
Preface

The use of proteomics for the study of complex diseases is increasing and is particularly applicable to cardiovascular diseases, the leading cause of death in developed countries. Proteomics is a rapidly expanding investigation platform in cardiovascular medicine and is becoming integrated and incorporated into cardiovascular research. Driven by major improvements in mass spectrometry instrumentation, methodology, and data analysis, the proteomics field has exponentially grown in recent years. These advancements serve not only to identify proteins with high sensitivity but increasingly to use proteomic technologies to assay the dynamic properties of proteins in high throughput and to characterize the structure and composition of large multiprotein complexes. These new approaches and techniques 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 heart pathology is a true reflection of this progress. Overall, the recent development of MS-based methods and advanced analytical tools are transforming our ability to profile proteins in the cardiovascular system. This book encompasses a selection of techniques and methods that target the numerous processes implicated in the pathophysiology of heart. Thus, we provide protocols and updated methods in the heart proteomic area with a particular focus on MS-based methods of protein and peptide quantification and the analysis of posttranslational modifications. The development of LC-MS/MS approaches has been a significant advancement in many areas of biomedical research, and heart proteomics is not an exception. Several chapters describe system biology approaches, which provide a better understanding of normal and pathological processes. We have followed a hierarchical order in the different chapters starting with methods dedicated to cardiac tissue (Large-scale characterization of the murine cardiac proteome; Determining protein concentration of the human ventricular proteome; Multidimensional protein identification technology for direct-tissue proteomic of heart; Global protein quantification of mouse heart tissue based on the SILAC mouse; Global proteomic profiling and enrichment maps of dilated cardiomyopathy; Characterization of the human myocardial proteome in dilated cardiomyopathy by label-free quantitative shotgun proteomics of heart biopsies), aortic valves (Differential protein expression analysis of degenerative aortic stenosis by iTRAQ labeling; Proteomic analysis of interstitial aortic valve cells acquiring a pro-calcific profile), organelle subproteomes (Proteomic analysis of brain mitochondrial proteome and mitochondrial complexes; Oxidative modifications of mitochondria complex II), posttranslational modifications (Detection of O-GlcNAc modifications on cardiac myofilament proteins; Quantification of mitochondrial S-Nitrosylation by CysTMT6 switch assay), analysis of secretomes (Optimized method for identification of the proteomes secreted by cardiac cells; Secretome of human aortic valves), and quantitation of specific proteins (Using pure protein to build a multiple reaction monitoring mass spectrometry assay for targeted detection and quantitation; Identification of Thioredoxin target protein networks in cardiac tissues of a transgenic mouse).

This book does not attempt to describe exhaustively all the techniques used in the field of heart 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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