

Agilent Lunchtime Seminar

Monday, March 8, 12:15 – 1:30 pm

Mattie Silks (Lower Level 1), Marriott City Center Hotel

[RSVP today to reserve your place.](#)

Quantitative Proteomic Profiling

Presenters:

Leigh Anderson (Plasma Proteome Institute) and Vadiraja Bhat (Agilent Technologies)

Part 1

In order to bridge the gap between biomarker discovery and clinical use, a new approach to verification is proposed: multiplexed panels of specific candidate assays based on hybrid immuno-mass spectrometric (SISCAPA) detection. By combining high sensitivity, high throughput, and precision with use of small plasma samples, a platform for systematic verification of hundreds of candidates in thousands of samples can be implemented. Such systematic studies will finally allow us to test the “strong biomarker hypothesis” that molecular biomarkers exist for all major disease states. An extension of this approach, the hPDQ project providing a library of specific tests for all 21,300 human proteins could provide the larger biomedical research community with direct quantitative access to the entire human proteome.

Part 2

Multiple, complex molecular events characterize cancer development and progression. Deciphering the molecular networks that distinguish organ-confined disease from metastatic disease may lead to the identification of biomarkers of cancer invasion and disease aggressiveness. Although alterations in gene expression have been extensively quantified during neoplastic progression, complementary analyses of proteomic changes have been limited. Here we interrogate the proteomic alterations in a cohort of 15 prostate-derived tissues that included five each from adjacent benign prostate (Benign), clinically localized prostate cancer (PCA) and metastatic disease from distant sites (Mets). The experimental strategy couples isobaric tags for relative and absolute quantitation (iTRAQ) with multi-dimensional liquid-phase peptide fractionation followed by tandem mass spectrometry. Over 1000 proteins were quantified across the specimens, and delineated into clinically localized and metastatic prostate cancer-specific signatures.