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Sample preparation for 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. MS has allowed it possible to analyze with various types of mass analyzers including ESI, MALDI, FT-MS, ion trap, time-of-flight, quadrupole, etc. Mass analysis of protein and proteomic(s) products have ranged in mass between 50-300.000 daltons, in attomole through nanomole quantities. Sample preparation technique for MS-analysis is an important step in the proteomics workflow. In the protein analysis, sample preparation is the most variable and time consuming step. In proteomics laboratory sample preparation, instrumentation and software are all critical to success and high quality results. There are different sample preparation techniques because we have no standard method for preparing including type, complexity, source etc. Proper sample preparation means better results.

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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