CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP130432

Project Title:
Protein Array and Analysis Core (PAAC)

Award Mechanism:
Core Facility Support Awards

Principal Investigator:
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Entity:
The University of Texas M.D. Anderson Cancer Center

Lay Summary:

A protein is a chain of amino acids. During protein synthesis, 20 different amino acids can be incorporated into a protein, which then folds to form a structure that will dictate its function in cells. Once synthesized, a protein can undergo further chemical modification to alter its cellular function through a process called posttranslational modification (PTM). PTMs can either alter the structure of a protein or generate a docking site for a binding protein. We are particularly interested in identifying and characterizing protein interactions that are driven by PTMs. Processes that regulate PTMs in normal cells become deregulated in cancer cells through altered functions of the enzymes that deposit these PTMs. The enzymes that are primarily deregulated in cancer are oncogenic kinases. To understand how the deregulation of these enzymes causes cancer, we need to know the network of protein-protein interactions that are altered by these uncontrolled enzymes. We have developed a chip-size array of proteins that can be used to identify the “readers” of specific PTMs. We are the only research group to have such a large collection of protein domains. Thus, many researchers, who have identified PTMs that are often unique signatures of a certain cancer, send us their modified proteins in the hopes that we can identify relevant binding partners. We are now expanding this facility to not only include state-of-the-art protein domain microarrays, but also to allow the further characterization of these protein-protein interactions in cells. In addition, we will provide the instrumentation and know-how to determine the strength of these protein-protein interactions. This basic knowledge is important because these deregulated protein networks can be targeted with drugs that inhibit the enzyme that deposits the PTM, or that inhibit protein-protein interactions directly. These findings will lay the groundwork, and identify the targets, for future cancer drug discovery projects.