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## Mass spectrometry technology for biomarker discovery

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Human tissues and organs have affected depending on pathological condition of diseases. Proteins are basic functioning molecules of cells accordingly to modification intensities. Protein modification can be differences in cellular interaction, localization, activity, protein concentration, and co-/posttranslational. Protein biomarker discovery has covered some subtitles or points such as differentially expressed proteins for disease specific protein isomers and abnormal protein activity. Proteomic analysis and conclusions have allowed the potential protein biomarker discovery and thus diagnosis of disease and prognosis can be possible. MS-based proteomic has correlated between protein modification and a certain disease platform to accurately and confidently measure the proteins in sera or plasma which are low-abundance concentration. MS-based quantitative platform use for tissue samples or several body fluids of protein biomarker discovery. Similar to whole tissue samples human fluids such as gastric fluid, urine, blood have also been evaluated in the last decade studies. Intensity of modifications of proteins as post translational can also be indicative of a disease or its progression. Activity-based protein platform changes have allowed for proteome researches of enzymatic and protein-drug interaction events.

### Biography

Sermin Tetik completed her PhD in 2003 years at University of Marmara (Istanbul-Turkey). She have been working an academican at the same University, Faculty of Pharmacy in Istanbul-Turkey as associated professor since five years and project director of her research team focusing on thrombosis -hemostasis area. She has published more than 30 papers and above 50 international abstract in reputed journals and conferences, serving as an editorial board member of repute.

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