulation of Oxidized Proteins 2 The Chemistry of Protein Modifications Elicited by Nitric Oxide and

1.

	Related Nitrogen Oxides2.1 Introduction; 2.2 Chemical Biology of NO; 2.2.1 Direct Effects; 2.2.2 Indirect Mechanisms; 2.3 Chemistry of Metabolite Formation; 2.3.1 Nitrite and Nitrate Formation; 2.3.2 Metal Nitrosyl Formation; 2.3.3 Nitrosation; 2.3.4 Nitration; 3 Mass Spectrometry Approaches for the Molecular Characterization of Oxidatively/Nitrosatively Modified Proteins; 3.1 Introduction; 3.2 Mass Spectrometry Analysis of Oxidatively/Nitrosatively Modified Proteins 3.2.1 Analysis of Oxidized/Nitrosated Products of Protein Thiols3.2.2 Analysis of Oxidized/Nitrosated Products of Protein Thiols3.2.2 Analysis of Oxidized/Nitrosated Products of Protein Carbonylation Products; 3.2.5 Analysis of Oxidatively/Nitr(s) atively Products of Tryptophan and Histidine; 3.3 Proteomic Strategies for the Identification of ROS/RNS Protein Targets in Biological Matrices; 3.4 Conclusions; 4 Thiol-Disulfide Oxidoreduction of Protein Cysteines: Old Methods Revisited for Proteomics; 4.1 Introduction: Protein Thiols from Oxidative Stress to Redox Regulation 4.2 Different Redox States of Protein Cysteines4.2.1 Disulfides; 4.2.2 Mixed Disulfides; 4.2.3 Higher Oxidation States; 4.3 Methodologies to Identify and Quantify the Redox State of Protein Cysteines; 4.3.1 Methods Based on Reagents That Label Free Cysteine; 4.3.2 Methods Based on Different Electrophoretic Mobility: Diagonal Electrophoresis; 4.4 Methods to Detect Specific Modifications; 4.4.1 Methods Based on a Series of Alkylation, Reduction, and Labeling Steps; 4.4.2 Methods Based on Incorporation of Labeled Glutathione to Identify Glutathionylated Proteins; 4.4.3 Immunological Methods 4.5 Methods for Enriching Redox-Regulated Proteins4.5.1 Enrichment of Proteins with Specific Forms of Cysteine Oxidation; 4.5.2 Membrane Proteins; 4.6 Structural and Physicochemical Determinants for the Susceptibility of Cysteines toward Oxidation; 4.7 Perspective; 5 Carbonylated Proteins and Their Implication in Physiology and Pathology; 5.1 Introduction; 5.2 Types of Oxidative Modifications and C
Sommario/riassunto	Methodology and applications of redox proteomicsThe relatively new and rapidly changing field of redox proteomics has the potential to revolutionize how we diagnose disease, assess risks, determine prognoses, and target therapeutic strategies for people with inflammatory and aging-associated diseases. This collection brings together, in one comprehensive volume, a broad array of information and insights into normal and altered physiology, molecular mechanisms of disease states, and new applications of the rapidly evolving techniques of proteomics.Written by some of the