Abstract:
The ultimate goal of MS-based clinical onco-proteomics is in-depth molecular profiling of human cancers and translation of these findings into biomarkers and assays that physicians can use on their patients. So far, the translation of proteomic findings into clinical tests has been disappointing. Innovative experimental designs coupled with high-resolution and high-accuracy shotgun proteomics for systematic profiling of human cancers may facilitate translation of proteomic findings to clinical tests. This presentation will look at results obtained from a pilot study that describes a method for cancer biomarker development via targeted shotgun proteomics. Using renal cell carcinoma (RCC) as a model disease, present strategy utilizes tissue-directed differential and subtractive shotgun proteomics to identify tumor proteins in peripheral blood of a patient diagnosed with non-metastatic RCC. The findings, cross validated using orthogonal immuno-assay indicate that tumor proteins can be detected by MS in the peripheral blood of a patient diagnosed with non-metastatic cancer.

Selected publications:
• Proteomic Profiling of H-Ras-G12V Induced Hypertrophic Cardiomyopathy in Transgenic Mice Using Comparative LC-MS Analysis of Thin Fresh-frozen Tissue Sections. J Proteome Res. 2012 Jan 4