

## Probing protein kinase signaling using proteomic approaches

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Protein phosphorylation is an important post-translational modification whereby proteins are covalently modified by attachment of a phosphate residue on serine, threonine and tyrosine resideus on peptides. Protein phosphorylation is a reversible phenomenon and catalyzed by protein kinases and protein phosphatases. Proteins modified by phosphorylation have changed confomation, activity, subcellular localization and can also be targeted for degradation. With the advent of mass spectrometry evolved the field of proteomics where by one can study the complete set of proteins in a cell (proteome). Mass spectrometry is a very useful tool in modern biology to study protein sequence and post-translational modification in a highthroughput manner. Protein kinases and phosphatases set up cascades of activation/inactivation events in cells where by signals arriving on the cell in the form of physiological stimuli are transduced to the nucleus until the desired cellular response is obtained. My main focus is on understaning the phenomenon of phosphorylation, identifying phosphorylated proteins, understnad the function of kinases in greater detail. Specifically I have worked on protein tyrosine kinase, c-Src which is key molecule in transducing growth factor derived signals and recently also on protein serine/threonine kinases (atypical PKCs zeta and iota) which have a close sequence homology but have opposing biological functions and are less understood. Identifying protein kinase substrates, phosphorylation sites, and interating proteins can often reveal a great deal about the function of the proteins and specific signal transduction pathways. Using proteomic approaches I have undertaken several projects where I identified the several substrates of c-Src and their sites of phosphorylation. For the last few years I have also taken up projects where my focus was to study the less understood atypical protein kinases and their interacting proteins..