Application of Mass Spectrometry in Proteomic Studies

Talat Yalçın
Izmir Institute of Technology, Faculty of Science, Department of Chemistry, Gulbahce
Urla-Izmir 35430

Mass spectrometry has been widely used to analyze proteins, especially, with the development of techniques such as matrix-assisted laser desorption ionization (MALDI) and electrospray ionization (ESI). Nonvolatile and large analytes, such as proteins and peptides can be easily ionized into the gas phase with these two new techniques without significant fragmentation.

The term ‘proteome’ or ‘proteomics’ has been introduced to the literature in 1995. Proteomics is the identification and sequencing of proteins isolated from cells, tissue, and body fluids. Comparison of global protein expression from stressed conditions against appropriate control samples allows for the detection of specific changes in the proteome. A proteome, therefore, provides a kind of snapshot view of a cell at a given point in time. Proteins are usually cleaved into small peptides by using enzymes digestion and analyzed by mass spectrometry to obtain peptides mass finger prints and then proteins can be identified by searching database.

In this talk, the role of mass spectrometry in proteomic studies and applications will be discussed.

References