E2-11 Peptide sequence information by partial acid hydrolysis: an analysis by matrix-assisted laser desorption ionization mass spectrometry

R V Coorey[1,2], P Hakansson[1], R A Zubarev[1], T R Ariyaratne[2]
([1]*Division of Ion Physics, Dept. of Radiation Sciences, Uppsala Univ. Sweden, Present address:* [2]*Dept. of Physics, Univ. of Colombo, Colombo 3*)

A method is described to deduce sequence information of a peptide using partial acid hydrolysis and subsequent analysis by Matrix-Assisted Laser Desorption Ionization Mass Spectrometry (MALDI-MS). The mass analysis of peptides which had been subjected to a partial acid hydrolysis revealed that the cleavage of the peptide bonds often occurs not randomly, but rather follows a ladder-like structure. In this structure, individual peptides miss one to several amino acids

exclusively from C-terminus or exclusively from N-terminus. A very rapid cleavage occurs at N-sides of Ser and Thr residues; as well as between 2 adjacent Gly residues. These characteristic features of partial acid hydrolysis are used for peptide sequencing. The sequencing is performed by identifying the amino acid residues based on the difference in the molecular weight between the major hydrolysis products, beginning from the molecular weight of the original (intact) peptide. This methodology could be used to confirm the identity of peptides during a peptide mapping.

Financial assistance by International Science Programs, Uppsala University, Sweden (Research grant SRI 01/2) is acknowledged.