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Sommario/riassunto

This book comprehensively reviews the fundamentals of biomarker discovery using mass-spectrometry-based proteomic and glycoproteomic methods. It also provides case studies of proteomic and glycoproteomic molecular signatures to illustrate the design and use of various mass spectrometry modes such as selected reaction monitoring (SRM), parallel reaction monitoring (PRM), and sequential window acquisition of all theoretical fragment ion spectra mass spectrometry (SWATH-MS). In turn, the book presents the challenges of the proteomic methods in biomarker discovery and approaches for overcoming these challenges by extending the performance by improving the sensitivity, throughput, and selectivity of the method. It also addresses the bottleneck of deriving useful biological interpretations from large multi-dimensional datasets emanating from these experiments by discussing data analysis pipelines and appropriate statistical analysis. Finally, a detailed discussion on the design, characterization, and application of protein/glycoprotein-based biosensors for clinical diagnostics is discussed. The book is intended to serve as a reliable resource for the students and researchers working in the area of biomarker discovery and validation using mass spectrometry-based methods and their subsequent applications for biosensor design.