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This volume 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. Attention is given to state-of-the-art techniques for the characterization of the phosphoproteome and tandem MS for detection of inborn errors of metabolism. This volume is an indispensable resource in the search for novel biomarkers.

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