Mass spectrometry is an analytical technique in which chemical compounds are ionized into charged molecules and ratio of their mass to charge (m/z) is measured. Though MS was discovered in the early 1900s, its scope was limited to the chemical sciences. However, the development of electron spray ionization (ESI) and matrix assisted laser desorption ionization (MALDI) in 1980s increased the applicability of MS to large biological molecules like proteins. In both ESI and MALDI, peptides are converted into ions by either addition or loss of one or more than one protons. Both are based on “soft ionization” methods where ion formation does not lead to a significant loss of sample integrity. MALDI-TOF MS has certain advantages over ESI-MS viz. (i) MALDI-TOF MS produces singly charged ions, thus interpretation of data is easy comparative to ESI-MS, (ii) for analysis by ESI-MS, prior separation by chromatography is required which is not needed for MALDI-TOF MS analysis (Everley et al., 2008). Consequently, the high throughput and speed associated with complete automation has made MALDI-TOF mass spectrometer an obvious choice for proteomics work on large-scale (Ekström et al., 2000) [1].

1)

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4525378/