

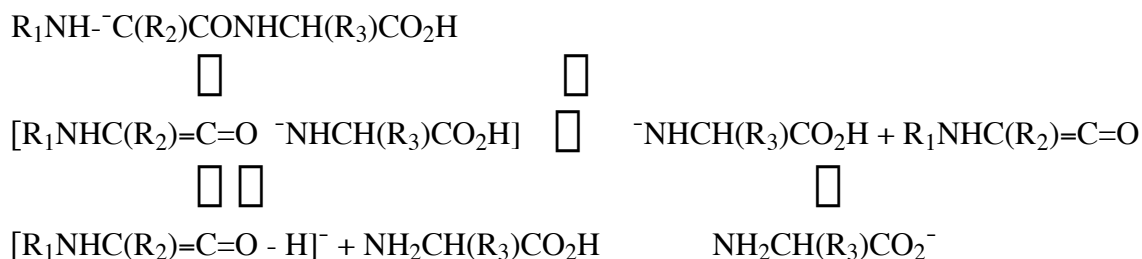
Fragmentation of Peptides Using Negative Ion Electrospray Mass Spectrometry

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The sequencing of peptides and proteins using mass spectrometry has revolutionised fields like that of proteomics. Large biomolecules can now be identified quickly and efficiently using the backbone fragmentations of such molecules. To date, such sequencing information has been derived predominantly from spectra run in the positive ion mode. Negative ion mass spectrometry of biological molecules has tended to be limited to merely the identifying of molecular ions.

This talk will discuss the fragmentation of $(M-H)^-$ ions of underivatised peptides. Two backbone fragmentation patterns, provide analogous information to that of the B and Y+2 fragmentation of positive ion mode. These fragmentations have been called \square (Scheme 1) which provides information analogous to Y+2 fragmentation and \square (Scheme 1) which provides information analogous to B fragmentation. Other backbone fragmentations will be discussed that are specific to and identify certain residues, including Asp, Asn, Glu and Gln.



Scheme 1