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Study on Structure of Biological Macromolecules by Mass Spectrometry

Satoko Akashi

(Int. Grad. Sch. Arts & Sci., Yokohama City University)

Mass Spectrometry is now an essential tool for rapid identification of proteins with a small amount of samples. The present paper demonstrates author's research that has contributed to construct a basis of the current methodology for characterization not only of the primary structure but also of the tertiary structure of proteins.

In late 1980's, we suggested the strategy of "top-down" analysis of primary structure of proteins; i.e. molecular mass of the protein is determined accurately at the first stage, then the protein is digested into fragment peptides whose molecular masses and sequences are successively elucidated by mass spectrometry. With this strategy, amino acid sequences, including post-translational modifications, have been characterized for various proteins, such as bovine serum albumin and IgG.

This "top-down" strategy has also been employed for characterization of the interface regions of protein-protein complexes and the tertiary structure of proteins. It has been demonstrated that interaction sites can be identified by this strategy in combination with H/D-exchange or chemical modification of amino acid on the protein surface, and that this method can give information also on the tertiary structure of proteins.

Application of new ionization methods to biological samples has also been carried out. We have shown that a new ionization technique, laser spray, which was developed by Prof. Hiraoka (Yamanashi Univ.) is effective for characterization of biological complexes.

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