Advanced enabling technologies for cancer proteomics

Brief Synopsis:

Mass spectrometry-based proteomics is a promising technology in characterization of human proteome at a genome scale, facilitating proteogenomic characterization of cancer specimens. Recent advances in mass spectrometry instrumentation, sample handling platforms, and proteomic analysis strategies allow for not only large-scale, comprehensive proteome profiling, but also focused systems biology studies, biomarker verification, as well as analysis of protein expression and phosphorylation in very small populations of cells. This will lead to significantly improved understanding of aberrant regulatory and signal transduction networks underlying cancer for translational applications.