

## **Peptide Sequencing by MS/MS (Code F):**

### **1. General Procedure**

Peptide sequencing by MS/MS is performed by tandem mass spectrometers. It requires two stages of mass analysis. A specific peptide molecular ion (precursor ion) is mass-selected by the first stage of mass analysis and is activated by collision with a neutral gas molecule in a collision cell to induce a fragmentation reaction. The ionic products of the fragmentation reaction are mass-analyzed in the second stage of mass analysis to produce a product ion spectrum (MS/MS spectrum). The fragment ions of a peptide can provide its amino acid sequence information.

### **2. How to Read the Spectrum?**

Two major series of fragment ions usually are formed in the fragmentation reaction of protonated peptides. The charge retained at N-terminus gives b-series ions; the charge retained at C-terminus gives y-series ions. The peptide sequence can be deduced from the masses of b and y series ions.

[An example of peptide MS/MS spectrum](#)