

# Strategies for Quantitative Proteomics and their Use in Biomedical Research

## **Abstract**

The vast majority of proteomic studies to date have relied on mass spectrometric techniques to identify, and in some cases quantify, peptides that have been generated by the enzymatic digestion of protein components of a proteome. A number of strategies have emerged over the past decade that differ in the type of instrument used, their performance profiles, the manner in which they interface with biological research strategies, and their reliance on and use of prior information.

Three main mass spectrometry based proteomic approaches used today will be discussed: shotgun or discovery proteomics, directed, and targeted proteomics, respectively. The principles of each technique, their respective strengths and weaknesses and the dependence of their performance profiles on the composition of the biological sample. The discussion is intended to provide biologists and proteomics scientists a rational basis for the selection of optimized strategies to address research questions specific to clinical applications.