



CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP120507

Project Title:
Massively Parallel Protein Identification for Cancer Biomarker Discovery

Award Mechanism:
High Impact/High Risk

Principal Investigator:
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Entity:
The University of Texas at Austin

Lay Summary:

The development of "NextGen" DNA sequencing methods for quickly acquiring genome and gene expression information has transformed biology. Unfortunately, a similar high-throughput method for the large-scale identification and quantification of specific proteins in complex mixtures remains unavailable, representing a critical bottleneck in many biochemical, molecular diagnostic and biomarker discovery assays. While nucleic acid mutations underlie nearly all cancers, these changes are most readily embodied by proteins and often expressed in bodily compartments (i.e. saliva, blood, urine) accessible without invasive procedures such as biopsies. Thus, an approach capable of sensitive identification and quantitative profiling of protein abundances in these compartments would significantly impact the search for and application of protein biomarkers in the diagnosis, characterization, and monitoring of most, if not all, cancers. Indeed, the value of diagnostic biomarkers is clear, as seen in the utility of e.g. thyroglobulin for monitoring thyroid cancer, and in only administering HERCEPTIN for breast cancers overexpressing HER2/neu. A variety of techniques have been applied to this problem, including mass spectrometry and antibody arrays, but in general, they lack the sensitivity and intrinsic digital quantification to be fully effective. In fact, what is specifically needed is a massively parallel method, akin to NextGen DNA sequencing, for identifying and quantifying individual peptides or proteins within a given sample. We propose such a novel high-throughput method for protein identification. This technology will be directly applicable to cancer diagnosis, characterization, and protein cancer biomarker discovery.