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## Preface

Proteomics is a rapidly expanding investigation platform in cardiovascular medicine. Driven by major improvements in Mass Spectrometry (MS) instrumentation and data analysis, the proteomics field has flourished in recent years particularly in the study of complex diseases. These recent advances are characterized by the development of quantitative MS-based methods that moved the field on from primarily identifying proteins to also providing measurements of relative changes in protein levels between different cell states, typically normal controls versus diseased samples. The application of proteomic techniques to the vascular pathology is a true reflection of this progress. Vascular proteomics of atherosclerotic lesions has become a major experimental group of tools in the last years notably by revealing novel proteins and signaling pathways to the processes involved in atherogenesis and its complications. This book encompasses a selection of techniques and methods that target the key processes implicated in atheroma plaque composition, formation, and development and the various components and plasma proteins involved in the atherosclerotic process. In this volume dedicated to Vascular Proteomics, we provide protocols and up-to-date methods for the analysis of arteries, cells, lipoproteins, body fluids (plasma, urine), and metabolites, with a particular focus on MS-based methods of protein and peptide quantification. The development of LC-MS/MS approaches has been a significant advance in many areas of biomedical research, and vascular proteomics is no exception. After an introductory chapter, we have followed a hierarchical order in the different chapters starting with methods dedicated to tissues (Laser microdissection for the analysis of human arteries; Use of SIMS-TOF in vascular Biology), cells (Vascular smooth cells treated with atenolol; Phosphoproteomic analysis of aortic endothelial cells; Characterization of membrane and cytosolic proteins of erythrocytes), lipoproteins (Quantitative analysis of apolipoproteins in HDL by top-down differential mass spectrometry; Quantitative proteomic analysis of high-density lipoproteins by stable 18-O-isotope labeling), plasma and plasma proteins, and metabolites (Biomarkers of abdominal aortic aneurysm by iTRAQ analysis of depleted plasma; Absolute Quantitation of proteins in human blood by multiplexed multiple reaction monitoring mass spectrometry; MRM of plasma proteins in cardiovascular proteomics; Metabolites secreted by human atherothrombotic aneurysm). We have also included several chapters on very specific samples such as the analysis of thrombus (Identification of novel biomarkers of abdominal aortic aneurysm from thrombus conditioned media), the secretome of arteries (Characterization of human arterial tissue secretome by 2-DE and nLC-MS/MS), and the study of exosomes (Proteomic analysis of urinary exosomes in cardiovascular and associated kidney diseases by 2-DE and LC-MS/MS). This type of sampling has great potential for the possible identification of new biomarkers, and their analysis is therefore of great interest.

This book does not attempt to describe exhaustively all the techniques used in the field of vascular proteomics, rather is a representative selection of methods that can be a useful resource for experienced proteomics practitioners and specially for newcomers, in order to

become acquainted with the practice of a selective group of proteomic techniques for cardiovascular research. The editors are especially grateful to all contributing authors for the time and effort they have put into writing their chapters, and particularly to the Methods in Molecular Biology series editor, John Walker, for his continuous advice and support through the editorial process.

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