

Proteomics as a toolbox for biomarker discovery

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Abstract: Proteomics tools have evolved a lot in recent past. In this talk, I will be discussing standard methods used for analysis of single protein to complex sets of proteins present in cell or tissue or different biofluids. Comparative proteomics by label-free and labeling methods provide unique opportunity to carry our high throughput proteome studies from biofluids collected from disease and healthy controls to identify important deregulated molecules as markers. I will also share some of our laboratory findings with respect to tuberculosis biomarker discovery using quantitative proteomics study at ICGEB New Delhi.