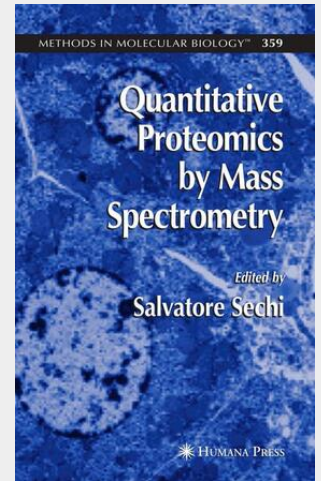


Quantitative Proteomics by Mass Spectrometry

Quantitative Proteomics by Mass Spectrometry, from the Methods in Molecular Biology™ series, is a compendium of cutting-edge protocols for quantitative proteomics, and presents the most significant methods used in the field today. The focus on mass spectrometry (MS) is integral, as MS has, and will continue to be, an essential tool in proteomics for studying complex biological systems and human diseases. This volume, written and compiled by leading quantitative proteomic experts, is an indispensable resource in the search for novel biomarkers. Quantitative Proteomics by Mass Spectrometry presents several innovative MS quantitative procedures, including a variety of methods for introducing isotopic labels and quantifying post-translational modifications. Some of these methods include growing an organism in isotope-enriched media, performing trypsin proteolysis in the presence of 18O-water, reacting protein samples with isotopically labeled reagents, quantifying relative amount of proteins without the use of any isotopic labels. Attention is also given to state-of-the-art techniques for the characterization of the phosphoproteome and tandem MS for detection of inborn errors of metabolism. Specifically, the procedure for determinations of enzymatic activity could be used for large-scale screening of newborns. The protocols in this volume expand both the breadth and depth of readily available methods for quantitative proteomic researchers using MS.

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