

# International Summit on **Current Trends in Mass Spectrometry** July 13-15, 2015 New Orleans, USA

## Overview of mass spectrometry

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Mass Spectrometry (MS) has become the method of fields and applications, including proteomics and proteomic analysis. MS is now routinely used to identify and quantify known and unknown proteins in our labs as a fundamental tool. Its accuracy, flexibility and sensitivity have allowed new approaches in the biological area, characterization of biopharmaceutics and diagnostic criteria. The utility of MS for simple and complex protein and peptide mixtures analyses gave us the ability to develop such accurate results within the last two decades. The development of high-throughput and quantitative MS proteomics workflows has supported to scope of what we know about protein structure, function, modification and global protein dynamics. This overview outlines the role of mass spectrometry in the field of proteomics, MS methodology and instrumentation.

## Biography

Sermin Tetik has completed her PhD at the 2003 years from University of Marmara (Istanbul-Turkey). She is an academician at the same University in Istanbul-Turkey as an Associated Professor and Project Director of a research team focusing on thrombosis -hemostasis area and she completed before 6 months in Cyprus as a Founder (vice-Dean) of a new Pharmacy Faculty at University of International Cyprus. She has published more than 20 papers and 50 international abstracts in reputed journals and conferences and is serving as an Editorial Board Member of repute.

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