Developing Comparative Proteomics for the Early Detection of Cancer Biomarkers

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Mass spectrometry based proteomics has found many applications in the discovery and validation of disease biomarkers. One particular application involves the identification of disease markers directly from serum/plasma. We have performed direct comparison of various protocols for reducing the complexity of the serum proteome by: a) reducing the number of peptides per protein (i.e. glyco-, phospho-, or cysteine-peptide capture), b) depleting abundant proteins (i.e. albumin, IGG depletion, size fractionation), and/or c) protein level fractionation schemes (i.e. C3, C8, WCX beads) prior to analyzing tryptic digests of serum proteome by nano-LC-MS. The comparisons were made based on the number of features detected, the depth of proteome coverage, as well as the reproducibility of each protocol. Additionally, we have further developed the SISCAPA protocol and implemented as a biomarker validation method.