

13th BCEIA Abstract SAMPLE

MASS SPECTROMETRY IN THE STRUCTURAL STUDY OF PROTEIN VARIANTS (14P) B.

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Many genetic diseases are caused by structurally aberrant proteins having single mutations in their amino acid sequences. To delineate the pathological mechanism with which these diseases develop, it is essential to elucidate the precise structure of the aberrant proteins. As described below, not a few advances in the mass spectrometric technologies for this purpose were remarkable among the protein and genetic technologies that have been developed in the last decade.

First, electrospray ionization mass spectrometry (MS) allows us to measure the molecular weight of the proteins with twenty or thirty kilo-daltons very.

conventional chemical methods for protein sequencing.

It is noteworthy that any of these analyses are rapid and the results are unambiguous compared with chemical methods for the same purposes.

REFERENCES

1. Y. Wada, T. matsuo and T. Sakurai. Mass Spectrom. Reviews. 8: 379-434(1989)
2. Y. Wada. Biol. Mass Spectrom., 21: 617-624 (1992)
3. Y. Wada, T. Matsuo, I. A. Papayannopoulos, C. E. Costello and K. Biemann. Int. J. Mass. Spectrom. Ion Processes, 122: 219-229 (1992)

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2. All lines should begin at the left-hand margin, leaving no space blank. Before subtitles, there should be an extra half line spacing. Numbers and captions of figures should be typed close to the bottom of the corresponding illustrations. Numbers and captions of tables should be typed close to the top of the table.
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