



CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP120613

Project Title:
Develop cutting-edge proteomics core facility based on high resolution, high accuracy mass spectrometry and high throughput, web-based bioinformatics technology

Award Mechanism:
Core Facility Support Awards

Principal Investigator:
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Entity:
The University of Texas Southwestern Medical Center

Lay Summary:

Cancer cells function differently from normal cells in order to accommodate their abnormal needs for rapid growth, reproduction, spreading etc. Proteins are in many ways responsible for allowing cancer cells to assume their destructive biology. Cells like large cities have complicated communication systems. In cancer cells, these communication systems are altered. Alteration of these communication systems can be accomplished by altering protein concentrations or modification patterns. Detecting these differences allows scientists to find the altered communication routes which could then be used to: 1) devise new strategies to battle cancer; or 2) provide new ways to detect cancer at its early stages when it can be more readily treated. Scientists active in almost all areas of cancer research will benefit from the technology that allows such changes to be detected. Proteomics, defined as the science of protein interrogation, is aimed at identification and quantification of proteins and their modifications. Modern proteomics predominantly relies on mass spectrometry, an analytical technique with superb accuracy in measuring the mass of molecules. We will build a facility that will house state of the art mass spectrometers for comprehensive and high throughput protein analysis. We will also develop the computational infrastructure necessary to store, process and interpret mass spectral data for cancer researchers. Finally we will establish standard operating protocols and provide assistance to those scientists who are interested in using proteomics. Having proteomics capabilities as described above will allow cancer researchers to establish detailed maps of various cancer cell proteomes (a collection of all the proteins within a cancer cell). Such maps can then be used to find the strategic spots within the cell's communication networks or to identify logistical routes that could be targeted to develop new therapies or diagnostic tools.