

Tandem mass spectrometry (MS/MS)

Tandem mass spectrometry (MS/MS) is used to generate compound specific structural information. The sample ions of interest are selected to enter the collision cell, in which are bombarded by the gas molecules and form fragment ions. The fragmentation pattern is usually specific to the particular molecule and can be used to identify the compound.

Peptides fragment in a reasonably well-documented manner, along the peptide backbone. The most common cleavage sites are at the CO-NH bonds which give rise to the "b" and/or the "y" ions. The mass difference between two adjacent "b" ions, or "y" ions, is corresponded to the mass of a particular amino acid.

An MS/MS ion spectrum can be searched against known protein database to identify the sequence of the peptide. Usually two or more identified unique peptides with good confidence score can prove the existence of the protein.

